Saidha, Tekchand

From: Saidha, Tekchand

**Sent:** Monday, June 23, 2003 2:47 PM

To: STIC-Biotech/ChemLib

Subject: sequence search request - 09/830751

### 09/830751

Please search the data base and interference files for :

SEQ ID Nos. 2, 4, 6 and 8

Thank you!

Jekchand Saidha Primary Examiner Art Unit 1652, CM1, Room No. 10D05 Mail Box 10D01 (703) 305-6595



# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number

TO: Tekchand Saidha

Location: CM1/10D05/10D01

Art Unit: 1652

**Tuesday, June 24, 2003** 

Case Serial Number: 830751

From: Edward Hart

**Location: Biotech-Chem Library** 

CM1-6B02

Phone: 305-9203

edward.hart@uspto.gov

### **Search Notes**

Examiner Saidha,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

**Edward Hart** 



#### STIC-Biotech/ChemLib

97247

From: Sent:

Saidha, Tekchand

To:

Monday, June 23, 2003 2:47 PM STIC-Biotech/ChemLib

Subject:

sequence search request - 09/830751

#### 09/830751

Please search the data base and interference files for :

SEQ ID Nos. 2, 4, 6 and 8

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CRIFE

Jekchand Saidha Primary Examiner Art Unit 1652, CM1, Room No. 10D05 Mail Box 10D01 (703) 305-6595

6/34/43 6/34/43 4-AA

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### STIC SEARCH RESULTS

### Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

oluntary Results Feedback Form	
> I am an examiner in Workgroup: Example: 1610	
> Relevant prior art found, search results used as follows:	
☐ 102 rejection	
☐ 103 rejection	
Cited as being of interest.	
Helped examiner better understand the invention.	
Helped examiner better understand the state of the art in their technology.	
Types of relevant prior art found:	
☐ Foreign Patent(s)	
<ul> <li>Non-Patent Literature         <ul> <li>(journal articles, conference proceedings, new product announcements etc.)</li> </ul> </li> </ul>	
Relevant prior art <b>not found:</b>	
Results verified the lack of relevant prior art (helped determine patentability).	
Results were not useful in determining patentability or understanding the invention.	
Comments:	

Droploff.or send completed forms to STIC/Biotech-Chem Library CM1/Circ Desk



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 20000000
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### SUMMARI

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Arabidopsis thalia		Arabidopsis thalia	L-sorbosone dehydr	Pseudomonas putida	Pseudomonas putida	Corynebacterium gl	c glutamicum prote	E. coli cellular p	V.cholerae VPI pha	Rhodococcus erythr	Aldebyde deydrogen	Phodomorals erythr	Rhodococcus picric	e koli aldobyde d	Pseudomonas aerugi	Arabidopsis thalia	Staphylococcus epi	s. epidermidis ope	Staphylononous aur	staphylococous aur	Minromosospora ove	staphylococcus epi	Staphylococcus aur	Arabidopsis thalia	Enternoonis faera	Prosophila melanog	Human aldehyde deh	Arabidopsis aldehy	Arabidopsis thalia	Aldohydo-dohydroge	Arabidopsis aldehy	Presephila melanog	Arabidopsis aldoby	Prosophila melanog

### ALIGNMENTS

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WFI; 2001-315988/33. N-PSDB; AAF92081.		30-AUG-1999; 99US-0151440.	30-A02-2000; 2000Wo-082-0878.	08-MAR-2001.	WO200116346-A1.	Saccharomyces cerevisiae.	polyhydroxyalkonate; copolymer; lactic acid.	beta-lactam; acrylic acid; trifluoromethylated alcohol; diol;	bacterial host, absorbable prosthetic device, surgical suture;	Aldohylo dobydrogeniase, gly orol dobydratisec 3 HP; glycerol; foodstook: 3 bydrogenopiumie acid, genetic engineering; glucose:	Teast ald-hyde dehydrogenas- Alfa protein segmena- SEQ 11 NO 2.	26-JUN-2001 (first entry)			AAR74923 standard, Protein: 49° AA.	LT 1 4923

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Best Local Similarity
   AAP60456 standard; Protein; 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preparing (FHP) is potentially cheaper than chemical synthesis. The present sequence represents the yeast aldehyde dehydrogenase ALD4, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or diols, polyhydroxyalkonates and copolymers with lactic acid. Incorporation of genes encoding two enzymes makes the host organisms able to produce (3-HP) from (1). The biotechnological method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GBHI) and aldehyde dehydrournase (ADH) capable of catalysing the production of (3-HP) from (1); or (iii) carries a genetic construct which expresses the dhalf gene form Klebsiella preumoniae and a gene for an ADH capable of catalysing the production of (3-HP) from (1), 3-HP is a monomer, and is useful e.g. in the production of absorbable prosthetic devices and surgical subures or for incorporation into beta-lactume, production of actylic acid or formation of trifluoromethylated alcohols
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or glucose, where the microorganism: (i) expresses genes for non-native enzymes which catalyse the production of (3-HP) from (1); (ii) carries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \ell Hydroxypropionic acid preparation, for use e.g. as monomer, by termenting recombinant microorganisms expressing genes for suitable
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                                                                                                                                                           DSEYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDA 480
                                                                                                                                                                                                                                                                                                    CCAGSRVYVEESTYDKFTEEFKAASESTKVGDPFDESTFQGAQTSQMQLNKTLKYVDTGK
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                                                                                        LONYLOVKAVRAKLD 495
                                                                                                                        LONYLOVKAVRAKLD 495
                                                                                                                                                                                          DSEYGLAAGIHTSNINTALKVADRVNAGIVWINIYNDEHHAVEFGGENASGLGKEMSVDA 480
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                                                                                                                                                                                                                             NEGATLITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMAN
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used. The DNA construct may contain a promoter region in operative association with a signal peptide coding region. The promoter/signal construct is suitably provided with a flanking restriction site to allow precise coupling of the protein coding region to the signal peptide coding region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1A; 75pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ALLE-) ALLELIX INC
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15-APR-1985;
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                                                                                                                                                                                                               237 VAFTGSTLVGPTILQAAAKSNLKKVTLELGGKSPNIVFDDADIDNAISWANFGIFFNHGQ
                                                                                                                                                                                                                                                                                    241 VAFTGSTATGRHIYQSAA-AGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGE
                                                                                                                                                                                                                                                                                                                                                            177 PAVAAGNTVYLKTAQQTPLSALYAAKLIKEAPFPAGVINVISGFGRTAGAAISSHMDIDK
360 KNEGATITTGGERIGSKGYFIKPTVEGDVKEDMRIVKEETEGPVVTVTKEKSADEVINMA 419
                                                                 297 CCCAGSELLVQEGIYEKEVARFKERAQKNKVONPFEQDLFQGFQVSQEQFDRIMEYINBG
                                                                                                                                                                                                                                                                                                                                                                                                                                     161 PALVTGNTVVLKTAESTPLSALYVSKY (PQAGTPPGVINIVSGFGK) VVEATTNHPKTKK
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                                                                                                                                  VCCAGSRVYVEESIYDKFIEEFKAASESIKVGDPFDESTFOGAOTSOMQLNKILKYVDIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIDVAVAAARAAF-EGPWEQVTPSERGILINKLADIMERDIDTLAAIESLIDUGKAFTMAKV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              497 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pickett M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88,
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                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                                                                                                              Spores of Cladosporium herbarum are the most common forgal spores found in the air; they can cause allergic reactions. Various Clah allergens and sequences encoding them have now been isolated. The mature Clah53 allergen has moi, wt. 53 kD and is encoded by cDNA sequence AAQB6278. The allergen has homology to alderyde dehydrogenases. Potential epitopic subfragments were identified by computer analysis of the amino acid sequence. See AAP71892-P71906 for potential B-cell epitopes and AAP72615-P72627 for potential T-cell
                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 - AUG - 1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fungal spore, allergen, Clahfa, allergy; aldehyde dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cladosporium herbarum allergen Clah53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1, Page 8 9; 35pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                allergy detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant DNA for expressing the allergens, useful for in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allergens derived from Cladosporium herbarum spores - also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ86278
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                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                             263;
                                   63 AARQAF-EGSWRLETPENBGKLINNLANLEEKNTULLAAVESLUNGKATSMARVTSACAS 121
                                                                                                                                                                 TVPIKLPNGLEYPQPTGLFINNKFVPSKQNKTFEVINPSTEEEIGHIYEGREDDVEEAVQ 66
                                                                                 AADRAFSNGSWNGIDPIDPGKALYFLAELIEGDKUVIASIETLUNGKAISSSEGUVDLVI 126
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                                                                                                                                        SVQLETPHSGKYEQPTGLFINNEFVKGQEGKTFDVINESDESVITQVHEATEKDVDIAVA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unger A;
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                                                                                                                                                                                                                                        Score 1399; DR 16;
Pred. No. 6.7e-110;
9, Mismatches 135;
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                                                                                                                                                                                                                                                                                           DB 16,
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                           Length 496;
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AAR71803
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Species of Alternatia diternata can cause allergic reactions. Various Aira allergens and sequences encoding them have now been isolated. The mature Alta53 allergen has mol. wt. 53 kD and is encoded by cDNA sequence AAQ2525. The allergen has benclony to aldebyde debyded operates. Potential epitopic subframents were identified by computer analysis of the amino and seriod sequence. See AAR71804-P71816 for potential R-cell epitopics and AAR71817-P71832 for potential T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alternaria alternata allergen Alta53.
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                                                                                                                                                                                                               Claim 7; Page 8; 26pp; German.
                                                                                                                                                                                                                                                                in-vitro allergy detection.
                                                                                                                                                                                                                                                                                           reacting sera from patients with fungal extracts; useful for
                                                                                                                                                                                                                                                                                                                    Allergens derived from Alternaria alternata - their isolation by
                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ86275
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-106851/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simon B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Achatz G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOM-) PIOMAY PRODN & HANDELSGES MBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 VETSSEKODKSTATATATATSTETENVINMOTVNOSTITATATATATATATATAT
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                  Puda A,
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                                                                                                                                                                                                                                                                             ALDH5; human; polymorphism; harlotype; aldebyde debydrogenase 5; binding attinity; drug targeting; alcoholism; alcohol induced disorder;
                                                                                                                                                         06 DEC 2001.
                                                                                                                                                                                                                                                                                                                                Human ALDH5 protein
                                                                                                                                                                                                                                                                                                                                                                 13 MAY 2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM49516 Standard; Protein; 517 AA
                                                   (GENA ) GENAISSANCE PHARM INC
                                                                                      25 MAY
                                                                                                                       29 MAY 2001; 2001WO US17253
                                                                                                                                                                                                                                                                                                                                                                                                       AAM49516;
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                                                                                      2000; 2000US-207508F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 TVPIKLPNGLEYEOPTGLEINNKEVPSKONKIFEVINPSTEEEICHIYEGKEDDVEEAVQ 66
                  Finked K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IOTKTVSIRL 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLSAAVHTSNETTATEVANALKAGTVWVNSYNTEHWQLFFGGYKESGIGRELGEAALDNY 479
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                  Kazemi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.4%; Score 1362.5; DB-16; Length 495; 54.3%; Pred. No. 8.3e-107;
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                  Messer C,
                  Sauchis
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protein. ALDH5 proteins may be used to generate antibodies. Haplotyping method can be used by scientists to validate ALDH5 as a candidate target for treating a specific condition or disease predicted to be associated with ALDH5 activity, and in the design of clinical trials of candidate drugs for treating a specific condition or disease predicted to be associated with ALDH5 activity. Information on polymorphisms on the ALDH5 gene can be applied for studying the biological function of ALDH5 as in identifying drugs targeting this protein for the treatment of disorders related to its abnormal expression or function. The products of the invention have antialcoholic activity. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       his invention describes a novel isolated genes and haplotypes of the human aldehyde dehydrogenase 5 (ALDH5) gene containing polymorphic sites. The polymorphic ALDH5 variant is useful in studying the effect of the variation on the biological activity of ALDH5 and on the binding affinity of candidate drugs targeting ALDH5 for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                     alcoholism and alcohol-induced disorders. Polynucleotides comprising polymorphic gene variant or fragment may be used for therapeutic purposes. ALDH5 protein isoforms may be used in assays to measure the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New genetic variants with polymorphisms in the aldehyde dehydrogenase 5 (ALDH5) gene, useful for studying the function of ALDH5, and for expressing ALDH5 protein which is useful in screening drugs for
Sequence
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                                                                              represents the human ALDHS protein described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                          binding affinities of one or more candidate drugs targeting the ALDHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating ALDH5-related diseases
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517 AA;
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Query Match Best Local Matches Local Similarity hes 248; Conserv 9 PIKLPNGLEYEQPTGLFINNKEYPSKQNKTFEVINPSTEEETCHTYEGREDUVEEAVQAA 68 Conservative 49.0%; Score 1248.5; DB 23; Length 517; 50.6%; Pred. No. 4.1e-97; ative 85; Mismatches 148; Indels 9;

PILNPD-IPYNQ---LFINNEWQDAVSKKTFPTVNPTTGEVIGHVAEGDRADVDRAVKAA 83

Вþ

밁 Ŷ Db Ŷ KVYKYFAGWADKWHGKTIPMHGQHFCFTKHEPVGVCGQIIPWNFPLVMQGWKLAPALATG NYLKSSAGFADKIDGRMIDTGRTHFSYTKKÖPLGVCGÖLLFWNFFLLMWAWKLAPALVTG REAERLGSPWRRMDASERGRILNILLADI.VERDRVYLASI.ETLDNGKPFQESYALDI.DEVI 14-3 DRAFSNGS-WNGIDPIDRGKALYRLAELIEQDKDVIASIETLDNGKAISSSRG-DVDLVI 126

187 204 NTVVMKVAEQTPLSALYLASLIKEAGFPPGVVNIITGYGPTAGAAIAOHMDVDKVAFTGS NTVVLKTAESTPLSALYVSKY I PQAGIPPGV I NI VSGFGK I VVEA LTNHPK I KKVAFTGS 263

TATGRHIYQSAA--AGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGEVCCAG

SRVYVEESTYDKFIEEFKAASES1KVGDPFDESTFOGAOTSOMOLNKILKYVDIGKNEGA TEVG-HLTOKAAGDSNLKRVTLELGGKSPSTVLADADMEHAVEUCHEALFFNMGQCCCAG

323 SRTFVEESIYNEFLERTVEKAKQRKVGNPFELDTQQGPQVDKEQFERVLGYIQLGQKEGA

383 KLLCGGERFGERGFFIKPTVFGGVQDDMRIAKEEIFGPVQPLFKFKK1EEVVERANNTKY TILITGGERLGSKGYFIKPTVFGDVKEDMRIVKFELFGPVVTVTKFKSADEVINMANDSEY 424

Цb QΥ Вb Ŷ DЬ Ş В Ş

Ş Ę, QY 485 LOVKAVRAKL 494 443 GLAAAVPTROLDKAMYFTQALQAGTVWVNTYNIVTGHTPEGGEKESGNGRELGEDGLKAY 425 GLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALQNY 484

503 TEVKTVTIKV 512

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RESULT 6
AAM49517
   This invention describes a novel isolated genes and haptotypes of the haman aldebyde dehydrogenase 5 (LDH5) genes containing polymorphic sites. The polymorphic ALDH5 variant is useful in studying the effect of the variation on the biological activity of ALDH5 and on the binding affinity of candidate drugs targeting ALDH5 for the treatment of affinity of candidate drugs targeting ALDH5 for the treatment of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALDHs, human, polymorphism, Eagletype, aldebyle Johydrogenase 5, binding affinity; drug targeting, alcoholism; alcohol induced disorder,
                                                conditate drugs for treating a specific condition or disease predicted to be associated with ALDH5 activity. Information on polymorphisms on the ALDH5 genee can be applied for studying the biological function of ALDH5 as well as in identifying drugs targering this protein for the
                                                                                                                     target for treating a specific condition or disease predicted to be associated with ALLHS activity, and in the design of clinical trials of
                                                                                                                                                         protein. ALDH5 proteins may be used to generate antibodies. Haplo method can be used by scientists to validate ALDH5 as a candidate
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3; 96pp; English
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                treatment of disorders related to its abnormal expression or function. The products of the invention have antialcoholic activity. This segmen
                                                                                                                                                                                         binding affinities of one or more candidate drugs targeting the ALDHS
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represents the human ALDH5 polymorphic variant protein described in
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                                                                                                                                                                                                                       bacterial host; absorbable prosthetic device; Surgical s
beta-lactam; acrylic acid; trifluoromethylated alcohol;
polyhydroxyalkonate; copolymer; lactic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disclosure of the invention
                                                                                                                                                                                                                                                                         Aldehyde dehydrogenase; glycerel dehydratase; 3 HP; glycerel; teedstock; 3 hydroxypropionic acid; genetic engineering; glucose;
              (WISC ) WISCONSIN ALUMNI RES FOUND
                                                                                                                                                         WO200116346-A1
                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                 Human aldehyde dehydrogenase ALDH2 protein sequence SEQ 1D NO:4.
                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     AAB74924;
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB74924 standard; Protein; 500 AA
                                                   KII-AIIG-] uuu;
                                                                                    40-AIIG-2000; 2000WO-0523878
                                                                                                                      08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I EČČI I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               503 TEVKTVT1KV 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443 GLAAAVETEELERAMII IQAE<sub>K</sub>ARIAWXXIIINIVI DIILEDRI KERRIKEELI KERRIKAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 GLAAGIHTSNINTALKVADRVNACTVWINTYNDEHHAVPEGGENASGIGREMSVDALQNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 KIILOGGEPFGEPGEPTKPTVPGGVVGDMPTAKEETEGPVQPILFKFKKIFFVVEPANNTPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity
247; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 PIKLPNGLEYEGPIGLEINNKEVPSKGNKIEEVINESIEEEICHIYEGKELCVEEAVQAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQVKAVRAKL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLEVERSTYNEFIER TVEKAKDRKVGNPFELLIDDUGPDVIK BDFERVIGY IDLIGDEBGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRVYVEESTYDKETEEFKAASESTKVRIPPEDESTEQRAQTSQMQLNKTLKYVDTRKNEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEVG-HLIQKAAGXSNLKKVTLELGGKSPSIVLADADMEHAVEQCHEALFFNMGQCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATGEHTYQSAA--AGLKKYTLEL/GKSPNIVEADAELKKAVONI IL//LYYNSGEVCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTVVMKVAEQTPLSALYLASLIKEAGFPPGVVNIITGYGPTAGAATAQHXDVDKVAFTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKKVAFTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVYKYEAGWADKWHGKTIEMHGQHECETKHEEXGVCGQITEWNEELVMQGWKLAEALATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYLKSSAGEACKITGEMICTGETHESYTKEQELGVCGQIIEWNEELLMWAWKIAPALVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | REXERTASPWRRMDASERGRILLNXLADIVERDRVYLASIETIJDNGKFEGESYALDIDEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRAFSNGS-WNGIDDIDRGKALYRLAELIEQDKDVIASIETLDNGKALSSSEG DVDIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILNPD-IPYNQ---LFINNEWQDAVSKKTEPTVNPTTGEVIGHVAEGDRADVDRAVKAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                   99115-0151440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.5%; Score 1239.5;
50.4%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.40-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23; Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151; Indels
                                                                                                                                                                                                                                                              suture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Incorporation of genes encoding two enzymes makes the host organisms able to produce (3-HP) from (1). The biotechnological method of preparing (3-HP) is potentially cheaper than chemical synthesis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an ADH capable of catalysing the production of (3-HP) from (1), 3-HD a monomer, and is useful e.g. in the production of absorbable prosti
devices and surgical subjects of for incorporation into beta-lactams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CDHT) and aldehyde dehydrogenase (ADH) capable of catalysing the production of (4 HP) from (1); or (iii) carries a genetic construct which expresses the dhaB gene from Klebsiella pneumoniae and a gene for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            shydroxypropionic acid (3-HP). The method comprises termenting a recombinant microordanism in the presence of a source of glycerol (1) or dincose, where the microordanism: (i) expresses genes for non-native enzymes which catalyse the production of (3-HP) from (1); (ii) carries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         production of acrylic acid or formation of trifluoromethylated alcohols of diols, polyhydroxyalkumates and espolymers with lactic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 32 35; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rementing recombinant microorganisms expressing genes for suitable enzymes in the presence of always less as a summer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic constructions for the expression of a glycerol dehydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzymes in the presence of glycerol or glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suthers PF, Cameron DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence represents the human aldehyde dehydrogenase ALBE2, is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSDB: AAF82082
482 GLOAYTEVKIVTVKV 496
                                                  480 ALGNYLOVKAVRAKI, 494
                                                                                                                                                    4.20 NIDSFYGLAAGTHTSNINTALKVADRVNAGTVWINTYNDFHHAVPEGGENASGLGREMSVD 479
                                                                                                                                                                                                          852 KQEGAKILICGGGTAADRGYFTQPTVFGDVQDGMTTAKEETFGPVMQILKFKTTEEVVGRA
                                                                                                                                                                                                                                                               460 KNEGATLITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVIKFKSADEVINMA 419
                                                                                                                                                                                                                                                                                                                                                                                                                         242 VAFTGSTEIGKVIQVAAGSSNEKKVILEEGGKSFNEIMSDADMDWAVEQAHFALFFNQGQ 301
                                                                                                                                                                                                                                                                                                                 302 CCCAGSKTFVQEDIYDEFVVRSVARAKSKVVGNPFDSKTEQGPQVDETQFKKILGYINTG
                                                                                                                                                                                                                                                                                                                                                                       400 VCCAGSRVYVEESTYDKFTEEFKAASESTKVCDPEDESTFQGAQTSQMQLNKTLKYVDIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 VAFTGSTATGRHIYQSA-AAGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 PALATGNYVYMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGEGPTAGAATASHEDVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 PALVEGNEVVLKTAESTPLSALYVSKYTPQAGTPPGVINIVSGEGKIVVEAITNHPKIKK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 DIDMVIKCIFYYAGWADKYHGKTIPINGDFFSYTRHEPVGVCGGTIPWNFPLIMQAWKIG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DVDLVINYLKSSAGFADKIDGRMIDTGRTHFSYTKKQPLGVCGQIIPWNFPLLMWAWKIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 KAREGRIGAFOLGSPWRRMDASHSGRILLNRLADIJIERDRTYLAALETIJNGKPYVISYLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 EAVQAADRAFSNGS-WNCIDPIDRGKALYKLAELIEQDKDVIASIETLDNGKA-ISSSRG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 TVP1KLPNGLEYEQP----TGLF1NNKFVPSKQNKTFEV1NPSTEEE1CH1YEGREDDVE 62
                                                                                                     NNSTYCLAAAVFTKOLDKANYLSQALQAGTVWVNCYDVFGAQSFFGGYKMSGSGRELGEY 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOAVPAPN - - - OOPEVECNOIFINNEWHDAVSPKTEPTVNPSTGEVICQVAEGDKEEVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86, Mismatches 154,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1225.5; DB 22; Length 500;
Pred. No. 3.5e 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Query Match Best Local : Matches

Local Similarity

Conservative

84, Mismatches

DB 23; Length 512; indels

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RESULT 8
ABG61842
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30-APR-2001;
04-MAY-2001;
                                                                             prostate cancer in mammals. The prostate cancer associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABG61800-ABG61944 represent prostate cancer associated proteins.
                                                                                                                                                                                                                                         comportassociated transcript in a cell from a patient. The method comportses contacting a biological sample from the patient with prostate concertassociated polynucleotides (designated polynucleotides to a sequence that is at least 80% identical to them. The prostate concertassociated polynucleotide sequences
                                                                                                                                                                             are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as bumans or other mammals (** 9 mor), shorp and dog The methods of the invention are useful for diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer associated g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                              Claim 27; Page 333-334; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gish KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96
                                                                                                                                                                                                                                                                                                                                                                                             are expressed in a prostate tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABK92157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JAN-2001;
16-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-080-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-00T-0001; 2001WO-US32045
                                                                                                                                                                                                                                                                                                                              The present invention relates to methods of detecting a prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :0007-DHG-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-00T-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WOLUULSULBB-AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostate cancer; prostate tumour tissue; human; mammal; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostate cancer associated protein #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AUG:2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG61842 standard; Protein; 512 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -APP-2001; 20018S 281922P.
-APR-2001; 20018S 286214P.
-APR-2001; 20018S-0847046.
-MAY-2001; 20018S-288589P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -MAP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MAR-1001; 1001US-176888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-471335/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mack DH,
                                                   512 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US 253957P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0733742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0733288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200008 0687576
47.8%; Score 1218.5; DB 50.4%; Pred. No. 1.4e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Afar D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hevezi
                                                                                                                                                                                                showp and dogs)
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The present invention relates to a method for the in vitro diagnosis of endometriosis by defermining the amount of gone product from at least one specific gene in a patient sample and comparing this with the amount of gene product in a control sample A reduced level is indicative of
DPIDESKALYPLAELIFGERFVTASIETLENGKA-ISSSRGFVI.VINYLKSSAGFADKI 139
                                                                     14.0 TOSEM IDTOSETHESYTERQPLOSVOSQITPWNPPLIJMMAWELJAPALVEONTVVLETAESEPPL TAA
                                                                                      SALYUSKYIPQAGIPPGVINIVSGFGKIVVEAITINHPKIKKVAFFGSTATGPHIYQSAA- 258
                                                                                                                                                            259 AGLKKVTLELGGKSPNIVPADARIKKAVQNIII.CIYYNSGBVÇCAGSPVYVEESIYDKPI 318
                                                                                                                                                                                                                                                   272 SNIKKVTILELGGKNECIV/ADADIDGAVE/JAHGGVEFNOGSSCTAASRVEVEEQVYSEFV 331
                                                                                                                                                                                                                                                                                          319 BEFKAASESIKVGDPFDESTFQGAQTSQMQLNKILKYVDIGKNEGATLITGGERLGSKGY 378
                                                                                                                                                                                                                                                                                                               379 FIKPTVEGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEYGLAAGIHTSNINTA 438
                                                                                                                                                                                                                                                                                                                                                                                                    392 FIKPTVESEVTDNMRIAKEEIFGPVQPILKFKSIEEVIKRANSTDYGLTAAVFTKNI,DKA 451
                            92 DAESPORTCHOLADLVERDRATLAALEEMOGARPEHAPPIDLEGGIFFTPYPAGWADKI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin; aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin; insulin-like growth factor binding protein-2; alpha-2 type IV collagen; transmembrane receptor PTK7; collagen type XVIII alpha 1; platelet derived growth factor receptor alpha; laminin M chain; subtilisin like protein PACE4; nidogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haendler B, Kraetzschmar J, Kreft B, Winterhager E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          In vitro diagnosis and monitoring of endometriosis, comprises detecting reduced expression of specific gene products, e.g. from the
                                                                                                                                                                                                                                                                                                                                                                                                                                     139 LKVAERVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVFALGNYLGVKAVRAKI. 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA017364 standard; protein; 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 RPSVEYAKKRPVGDPFDVKTEQGPQIPQKQFDKILELIESGRKFGAKLEGGGSAMFDKGL 341
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endometriosis. The gene products may be fibrocettin, p27, referilocalbin, alabahide dehylidgense 6, gravin, phosphelipase C epsilon, elastin, insulic-like growth factor binding protein-2, alpha-2 type IV collagen, transmembrane receptor PTK7, collagen type XVIII alpha 1,
                                                                               plathlet derived growth factor receptor alpha, laminin M chain, subtilisin like pro-left PATS4 or indomen. The method is useful for included diagnosts of endometriosis, and also for monitoring progress and treatment of the disease. The present sequence is human aldehyde.
                                                                                                                                                                                                                                                                                                                               22 TGLFINNKEVPSKONKTFEVINPSTEEEICHIYEGREDDVEEAVQAADRAFSNGS-WNGI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                      92 PALSPGRILHQLADLVEPPPATLAALFTMPTGKPFLHAFFIDLEGTFFLPYFAGWADKL
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                                                                                                                                                                                                                                         Score 1218.5, DB 23, Length 512;
Pred, No. 1 4e-94;
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                                                                                                                                                                                                                                                                                      149; indels
                                                                                                                                                                                                                                                                                    84, Mismatches
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                                                                                                                                                                                                                                                                                        240; Conservative
                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                dehydrogenase 6.
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for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving (11) (11) is useful for generating antibodies against it, detecting or
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Note. The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and given mapping, and in re-ambinant production of (II). The polymelegides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 QGKTIPTDDNVVCFTPHEPIGVCGAITPWNFPLLMLVWKLAPALCCGNTMVLKPAEQTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 SALYVSKYIPQAGIPPGVINIVSGFGKIVVEAJTNHPKIKKVAFTGSTATGRHIYQSAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 LKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALONYLQVKAVRAKI, 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 469 LKLASALESGIVWINCYNALYAQAPFGGFKMSONGRELGEYALAEYTEVKTVTIKL 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (1) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.8%; Scere 1218.5; DB 50.4%; Pred No 1 5e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 36936; 103pp; English.
                                                                                                                                                    Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240; Conservative
                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                         WP1; 2001-639362/74
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS70764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biodiversity
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the invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 DASPROPLIYELADI MEREZVYLASI ETLIDMAKPYSMSYNVITLETATENLIKYFAGWADEN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 HGKTIPMIGDEFTYTRHEPVGV/GQTIPWNFPILAMAWKIAPALATATION I VLAPACISI, 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 SALVŲSKY IPQAGIPPAVINIVSTPAKIVVEATTNIIPKIKKVAPPASTAIDAHI YUSAA 25B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HITTELL HITTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.0 DGRMIDTGRTHESYTKRQPLGVCGGTTFWNFFLLAMMAWKIAPALVTGNTVVLKTAESTFFL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 TGLETNNKFVPSKONKTFEVINPSTEEETCHTYEGREDOVEEAVOAADRAFSRASS WAST BO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.0. TGVFINNEWHKSKSGKIFETINPTTAEVIAEIOCADKEDIDIAVQAAKNAFKLASIPWRRM 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formal directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes from Drosophila and for elucidating cell signalling and cell cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful in developmental biology and in elucidating cell signalling and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pr Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell-cell interactions in higher eukaryotes for the development of inserticias, therapout ics and pharmacentical dinas. The invention discloses general DNA sequences (ARLDel76 ARLDel1), expressed DNA sequences (ARLDel15) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                            Prosophila, developmental biology, cell signalling, insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.2%; Score 1203.5; DB 22; Length 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ 1D NO 7212; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150; Indels
                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID No 7212.
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tive 82; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li PWD, Myers FW;
                                                                       ABB60140 standard, Protein, 520 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                             (first entry)
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Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABB57737-ABB72072).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceut.ical
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                                                                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001.
                                                                                                                                                  ABB60140;
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RESULT 11
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of acetyl CoA.

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acetyl CoA synthetase (ACS), various subunits (specifically the E3 subunits) of plant plastidic pyrovare dohydrogense (PEH), the A and B subunits of a plant ATP citrate lysek (ACL), Arabidopsis pyruvate denytrogense (ALH). Arabidopsis aldohydrogense (ALH). Secretifically ALH-2 and ALH-4. The polypeptides can be expressed by standard recombinant methodology. The ACS, pPBH, ACL, PBC and ALDH polypeptides, methods and nucleic acid molecules of the invention are used to alter the level of acetyl CoA is expected to affect the biosynthesis of very long chain fatty acids and flavonoids. The enzymes may also be used for in vitro synthesis of acetyl CoA, which in turn can be used to produce acetyl CoA plastidic ACS, pPBH, ACL, pyruvate decarboxylase, acetyl CoA hydrodase, mitochondrial pyruvate dehydrogenase and aldehyde dehydrogenase are involved in the biosynthesis
                                                                                                                                                                                             399 YFVQPTVFADVQDDMTIAREFIFGPVQQLIRFKKI,DEVIERANNSFYGI,AAAVFTKDLDK 458
259 AGLKKVTLELGGKSPNIVFADAELKKAVQNITIGIYYNSGEVÇPAGSPVYVEESIYDKFI 318
                                     279 INLARVILLIAGSKSPNIILSDIDMDYAVETAHFGLFFNMGQCCCAGSRTFVEDKIYDEFV 338
                                                                            319 EEFKAASESIKVGDPFDESTPQGAQTSQMQUNKILKYVDIGKNEGATLITGGER-LGSKG 377
                                                                                                  378 YFIKPTVEGDVKEDMPTVKEETFGPVVTVTKFKSADEVINMANDSEYGLAAGIHTSNINT 437
                                                                                                                                                                                                                                                                       459 ANYTVGGLRAGTVWVNTYNVLAAQAPFGGYKMSGHGRENGEYALSNYTEVKSVIVKV 515
                                                                                                                                                                                                                                             438 ALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALQNYLQVKAVRAKL, 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant plastidic pyruvate dehydrogenase; ppDH; ATP citrate lyase; ACL; pyruvate decarboxylase; DC; aldehyde dehydrogenase, ALDH, aretyl CoA, fatty acid; flavozcid; envyme, phytochemicul; pyruvate dearboxylase; acetyl CoA hydrolase; mitochondrial pyruvate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel acetyl CoA synthetise (ACS), plastidic pyruvate dehydrogenase (PPDH), ATP citrate lyase (ACL), pyruvate decarboxylase (PDC) and aldehyde dehydrogenase (ALDH) polypeptides used to alter acetyl CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides nucleic acids encoding Arabidopsis plastidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis; plant plastid; acetyl CoA synthetase; E3 subunit; ACS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ke J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schnable PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oliver DJ, Behal R, S
Fatland B, Lutziger I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis aldehyde dehydrogenase (ALDH):1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IOWA ) HINIV TOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                         AAY67412 standard; protein; 538 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examples; Fig 10R; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US14382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wurtele ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allred CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-160678/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           levels in plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nikolau BJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY67412;
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141 GRMIDTGRTHFSYTKROPLGVCGOTIPWNFPLLMMAWKIAPALVTGNTVVLKTAESTPLS 200
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                                                                                                                                                                           58 TOLLINGNEVDSASGKTEPTLDPPTGEVTAHVAFGDAEDTNPAVKAAPTAFDEGFWPKMS 117
                                                                                                                                                                                                               82 PIDRGKALYRLAELIEQDKDVIASIETLDNGKAISSS-RGDVDLVINYLKSSAGFADKID 140
                                                                                                                                                                                                                                                                                                                        178 GLTIPADGNYQVHTLHEPJGVAGQIIPWNFPLIMFAWKVGPALAGGNTIVLKTAFQTPLT 237
                                                                                                                                                                                                                                                                                                                                                            201 ALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKKVAFTGSTATGRHIYOSAA-A 259
                                                                                                                                                                                                                                                                                                                                                                                             238 AFYAGKLFLEAGLPPGVLNIVSGFGATAGAALASHMDVDKLAFTGSTDTGKVILGLAANS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                   260 GLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGEVCCAGSRVYVEESIYDKFIE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 NLKPVTLELGGKSPFIVFEDADIDKAVELAHFALFFNQGQCCCAGSRTFVHEKYYDEFVE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 EFKAASESIKVGDPFDESTFÖGAQTSQMQLNKILKYVDIGKNEGAFLLIGGERLGSKGYF 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 KSKAPALKPVVGTPFPRGTPGGPQTFLKQFEKVMKYTKSGTESNATFFGGGFQTGFKGYF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                418 IQPTVFSNVKDPMLJAQDETFGPVQSILKFSDVDEVIKPANFTKYGLAAGVFTKNLDTAN 477
                                                                                                                                           22 TGLFINNKFVPSKQNKTPEVINPSIEEFICHLYEGREDDVEEAVQAADRAFSNGSWNGID 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 KVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALQNYLQVKAVRAKLD 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478 RVSRALKAGTVWVNCFDVFDAAIPFGGYKMSGNGREKGIYSLNNYLQIKAVVTALN 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila, developmental biology; cell signalling, insecticide;
                                                                  Length 538;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID No 13560
                                                                  DB 21;
                                                              Cuery Match 47.1%; Score 1201; DB 21; Best Local Similarity 48.9%; Pred. No. 4.6e-93; Matches 233, Conservative 82, Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB62256 standard; Protein; 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2900018-191637P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 MAR 2001; 2501W--8S09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860∕75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY.
                                  538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABLU6359
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                                  Seguence
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New isolated nucleic acid detection reagent for detecting 1000 or more

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in Pluridating cell signaling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 TKLFINNEFVDSVSGKTFATFNPATSKEIVQVSEGDKADIDLAVKAAKKAFHRESEWRKL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 DPIDRGKALYRLAELIEODKRVIASIFTLDNGKAISSSRGDVDLVINYLKSSAGFADKID 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 GPMITYTGPTHFSYTKRQPLGVCGQIIPWNFPLLMWAWKIAPALVTGNTVVLKTAESTPLS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 GDTIPAG-GFVSMTRKEPVGVVGQIIPWNYPLLMLAWKWGPALAVGCTIIMKPAEQTPLT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 ALYVSKYIPQAGIPPGVINIVSGFGKIVVEALINHFKIKKVAFTGSTATGRHIYQSAA-A 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 ALHMAALAKEAGFPAGVINVVNGFGPTAGAAISAHPDIAKVAFTGSVEIGRIVMQAAATS 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 IKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEYGLAAGIHTSNINTAL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 VEPTVFSDVKDDMRIAQEE1FGPVQSIFKFSSLEEMIDRANNVQYGLAAGVITNDINKAL 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 SPLORTNLMNKI.CALMDRDKAFLASLETQDNGKPYAEALFDVTYSILTLOYYAGWTDKFF 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 GLKKVTLELGGKSPNIVFADAELKRAVQNIILGIYYNSGEVCCAGSRVYVEESIYDKFIE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 EFKAASESIKVGDPFDESTFQGAQTSQMQLNKILKYVDIGKNEGATLITGGERLGSKGYF 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 KAAAKAKARKVGNPFFQNVQQCPQTDDDMLTKVLGYTESGKKEGAKLQAGGKRLGNVGFF 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 TGLFINNKFVPSKQNKTFEVINPSTEEEICHIYEGREDDVEEAVQAADRAFSNGS-WNGI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification, but was obtained in electronic format directly from WIPO
genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis; plant plastid; acetyl CoA synthetase; E3 subunit; ACS; plant plastidic pyruvale dehydrogenase, PPCH; ATP mitrate lyase; ALL; pyruvate decarboxylase; PDC; aldehyde dehydrogenase; ALDH; acetyl CoA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fatty acid; flavoncid; enzyme; phytochemical; pyruvate decaiboxýlase, acetyl CoA hydrolase; mitochondrial pyruvate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440 KVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALQNYLQVKAVRAKI, 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.2%; Score 1178.5; DB 22; Length 659; 49.1%; Pred. No. 5e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                      Disclosure; SEQ ID NO 13560; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91; Mismatches 148, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis aldehyde dehydrogenase (ALDH)-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  659 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis sp.
                                                interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 CGNTVVLKTAEQTPLSALLVGKLLHEAGLPGVVNTVSGFGATAGALASHMDVDKVAFT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 GSRTEVHERVYDEF VENAKARALARNVGFF NSGTEGGGGGGGENATURYTAHGVEAG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 ATLITOGEPLOSKOPETKETVPODOVREDMPLVREELPODVTVTKERSADEVINMANDSE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66. QAADKAFSNGSWNGIDPIDKGKALZPLIPQHTIPQHIDDASFFII DNGKAL-SSSPRDVDT - 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 AAARKAFIPGPWPKMTAYFPSKIIFPFADI IFKHNDEIAALETWDNGKPYEQSAUIEVPM 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 VINYLKSSAGFADKTIKIRMIDTGKTHFSYTKROPLGVCGG11PWNFPLLMWAWKTAPALV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 ITPPVKV-----EHTQLLIGGREVDAVSGKTFPTLDPRNGEVIAOVSEGDAEDVNRAV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or organs. A decrease in acetyl CoA is expected to affect the
biosynthesis of very long chain fatty acids and flavonoids. The enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used to alter the level of acetyl COA in a plant or plant cell, tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acet; CoA synthetase (ACS), carious cabonits (specifically the Ed subunits) of plant plastidic pyrovate dehydrogenase (pphH), the A and B subunits of a plant ATF eitrate lyase (ACL), Arabidopsis pyrovate decarbox; ase (PCC), Arabidopsis alidebyde dehydrogenase (ADH), specifically ADH-2 and ALDH-4. The polypoptides can be expressed by standard recombinant methodology. The ACS, pppH, ACL, ppc and ALDH polypoptides, methods and nucleic acid molecules of the invention are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 LARVERYYAGWADRIHGMTMPGDGPHHVQTLHEPTGVAGGTTPWHFDLLMLSWKLGPALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           004 GSRVYVEESTYDKETEEFRAASESTRV-OOFDESTFOGAGTSOMGUNETLAYVDTGKNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 TONTVVLKTAPSTPLSALEVSKELPGASTPPOSTNIVSGFORTVVEALLNHPLIKRVAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 GSTATGRHTYQSAA-AGLKKVTLELGGKSPNIVEADAELKKAVQNTTIGTYYNSGEVOOA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 GSTDVGKI ILELASKSNLKAVTLELESHHSFVCEDADVDQAVELAHFALFFNQGQCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 MTVPIKLPNGLEYEQPTGLFINNKFVPSKQNKTFFVINPSTEEFICHTYEGREDGVEEAV
                                                                                                                                                                                                                                                                                                                                                                                                      (pPDH), ATP citrate lyase (ACL), pyrnwate decarboxylase (PPC) and aldehyde dehydrogenase (ALDH) polypeptides used to alter acetyl CoA
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П
                                                                                                                                                                                                                                                                                                                                                                          Novel acetyl CoA synthetase (ACS), plastidie pyraste debydroqenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides noticity acids encoding Arabidopsis plastidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 544;
                                                                                                                                                                                                                                            Schnable PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162; Indels
                                                                                                                                                                                                                                          oliver DJ, Behal B, Schnable
Fatland B, Dutziger I, Wen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.1e-90;
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                                                                                                                                                                                                  (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Examples; Fig 12B; 79pp; English.
                                                                                                            99WO-US14382.
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nes 238; Conserv
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                                                424 YGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALQN 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 ADK1--DGRMIDIGRIHESYTKRQFLGVCGQIIPWNFFLLMWAWKIAPALVIGNIVVLKT 193
398 ATLQAGGDKLGSKGYYIQPTVFSDVKIDMLIATDFIFGPVQTILKFKDLDEVIARANNSR 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A novel retro virus vector encodes human cytosolic aldehydedehydrogenase and/or human glutamylcysteine-synthetase (AAR63673). Hematopoietic cells transfected by the vector are resistant to cyclophosphamide, providing a means of gene therapy that allows higher doses of toxic drugs to be used in cancer chemotherapy. The human genes may also be used as selectable markers for mammalian cell transfection and for transgenic animal breeding.
                                                                                                                                                                                                                                                                                                                                       glutamylcysteine synthetasé, hematopojetic cell, cyclophosphamide, chemotherapy, transyenic animal, yene therapy, cancer therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petroviral vectors encoding human cytosolic aldehyde dehydrogenase or glutamyl cysteine synthetase - used to transform a subject's haematopoietic cells to reduce the toxic effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 2%; Score 1153 5; DB 15; Length 521; 48.5%; Pred. No. 4.7e-89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 4.7e-89;
88; Mismatches 153;
                                                                                                                                                                                                                                                                                                                         Retro virus; vector; aldehyde-dehydrogenase;
                                                                                                                                                                                                  AAR63672 standard; Protein; 521 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYCO ) UNIV COLUMBIA NEW YORK.
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                                                                                          484 YI.QVKAVRAKL 494
                                                                                                                        518 YLQVKAVVTSL 528
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                                                                                                                                                                                                                                                                                                                                                                      selectable marker,
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OM protein - protein search, using sw model

June 24, 2003, 10-14-85; Search time 13-7085 Seconds (without alignments) 1062-435 Million cell updates/sec Run on.

US-Ú9-830-751-2 2550

MSVPALQNYLQVKAVRAKLIN 495 1 MSHLPMTVPIKLPNGLEYEQ Perfect score: Sequence.

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

Maximum DB seq length. 200000000 Minimum DB seq length: 0

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum March O&

Agn2\_6/ptodata/1/iaa/5A\_COMR.pep.\*
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/cqn2\_6/ptodata/1/iaa/pcTTIS\_COMR.pep.\* Issued\_Patents\_AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ			SUMMARIES	
Result		Query				
NO.	Score	Match	Length	DB	QI	Description
1	1158.5	45.4	521	4	US-09-221-294-2	Sequence 2, Appli
7	982.5	38 5		~	US-09-134-0010-4541	4541
m	949.5	37.2		4	US-09-134-001C-4383	Sequence 4383, Ap
4	921.5	36.1		4	US-09-651-941-9	9, App
S	921 5	36 1		4		5
9	921.5	36 1	SOR	4	US-09-655-270A-9	Sequence 9, Appli
7	888		497	-	US-08-513-841-2	~
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5	888		497	-1	US-08-942-67:2	ci
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11	775.5	30.4	4 A H	↔	78-74-144-6010-4246	7
12	763.5	29.9	493	4	09-1	43
13	685 5	C	F. 1.8	4	115-00-134-0010-4451	4451,
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15	657.5	25.8	482	4	11S-09-155-183-4	4
16	365	14	464	4	118-09-134-0010-4701	47
17	338.5	13	133	_	1	C1
18	338.5	13.3	133	C1	US-08-794-494-2	۲ì
19	194 5	7	15.5	₹	11S-08-952-061 2	Sequence 2, Appli
20	152	6.0	711	₹	-134-	6,46
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23		4.5	510	C4	-08-663	1, 1
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58	104	4.1	495	4	-09-134-	3128
27	104	4	1491	4	11S - 09 - 376 - 330 - 16	16,

79 GIUPTUPGKALYPLAELIEGEK - IVVIASIETLUNGKAISSS-PGEVELVINVLKSSAGF 135

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Sequence 33, Appl	Sequence 18, Appl	Sequence 6, Appli	Sequence 49, Appl	Sequence 31, Appl	Sequence 33, Appl	=	Sequence 33, Appl	2	Ç.	70,	Q	Sequence 3464, Ap	ě	Sequence 2, Appli		94,	્.
US-09-655-270A-33						115-08-583-799-31	US-08-583-799-33	US-08-164-839-70	US-08-164-839-72	US-08-583-799-70	US UB-583 739-72	tig-09-134-001c-3464	US-08-984-618-13	US-09-217-490-2	US-08-224-657-94	US-09-354-138-94	TIS-09-724-519-2
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# ALIGNMENTS

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7; Gaps
                                                                                                      APPLICANT: Riccardo Dalla-Favera and APPLICANT: Alessandro Massimo Gianni
1111E DE TUNENTION: A FETTOVITAL VECTOR Capable of Transducing the ILILE DE INVENTION: Additional design assert Cope and Cases of Said ILILE DE INVENTION: Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 45.4%, Score 1158.5, DB 4, Length 521;
Rest Local Similarity 48.8%; Fred. No. 8.20-100,
Matches 235, Conservative 88, Mismatches 152; Indels 7;
                                                                                                                                                                                                                                                                 E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER PRACARLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM 330 466 DX2
OPERATIN: SYSTEM: PC-IONS/MS-DOS
SOFTWARE: Palentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: IIS/09/221,294
FILING DATE:
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                       Sequence 2, Application us/09221294
Patent No. 6268138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPEKENCE/DOCKET NUMBER 429
TELECOMMUNICATION INFORMATION:
TELEPHONE, 212.278.0400
TELEPA. 212.278.0400
TELEPA. 212.291.0525
INFORMATION FOR SL. IL NO. 2.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: White, John P. PECISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTOPNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 521 amino acids
amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                            CURRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  New York
                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           New York
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440 KVADPVNAGTVWINTYNDEHHAVPEGGENASGI GREMSVDALONYLOVKAV 490
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PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4383, Application US/091340010 Patent No. 6380370
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TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
STAMDASEPGELLYKLADLIERDFILATMESMESMESKRIYSNAYLNDLAGOTKTLRYGAGW 154
                                                             136 ADKI--DGRMIDTGPTHESYTKPOPLGVCGQIIPWNFPLLMWAWKIAPALVTGNTVVLKT 193
                                                                                     194 AESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKKVAFTGSTATGRHI 253
                                                                                                                                                                                     215 AEQTPLTALHVASLIKEAGFPPGVVNIVPGYGPTAGAAISSHMDIDKVAFTGSTEVGKLI 274
                                                                                                                                                                                                                              254 YÖSAA-AGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGEVCCAGSRVYVEES 312
                                                                                                                                                                                                                                                    313 IYDKFIEEFKAASESIKVGDPFDESTFQGAQTSQMQLNKILKYVDIGKNEGATLITGGER 372
                                                                                                                                                                                                                                                                                                                                           373 LGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEYGLAAGIHT 432
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CURRENT PAPLICATION NUMBER: US/09/134, 001C
CURRENT PILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064, 964
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PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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; Patent No. 6380370
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Matches 203, Conservative
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US-09-134-001C-4541
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APPLICANT: Lynd Doucette-Stamm et al TILLE OF THE SENDENTES RELATING TO STAPHYLOCHEN TILLE OF INVENTION: NUCLEIC ALLD AND AMINO ACID SEQUENTES RELATING TO STAPHYLOCHEN TILLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                           321 JPKEKEAFENIKVGOPPDEDIKMSAQTGPEQIDKIBSYIKIAEEDPKANIETGGHRITDN 380
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84 DRGKALYPLAELIEQDKPVIASIETLINGKAISSSPG-DVDLVINYLKSSAGFAPKINGP 142
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36 1%; Score 921.5; DR 4; Length 485; 39 6%; Pred. No. 1.1e-77; Live 90, Mishaltches 191, Indels 7,
                                                                                                                                                                                                                                                                                   ON: Genes Encoding Picric Acid Degradation BC1022 US NA
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APPLICANT: WALTERS, DANA M
APPLICANT: RAINER, RUSS
TITLE OF INVENTION: Genes Encoding Pictic Acid Degradation
FILE REFERENCE: RC1022 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM. Rhodococcus erythropolis HD PM-1
                                                                                                                                                                                                                                                                                                                               CUPRENT APPLICATION NUMBER HS/05/551, 941
CURRENT FILING DATE: 2006-08-31
PRIOR APPLICATION NUMBER: 60/152,545
PRIOR FILING DATE: 1999-10-03
                                                                                                                                       ; Sequence 9, Application US/09651941
; Patent No. 6355470
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Patent No. 6461856
GENERAL INFORMATION:
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                                                                                                                                                                                                         APPLICANT: ROUVIER, PIERRE E APPLICANT: WALTERS, DANA M
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Matches 189; Conseivative
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TITLE OF INVENTION: Gene
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                                                                                                                                                                                          ; GENERAL INFORMATION:
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TITLE OF INVENITOR High Febrity Sampling of Differentially Expressed Prokaryotic
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                                                                                                                                                                                                                                                                                         Query Match 36 1%; Score 921 5; DR 4; Length 485; Best Local Similarity 39.6%; Pred. No. 1.1e-77;
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CUPRENT APPLICATION NUMBER: US/09/655,270A
CURRENT FILLING DATE: 2090-09-05
FFICE APPLICATION NUMBER: 66/170,702
CURPENT APPLICATION NUMBER US/09/955,597 CURPENT FILLING MATE: 2001-09-17 PPIOR APPLICATION NUMBER (6/152,545 PRIOR FILING DATE: 1999-10-03
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PRIOR APPLICATION NUMBER: 60/152,542
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APPLICANT: Rouviere, Pierre E.
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                                                                                                                          SOFTWARE: Microsoft Office 97
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66. UAADEAESIGSWINGTIP TIPEGEALTYRIAELI EUDEDVIASTELLIJONIJEALSSSEKUDDIJV. 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 VSEPEK - - - - - PREFGFF HAISWRAGKO - FFDRSSPAHDVPVTR I PRCTREDLDEAV 57
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APPLICANT: FOSHIGA, MASATU
APPLICANT: Hypash, Hiromi
TITLE OF INVENTION: Method for Producing 2-Keto L Galonic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.8%; Score 888; DB 1; Length 497;
39.8%; Pred. No. 1.5e-74;
ive 93; Mismatches 189; Indels 12;
          REFERENCE/DOCKET NUMBER: 18-909-0 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD: experimentally
                                                                                                                                                                                                                                                                                                                                                                                                                 Gluconobacter oxydans
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                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000
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Saito, Yoshimasa
Ishii, Yoshinori
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Matches 194; Conservative 9
                                                                                                                                                                                                                                               497 amino acids
                                                                                                                              TELFX 248855 OPAT UN
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                 TELEPHONE: 703-4.
TELEPHONE: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mat.peptide
LOCATION: 1.497
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
ORIGINAL SOURCE:
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APPLICANT: Saito, Yoshimasa
APPLICANT: Saito, Yoshida, Masaru
APPLICANT: Suzuki, Hiromi
APPLICANT: Saita APPLICANT: APPLICA
                                                                                                                                                                                                        84 DRGKALYRLAELIEQDKDVIASIETLDNGKAISSSRG-DVDLVINYLKSSAGFADKIDGR 142
                                                                                                                                                                                                                                                                    91 ORTKLMFKYAALIEEHKTELAQLOSKUMGKPIRESLGIDLPIMIETLEYFAGLVTKIEGR 150
                                                                                                                                                                                                                                                                                                                                          143 MIDTGRTHFSYTKROPLGVCGGIIPWNFPLLMMAWKIAPALVTGNTVVLKTAESTPLSAL 202
                                                                                                                                                                                                                                                                                                                                                                          151 TTPAPGRFLNYTLREPIGVVGAITPWNFPAVQAVWKIAPALAMGNAIVLKPAQLAPLVPV 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 YVSKYIPQAGIPPGVINIVSGFGKIVVEALTNHPKIKKVAFTGSTATCRHIYQSAAAGLK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 KVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGEVCCAGSRVYVEESIYDKFIEEFK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 TASLELGGKSALVAFGDSSPKAVAAVVFQAMYSNQGETCTAPSRLLVERPIYDEVVELVQ 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 FIKPTVFGDVKEDMRIVKEEIFGDVVTVTKFKSADEVINMANDSEYGLAAGIHTSNINTA 438
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                                                                      24 LFINNKFVPSKQNKTFEVINPSTEEEICHLYEGREDDVEEAVQAADRAFSNGSWNGIDPI 83
                                                                                                                                     33 LVIGDØLTPSSTGATFDSINPADGSHLASVAEATAADVARAVKAAKAAAR--TWORMPPA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 LKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALQNYLQVKAVRAKLD 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 LRFAQTLDAGNVWINSWGVLNPASPYRGFGQSGYGSDLAQAATESFTKFKSTWARLD 507
          7; Gaps
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1755 Jefferson Davis Highway, Suite 400
Matches 189; Conservative 90; Mismatches 191; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette, 3.50 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 241851/1993
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 01-NOV-1995
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FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08513841
Patent No. 5753481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24,618
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MEDIUM TYPE: Diskett
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423 EYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGPEMSVDALQ 482
358 AKLLCGGGIVDFGKGQYIQPILFTDVKPSMGIAPDFFFGPVLASFHFDTVDEAIAIANDT 417
                                                                                                                    483 NYLQVKAV 490
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US-08-942-673-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 AAARRAFENGSWAGLAAADRAAVLIKAAGLIRERRPDTAYWEVLENGKPISQAKGEIDHC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 TGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHFKIKKVAFT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 GSTAIGEH-IYGSAAAGLKKVILELGGKSPNIVFALAHTKKAVQNLILGIYYNSGEVCCA 3U3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 INYLKSSAGFADKIDGPMINT-GRTHFSYTKRQPLGVCGQIIPWNFPLLMWAWKIAFALV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 MIVPIKLPNGLEYEQPIGLFINNKFVPSKQNKTFEVINPSTEEFICHTYEGREDDVEEAV 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93; Mismatches 189; Indels 12; Gaps
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              ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt,
ADDRESSEE: P ^
                                                                                                                                                                        MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage COMPUTER: IBM PC compatible
                STREET: 1755 Jefferson Davis Highway, Suite 400 CITY: Arlington STATE: Virginia.
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                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 28612/1994 FILLING DATE: 25-FEB-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 118/08/696,834
FILING DATE: 24-SEP-1996
                                                                                                                                                                                                                     PC-DOS/MS-DOS
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STRAIN: T-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
TELECHMANNIATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX. (703) 413-2220
TELEFAX. 24885.0PAT UR
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497 amino acids
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                                                                                                                                                       COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER.
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APPLICANT: SLEUKI, Hiromi
TITLE OF INVENTION. No. ER6129201 L.sorbose Dobydrogenase and No. ER6129201
TITLE OF INVENTION. L-sorbosone Dehydrogenase Obtained from Glucomobacter
TITLE OF INVENTION: oxydans T-100
NUMBER OF SEQUENCES: 22
CURPERSPONDENCE ADPRESS:
                                                                                                                                                                                                                                                                                                    . Oblon, Spivak, McCleiland, Maier & Neustadt, P.C.
1755 Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette, 3.50 inch, 1.44 Mb storage
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FILING DATE: Z8-SEP-1993
ATTORNEY/AGENT INPOPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: MS-DOS Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: UK 9304700.9 FILING DATE: UB-MAR-1993 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMGANISM: Gluconobacter oxydans STRAIN: T-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513,841
FILING DATE: 01-NOV-1995
Sequence 2, Application US/08942673
Patent No. 5861292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
                                         GENERAL INFORMATION:
APPLICANT: Niwa, Mineo
APPLICANT: Saito, Yoshimasa
APPLICANT: Ishli, Yoshimori
APPLICANT: Yoshida, Masaru
APPLICANT: Suzuki, Hiromi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24,618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 248855 OPAT HP
INFOPMACTION POP SEQ ID NO
SEQUENCE CHARACTERISTICS:
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TELEPHONE: /US ==
TOS = 703 - 413 - 2220
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34.8%; Score 888; DB 2; Length 497;

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No. 6197562el Lisorthise Dehydrogenase and No. 6197552el
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                                                                                                                                                           66 QAADRAFSNGSWNGIDPIDRGKALYRLAELIEQDKDVIASIETLDNGKAISSSRGDVDLV 125
                                                                                                                                                                                                                                                                                                                                                                 357
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                                                                                                                                                                                                                                                 126 INYLKSSAGFADKIDGRMIET-GRTHFSYTKRÖPLGVCGQIIPWNFPLLMWAWKIAPALV 184
                                                                                                                                                                                                                                                                                              118 IACFEMAAGAARMLHGDTFNNLGEGLFGMVLREPIGVVGLITPWNFPFMILCERAPFILA 177
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                                                                6 MIVPIKLPNGLEYEQPIGLFINNKFVPSKQNKTFEVINPSTEEEICHIYEGREDDVEEAV 65
                                                                                                             7 VSLPLK-----PREFGFFIDGEWRAGKD--FFDRSSPAHDVPVTFIPPGTPEDLDEAV 57
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                       12;
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1755 Jefferson Davis Highway, Suite 400
39.8%; Pred. No. 1.5e-74;
tive 93; Mismatches 189; Indels
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APPLICATION NUMBER- 08/513,841
FILING DATE: 01-NOV-1995
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Patent No. 6197562
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Ishii, Yoshinori
Yoshida, Masaru
Suzuki, Hiromi
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                     Matches 194; Conservative
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MEDIUM TYPE: Diskett
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Best Local Similarity
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66 OAADRAFSNGSWNGIDPIDRGKALFRIJEODRDVIASIEILDNGKAISSSRUDVDLV 125
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                                                                                                                                     24,618
3R: 18-909-0-PCT
            FILING DATE: 08 MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 241851/1993
FILING NATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: UK 9404700.9
                                                                                                                                                                                                                                                                                                                                                                                          OPGANISM: Gluconobacter exydans
                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                             703-413-4000
                                                                                                                                                      PEFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                           497 amino acids
                                                                                                                                                                                          TELEPHONE: 703-413-520
TELEFAX: 704-413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                   NORMAN F. OBLON
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                                                                                                                                     REGISTRATION NUMBER:
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MOLECULE TYPE: F
ORIGINAL SOURCE:
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// Sequence 4246, Application US/09134001c // Patent No. 6380370

US-09-134-001C-4246

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RESULT 13
US-09-134-001C-4451
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  TYPE: PRT
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                                         TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES FELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                       36.6%; Share 775 %; DR 4, 36.6%; Pred, No. 5e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 188;
                                                                                        FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER OS/09/134,0010
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CURRENT APPLICATION NUMBER: US/09/134,0010
                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/064,964 PRIOF FILLING DATE: 1947-11-08 PRIOR APPLICATION NUMBER: US 60/055,779
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PRIOR APPLICATION NUMBER: US 60/055,779
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PRIOR APPLICATION NUMBER: US 60/064,964
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                                                                                                                                                                                                                                                                                                                          TYPE, PRT OPGANISM: Staphylococcus epidermidis
                      APPLICANT: Lynn DoucetterStamm et al
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                                                                                                                                         1998-08-13
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NUMBER OF SEQ ID NOS: 5674
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SEQ ID NO 4388
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                                                                                                                                      CURRENT FILING DATE:
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACTE AND AMINO ACTE SEQUENTES FELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIPEPMINIS POF PIAGNOSTICS AND THEFAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 TKAEHVKLLIPLLEKNKDEIAULYVKEÖGKTLAUAYGEIDKSISFIDYMTSLSMSDK--G 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 PMILPTREFFES-YTKBQFL/ZVOZGTTPWNPFLLMWAWKTAPALVTGNTVVLKTAPSTPLS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 ALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKKVAFTGSTATGRHIYQSAAAG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 LKKVTLELGGRSPNIVFADAFLKKAVQNITLGTYYNSGEVCCAGSFVYVEESIYDKFLEE 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                        84 DPGKALYPLAELTEQPKIVTASTETT. DNGKATSSSRGIVUL. VINYL. - KSSAGFARKTIG 141
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                                                                                                                                                                                                                                                                                 24 LEINNKFVPSKONKTFEVINPSTEEEICHIYFGREDVEEAVQAADAAFSNGSWNGIDPI 83
                                                                                                                                                                                                                                                                                                                              24 LFINNEFIESOSKETMDVINPATGEAFDTITLATEEEVNDATEKSOOA--OLEMERVPOP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 MYVVPFKNEPGIDFSVQTNVERFNEELRKVKAQLGQDIPLVINGFKL--TKTDTFNSVNPA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 TERAKERPASTIPATEQIVOTOKAVIQOASHKOTQOSCIGSMAAKSTASVIPAAAQT
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                                                                                                                          Length 493;
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                                                                                                                          DB 4;
                                                                                                                                                                                                   Conservative 109; Mismatches 181;
                                                                                                                          29.9%; Score 763.5; DB 4; 34.5%; Pred. No. 6.8e-63;
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CUPPENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 59/064, 964
PRIOR FILING DATE: 1997-11-08
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, OMSANISM. Staphylococcus epidermidis
US-09-134-001C-4388
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SEQ ID NO 4451
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                                105 SIETLIONGKAISSSRGD----VDLVINYLKSSAGFADKIDGR-MIDTGRTHFSYTKRQPL 159
                                                                                                                              274 NIVFADAELKKAVQNIILGIYYNSGEVCCAGSRVYVEESIYDKFIEEFKAASESIKVGDP 333
                                                                                                                                                                                                                                                                                                                                                                                                                           63 NTSQLJAKVSKATGDDIFKAFESANHAYG--SWKKWSHKDRAELIJLRVAAIIRRRKEEFS 120
                                                                     121 AIMVYEAGKPWDEAVGDAAEGIDFIEYYARSMMELA---DGKPVLDREGEHNRYFYK-PI 176
                                                                                                        160 GVCGQIIPWNFPLLMMAWKIAPALVTGNTVVLKTAESTFLSALYVSKY1FQAGIFFGVIN 219
                                                                                                                                                                                220 IVSGFGKIVVEALTNHPKIKKVAFTGSTATGRHIYQSAAA ·····GLKKVTLELGGKSP 273
                                                                                                                                                                                                                                                                                         297 IVVDNNVDIDLAAEAIVISAFGFSGUKCSACSKAIVHUDVHDEILEKAIULIUKLILGNI 356
                                                                                                                                                                                                                                                                                                                              334 FDESTFOGAQTSQMQLNKILKYVDIGKNEGATLITGGERLGSKGYFIKPTVFGDVKEDMR 393
                                                                                                                                                                                                                                                                                                                                                   394 IVKEEIFGPVVTVTKFKSADEVINMANDSEYGLAAGIHTSNINTALKVADRVNAGTVWIN 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 KKFTGAQRAACMLKFADLAEKNAEKLARLESLPTGRPVSMITHFDIPNMVSVFRYYAGWA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 NGIDPIDRGKALYRLAELIEQDKDVIASIETLDNGKAISS-SRGDVDLVINYLKSSAGFA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 DK IDGRMI - - DTGRTHFSYTKRQPLGVCGQ I I PWNFPLLIMWAWK I APALVTGNTVVLKTA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 DKIAGKTFPEDNGKPNWRY---EPMGVCAGIASWNATFLYVGWKIAPALAAGCSFIFKAS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 ESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKKVAFTGSTATGRHIY 254
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33.4%, Pred Na. 1 8⊷-55;
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APPLICANT: FOLKERS, OLTO
TITLE OF INVENTION: Compositions and Methods for Fumonisin
FILE REFERENCE: 5718-111
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NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSPQ for Windows Version 4.0
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APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
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Matches 164: Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 LETINKEVPSKONKTFEVINPSTEEETCHTYBTREDDVEEAVOAADRAFSNISWIGDPT HA
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255 OSA-AAGLKKVTLELGGKSPNIVFADAELKKAVONITLGTYYNSGEVYYGAGSK
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                                    APPLICANT: Gasson, Michael J.
APPLICANT: Walton, Nicholas J.
TITLE OF INVENTION: PRODUCTION OF VANILE.N
FILE REFERENCE: 20747/100
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EARLIER FILLING DATE: 1997-04-24
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EARLIER FILLING DATE: 1996-03-23
NUMBER OF SEQ ID NOS: 14
                                                                                                                                     411 EST----YDKFTEEFKAASESTKVG
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Patent No. 6323011
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Published\_Applications\_AA:\* Database :

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/cgn2\_5/ptodata/2/pubpas/US60\_NEW\_FUB\_pcp + /cgn2\_6/ptodata/2/pubpas/US60\_PUBCOMB.pep.\*

# SUMMARIES

	Query				
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	54.9	496	σ	US-09-847-208-59	Sequence 59, Appl
1362.5	53.4	495	CT)	US-09-847-208-11	11,
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	47.8	512	ď	US-10-268-518 2	,,
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1201	47 ;	9.5	c	TIS-09-344-882-20	20
1201	47 1	5.38	c	US-10-293-865-20	20.
1169.5	45.9	534	c	US-09-344 882-24	4.4
1169.5	45.9	534	6	US-10-293-865 24	Sequence 24, Appl
146 5	45.0	50]	7	US-09-444-882-22	ci
146.5	45.0	501	c	US-10-294-865-22	01
1067	41 B	402	c	US 10-268-518-4	Sequence 4, Appli
1056.5	41 4	493	σ	118-10-175-696-21	. 1.
056.5	41.4	493	10	US-09-823-901-9	9
1025	40.2	496	-	08-09-815-242-10450	Sequence lossa, A
1015	39 R	508		US-08-781-986A-5241	Sequence 5241, Ap
984	38 6	υύs	σ	02-10-166-087-4	Sequence 4, Appli
970.5	38.1	496	10	US-09-815-242-5644	Seguence 5644, Ap
970.5	38 1	496	10	US-09-815-242-12657	Soquence 12657, A

	Sequence 1348, Apsequence 13829, A sequence 1254, A sequence 4108, Apsequence 4108, Apsequence 358, Appequence	Sequence 5, Appli Sequence 4, Appli Sequence 12, Appl Sequence 28, Appl Sequence 28, Appl Sequence 4482, Appl Sequence 4037, Appli Sequence 4037, Appli
10 08-09-815-542-12102 10 08-09-815-242-10057 9 08-09-28-552 10 08-09-919-038-143 9 08-10-175-896-17 10 08-10-175-896-17	10 05 09 925 - 330 1248 10 05 09 815 - 242 12475 10 05 09 - 815 - 242 12475 9 05 - 09 - 815 - 242 12476 9 05 - 09 - 178 - 60 - 1024 10 05 - 09 - 178 - 60 - 60 - 60 10 05 - 09 - 178 - 60 - 60 10 05 - 09 - 178 - 60 - 60 10 05 - 09 - 178 - 60 - 60 10 05 - 09 - 178 - 60 - 60 10 05 - 09 - 178 - 60 - 60 10 05 - 09 - 178 - 60 - 60 10 05 - 09 - 178 - 60 - 60 10 05 - 09 - 178 - 60 - 60 10 05 - 09 - 178 - 60 - 60 10 05 - 09 - 178 - 60 - 60 10 05 - 09 - 178 - 60 10 05 - 0	10 US-09-44-5 10 US-09-494-5 10 US-09-733-383-4 10 US-09-722-419-12 10 US-08-976-06-02-28 10 US-09-138-626-6487 10 US-09-138-626-6487 10 US-09-138-626-6487 10 US-09-138-626-6487 11 US-04-138-626-6487 11 US-04-138-626-6483 12 US-04-138-626-6483
6440 6440 518 6487	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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# ALIGNMENTS

FEEULT 1  Sequence 59, Application US/ORA47208  Sequence 59, Application US/ORA47208  Publication No. US20330082190A1  FabelEcation No. US20330082190A1  APPLICANT: Saxon, Andrew  APPLICANT: Saxon, Andrew  APPLICANT: Exb. Dacocheng  TITLE OF INVENTION: 19E-MEDIAIED ALLERGIC DISEASES  FILE PEFFENCE. USC/OR2A  CURPENT APPLICATION VORSE US/OP/847,208  SOFTWARE: PASSED FOR WINDOWS VORSEON 4.0  SEQ ID NO 59  TENOTIFE OF INVENTION NORSE US/OF/847,208  TYPE: PRT  CORANISM: Cladosportum herbarum  US-09-847-208-59	Query Watch Best Local Similarity 53 RM; Pred No 4 4e-98; Matches 263; Conservative 89; Mismatches 135; Indels 2; Gaps	7 IVI.ELENGLEYEGFTGLFINNKEVFSKONKIFEVINFSTEELTHIYEGFEDDVERAVQ :   ::   ::     :	67 AAUGAPSNOSWNSTDFIDEGRALVELAETIEGERIVIASIETIENGRAISSFGLVDLVI 	127 NYLKSSAGFADKIDGRMIDTGPTHESYTKROPLGVGQIIDWNFDLLMMAMKIAPALVIG 1	187 NIVVLKTAESTPLSALYVSKYTPSACILPOVINTVSGFOK LVVEALTNHFK IKKVAETGS 
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425 GLAAGTHTSNINTALKVADRVNAGTVWINTYNDFHHAVPROGFNASGLGREMSVDALONY 4H4
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Publication No. US20030077589A1
                                                                                                                                                                                                                                                                                          KRAETZSCHMAR, JOERN
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                                                                                                                                                                                                                                                                                        APPLICANT: KRAETZSCHMAR, JC APPLICANT: KREFT, BERTHOLT
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                                                                                                           480 IUTKTVSIRI, 489
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US-10-268-518-2
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                                                                                                                                             306 RVYVEESIYDKFIEEFKAASESIKVGDPFDESTFQGAQTSQMQLNKILKYVDIGKNEGAT 365
                                                                                      362 RVYVQESTYDKFVQKFKEKAQKNVVGDPFAADTFQGPQVSKVQFDRTMEYTQAGKDAGAT 361
                                                                                                                                                                                              426 LAAGIHTSNINTALKVADRVNAGTVWINTYNDEHHAVPFGGENASGLGREMSVDALQNYL 485
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84, Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF TITLE OF INVENTION: 19E-MEDIATED ALLERGIC DISFASES FILE REFERENCE: UC67.002A
53 4%; Soore 1362 5; 54.3%; Pred No. 2.6e
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CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09847208
Publication No IS20030082190A1
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ORGANISM: Alternaria alternata
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APPLICANT: Zhu, Daocheng
                                                                                                                                                                                                                                                                                                       482 QTKTVSIRL 490
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                                                                                                                                                                                                                                                                     486 OVKAVRAKL 494
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Best Local Similarity
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92 DALSKGRIJJAQLADIVEKDKATIJAALETMOTGKPFIJJAFFIDJEGCTRTIRYFAGWADKT 151
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APPLICANT: SCOTTI, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETHIOSIS
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50.4%; Pred. No. 2.2e-84;
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CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
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TITLE OF INVENTION: MOVEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTION: METHORS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.8%, Score 1218 5; DR 9; Length 512; Best Local Similarity 50.4%; Pred No. 2 26-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84; Mismatches 149; Indels
                                                               TITLE OF INVENTION 0136. A HUMAN ALBERTOE DEHYDROCENASE
TITLE OF INVENTION FAMILY MEMBER AND USES THEREPOR
FILE REFERENCE: MPIO1-234PIRM
                                                                                                                                   CURPENT APPLICATION WIMBER US/10/268,518 CUPPENT FILLNS DATE: 2002-10-10 PRICE PRICE TO DATE: 2002-10-10 PRICE FLING DATE: 2001-10-16 NUMBER OF SEQ ID NOS-10 SOFTWAPE: PastSEQ for Windows Version 4.0
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Gorbatcheva, Bella
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// Publication No. US20030100034A1
// GENERAL INFORMATION:
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                                             APPLICANT: Hunter, John Joseph
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Zhao, Xumei
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                                                                                                                                                                                                                                                                                                            LENGTH 512
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8] PPIPPGKAL/PELAELLEGUKEVIASTETLONGKA+1SSSRAT/VOLVINYLKSSAGFADKI 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.8%; Score 1218.5; DB 9; Length 512; 50.4%; Pred No. 2.2e-84; (ive 84; Mismatches 149; Indels 3;
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
                        FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 455
SÜRTWARE: FastSEQ for Windows Version 4
                                                                CURRENT FILING PARE TOTAL 17.25

PRIOR APPLICATION NUMBER: 60/307, 982

PRIOR FILING DATE: 2001.07-25

PRIOR PELICATION NUMBER: 60/314,356

PRIOR PELICATION NUMBER: 60/314,356

PRIOR PELICATION NUMBER: 60/314,746

PRIOR APPLICATION NUMBER: 60/311,746

PRIOR APPLICATION NUMBER: 60/311,746

PRIOR APPLICATION NUMBER: 60/311,746

PRIOR APPLICATION NUMBER: 60/311,746

PRIOR PILING DATE: 2001.12.12

PRIOR PILING PATE: 2001.12.12
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; Patent No. USESSESSESTA1
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Wurtele, Eve S
Oliver, David J
Behal, Robert
Schnable, Patrick S
Ke, Jinshan
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Allred, Carolyn C
Fatland, Beth
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Best Local Similarity 50.4%
Matches 240; conservative
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CURRENT APPLICATION NUMBER OF US/10/293,865

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APPLICANT: Wen, Tsui-Jung TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and TITLE OF INVENTION: Acetyl CoA Levels in Plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 GRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAWKIAPALVTGNTVVLKTAESTPLS 200
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48.9%; Pred. No. 5e-83;
tive 82; Mismatches 159, Indels
                                                                            PILE REFERENCE: 201573
CURRENT APPLICATION NUMBER: US/09/344,882
CURKENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/090,717
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                                                                                                                                                                    1998-06-26
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APPLICANT: Lutziger, Isabelle
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Wen, Tsui-Jung
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APPLICANT: Johnson, Jerry L
APPLICANT: Allred, Carolyn C
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Oliver, David J
Behal, Robert
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des 233; Conservative
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NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                               SEQ ID NO 20
LENGTH: 518
                                                                                                                                                                                                                                                                               TYPE: PRT
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APPLICANT: Jutziger, Isabelle
APPLICANT: Wen, Tsui-Jung
TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Acetyl CoA Levels in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                58 TOLLINGNEVDSASGKTEPTLDPRTGEVIAHVAEGDAEDINHAVKAARTAFDEGPWEKMS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 PIDRGKALYRLAELIEODKDVIASIETLDNGKAISSS-RGEVUNGEVINYEKSSAGFADKID 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 ALYVSKYTPQAGIFPGVINIVSSFGKIVVEAITNHFKIKKVAFTSSTATGPHIYQSAA-A 259
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CURRENT APPLICATION NUMBER: US/09/344,882
CURRENT FILING DATE: 1999-06-25
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PRIOR FILING DATE: 1998 06-26
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 3.1
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Patent No. US26020162137A1
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Wurtele, Eve S
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APPLICANT: Lutziger, Isabelle
APPLICANT: Wen, Tsui-Jung
TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Asteryl CoA Levels in Plants
                                                                                                                                                                                                                                                                                         6 MTVPIKLPNGLEYEQPTGLFINNKFVPSKQNKTFEVINPSTEEEICHIYEGREDDVEEAV 65
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                                                                                                                                                                                                 45.9%; Score 1169.5; DB 9; Length 534; 48.5%; Pred. No. 1.2e-80;
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CHPPENT APPLICATION NUMBEP- HS/10/293,865
CUPPENT FILINS DATE: 2002-11-13
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PRIOR APPLICATION NUMBER: US 09/344,882
PRIOR FILLING DATE: 1999-06-25
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Oliver, David J
Rehal, Robert
Schnable, Patrick S
                                                                                                                                 ORGANISM: Arabidopsis Thaliana
PRIOR FILLING DATE: 1998-06-26
NUMBER OF SEQ 1D NOS: 38
SOFTWARE: Patentin Ver. 2.2
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Johnson, Jerry L
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APPLICANT: Wurtele, Eve S
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48.5%; Fred. No. 1.2e-80;
tive 77; Mismatches 167; Indels 9;
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CUPPERNT APPLICATION NUMBER: US/09/244,882
COMPENT FILING DATE: 1999-06-25
PPIOP APPLICATION NUMBER- US 6//090,717
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ARR: US 60/090,717
PRIOP APPLICATION NUMBER HS 40/090,717 PRIOR PLIANS HARF. 1998-06-26 NUMBER OF SEQ ID NOS: 38 SOFTWARE PATENTIN VOT 3.1
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APPLICANT: Johnson, Jerry L
APPLICANT: Allred, Carolyn C
APPLICANT: Ealland, Beth
APPLICANT: Lutziger, Isabelle
APPLICANT: Wen, Tsul-Jung
TITLE OF INVENTION: Materials an
TITLE OF INVENTION: Acetyl CoA L
FILE PEFERENCE: 201573
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Oliver, David J
Behal, Robert
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Matches 238; Conservative
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PEPLICANT: Wen, TSUL-JUN-TSUL-LUTSUL TSULTANT WEN, TSUL-LUN-TSULTANT AGENTY AGENTY AGENTY AGENTY TITLE OF INVENTION: AGENTY COA Levels in Plants
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                       45.0%; Score 1146.5; DB 9; Length 501; 47.1%; Pred. No. 6 2e-79; tive 95; Mismatches 154; Indels 7;
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PRIOR APPLICATION NUMBER: US 09/344,882
PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/10293865 Publication No. US20030106090A1 GENERAL INFORMATION:
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APPLICANT: Oliver, David J
APPLICANT: Behal, Robert
APPLICANT: Schnable, Patrick S
                                                                                                                                       ORGANISM: Arabidopsis Thallana
  1998-06-26
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Johnson, Jerry L
Allred, Carolyn C
PRIOP FILING DATF: 1998-06-2
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.2
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Matches 228; Conservative
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                                                                                                                                                             US-09-344-882-22
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                                                                  SEQ ID NO 22
LENGTH: 501
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70. PAESNGSWIGTDPTDPGRALYPLAELTELJOKOVIASTETTONGRATISSEP GOVDLYTNY 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        667 TEGGERUGSKGYFIKPTVFGOVETOMFTOVEFTFODVVTVTKFKSADEVINMANOSEYGL 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 TVVLKTAESTPLSALYVSKYTPGACTPFOVINTVSOFOKTVVEATTNHFETERVAFTOST
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TITLE OF INVENTION: 9136, A HUMAN ALDEHYDE DEHYDROGENASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREFOR
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CHEMENT APPLICATION NUMBEE: US/10/268,518
CURRENT FILING DATE: 2002-10-10
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PRIOR PLINGATION NUMBER: US 40,000,717
PRIOR PLING DATE: 1998-06-26
NUMBER OF SEQ ID NUS: 48
SUFTWARE: Patentin Ver. 3.1
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PRIOR FILING DATE: 2001-10-16
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                                                                                                                                                                          ORGANISM: Arabidopsis Thaliana
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general information:
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ORGANISM: Artificial Sequence
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Matches 228; Conservative
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                                                                                                      SEQ ID NO 22
LENGTH: 501
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                                                                                                                                                        TYPE: PRI
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NUMBER OF SEQ 1D NOS. 31 SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 21

PRIOR FILING DATE: 2001-06-15 PRIOR APPLICATION NUMBER: 60/211,727

PRIOP FILING DATE: 2000-06-15

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87 KALYRLAELIEQDKDVIASIETLDNGKAISSSRGDVDL--VINYLKSSAGFADKIDG--R 142
                                                                                                                                                                                                               61 RILRKIADLIEEREDEIAALETIDLGKPIAEAKGDTEVGPAIDEIPYYAGWAPKIMGERP 120
                                                                                                                                                                                                                                                         143 MIDT----GRTHFSYTKRQPLGVCGQITPWNFPLLMWAWKTAPALVTGNTVVLKTAESTP 198
                                                                                                                                                                                                                                                                                                                                         199 LSALYVSKYIPGAG---IPPGVINIVSGFGKIVVEALTNHPKIKKVAFTGSTATGRHIYQ 255
                                                                                                                                                                                                                                                                                                                                                                                                                        256 SAAA-GLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGEVYYYAGSLYYVEESIY 314
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                                                                                   29 KFVPSKQNKTFEVINPSTEEELC-HIYEGKEDDVEEAVQAADKAFSNGSWNGIDPI-DRG 86
                                                                                                                             1 EWVDSASGKTFEVVNPANKGEVIGRVPEATAEDVDAAVKAAKEAFKSGPWWAKVPASEPA 60
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APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: NOVEL HIMAN ENZYME FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 10448-193001
                                            Indels 28,
Query Match 41.8%; Score 1067; 186 9; Longth 492; Best Local Similarity 46.9%; Pred No. 6.5e-73; Matches 231, Conservative 98, Mismatches 136; Indels 20
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PRIOR APPLICATION NIMHER: 10:067, KER
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60,266,140
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FILING DATE: 2001-05-21
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APPLICATION NUMBER: 60/205,675
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APPLICATION NUMBER: 09/823,901
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; Publication No. HS200 (0092658A)
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US-10-175-696-21
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                                                                                                                                                                                                                                                                                                                                                                                                                               143 MIGT----GRIHESYTKEGEFGVGGIIPWNFPLLMWAWKIAPALVIGNIVVLKIAESIP 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 DKFIEEFKAASESIK-VGDFFLEST-FWGAQTSWWQLNKIL-KYVDIGKNEGATLITGGE 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 PLGSK-----GYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEYGL 426
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                                                                                                                                                                                                                                                                                           1 EWVDSASGKTFEVVNPANKGEV1GKVPEATAEDVDAAVKAAKEAFKSGPWWAKVPASEKA 60
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Best Local Similarity 46.8%; Fred. No. 4.1e-72,
Matches 231; Conservative 98, Mismatches 136, Indeks 29;
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Fateri No. US.DGCC001807A1
GENERAL HOROMATION:
APPLICANT: Meyers, Rachel
TITLE OF INVENTON: DEHYCEGENASES AND USES THEREOF
FILE PERVENCEN: DEHYCEGENASES AND USES THEREOF
FILE PERVENCE: 10448-036001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURPENT APPLICATION NUMBER: US/09/823,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER IS 60,7193,920
                                                                                     OTHER INFORMATION COURSESSUS Sequence
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                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                199 LSALYVSKYIPQAG---IPPGVINIVSGFGKIVVEAITNHPKIKKVAFTGSTATGPHIYÖ 255
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                                                                                                                                                                      1 EWVDSASGKTFEVVNPANKGEVIGRVPEATAEDVDAAVKAAKEAFKSGPWWAKVPASEPA 60
                                                                                                                                  29 KFVPSKQNKTFEVINPSTEEELC-HIYEGREDDVEFAVQAADRAFSNGSWNGIDPI-DRG 86
                                                                                                  Gaps
                                                    Query Match 41.4%; Score 1056.5; DB 10; Length 493; Best Local Similarity 46 %; Prod No. 4 1e-72; Matches 231; Conservative 98; Mismatches 136; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CUKKENT FILING DATE: Z001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10550, Application US/09815242 Patent No. US20020061569A1
OTHER INFORMATION: consensus sequence
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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FILING DATE: 2000-11-27
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Zyskind, Judith W.
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480 LEEYTEIKTVTIRL 493
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APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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US-09-815-242-10550
                  US-09-823-901-9
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24 TESNLLLKTADLIEENQEHLAMVETLDNGKPLRETQSIDVPASADHFRYFASV1RGEEGS 133
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                                                                                                                       NUMBER OF SEQ ID Nos: 14110
SGFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10550
                     PRIOR FILLING DATE: 2000 12-22
PRIOR APPLICATION NUMBER: 60/269,408
PRIOR FILLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 43,6%;
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Search completed: June 24, 2003, 10:47:03 Job time : 24,9275 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

(Without alignments) 1780 862 Million cell updates/sec June 24, 2003, 10:11:00 ; Search time 179,207 Seconds Run on.

US-09-830-751-2 2550

MSVDALQNYLQVKAVPAKLD 495 1 MSHLPMIVPIKLPNGLEYEQ... Perfect score: Sequence.

Scoring table:

RIOSHM62 Gapop 10 0 , Gapext 0.5

4559144 Total number of hits satisfying chosen parameters:

4569144 seqs, 5447+4110 residues

Searched:

Minimum DB seq length. O

Maximum DB seq jength: Zunuununu

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 08

Database ·

/rgn2\_6/ptodata/1/paa/pcrus\_comm.pep.\* /rgu2\_6/ptcdata/1/paa/US06\_comm.pep.\* /cgu2\_6/ptcdata/1/paa/US07\_comm.pep.\* Pending\_Patents\_AA\_Main·\*

/ Cydic\_A/Products// Pass/NS(0.10MH pop. 1. Cydic\_A/Products// Pass/NS(0

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/cgn2\_6/ptodata/1/paa/CS150\_coMb.pcp.\* /cgn2\_6/ptodata/1/paa/US10\_coMp.pp:\* /cgn2\_6/ptodata/1/paa/US60\_coMp.pcp:\* /cgn2\_6/ptodata/1/paa/US60\_coMh.prp.\* 6/ptodata/1/paa/US049\_cOMB\_pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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bescription	Sequence 47094, A	Sequence 22438, A	Sequence 38066, A	Sequence 105395,	Sequence 1749, Ap	Sequence 70612, A
QT	08-09-741-547-094	US-60-360-039-22438	US-09-791-537-38066	US 09-791-537-105395	08-60-360-039-1749	08-09-791-547 70612
DB	21	27	21	2.1	27	5
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Score	2538	2538	1807	1728.5	1728.5	1695
Result No.	7	C1	3	4	S	9

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10 179-131	-69-791-537-	- 60 - 360 - 939 -	-04-741-547-	-680-660-686-	-08-512-853-1	-09-791-537-7	08-612	-09-791-537-	-09-847-208-59	US-09-847-208B-59	-08-612-855-	-08-51	08-512-855	-09-79]-537-	-09-84/-208-	.09	9-80-	09 791	6.60	-00-	0-04-	104-7	2-60-	-10 - 1	-00-	¥ - 014-	-60-412-418-1227	-60-3	3-60-	4-60-	-60-3	P - D - 4	1-60-	-60-360-039-2316	04-24]-542-40	- 04-74] -537 - 6465	US-09-791-537-71773
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APFLICANT: Debe, berek
APPLICANT: Panger, Toseph
IITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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Pred. No. 5e-230;
0; Mismatches 1
                                                                                                                                                                                            FILE REFERENCE, 201/210
CHEFENT APPLICATION NUMBER HS/N9/741,537
CURRENT FILING DATE: 2001 02 22
NUMBER OF SPQ IN NUS: 15,4055
SOFTWARE PARENTN VERSION 3 0
                                   Sequence 47094, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Saccharomyces cerevisiae
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99.88;
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              US-09-791-537-47094
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-791-537-47094
                                                                                                                                                                                                                                                                                                          SEQ ID NO 47094
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SEQ ID NO 38066
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APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REPRENCE: 38-10(52052)A
CURRENT APPLICANTION NUMBER: US/60/360,039
CURRENT PILING DATE: 2002-02-21
                                                             85 EEAVQAADRAFSNGSWNGIDPIDRGKALYPLAEHIEQDKDVIASIETLDNGKAISSSRGD 144
                                            122 VDLVINYLKSSAGFADKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAWKIAP 181
                                                                                                           ALVTGNTVVI.KTAESTPI.SALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKKV 241
                                                                                                                            242 AFTGSTATGKHIYQSAAAGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGEVC 301
                                                                                                                                                                                                           265 AFTGSTATGRHIYQSAAAGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGEVC 324
                                                                                                                                                                                                                                                             362 EGATLITGGERLASKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMAND 421
                                                                                                                                                                                                                                                                                                                                                                       422 SEYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDAL 481
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                 302 CASSPAYVEBSTYDKETEPPRAASPSTRVCHPEDPSTPQCAGEGMGTNRTTRYVDTCKN 361
                                                                                                                                                     * H 7
                                                                                                                                                                                                        362 EGATLITGGERLGSKGYFIKPTVFGDVKEDMKIVKEELFGPVVTVTKFKSADEVINMAND 421
                                                                                                                                                                                                                                 SEYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDAL, 481
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242 AFTGSTATGRH1YOSAAAGD.KKVTDEDGGKSPN1VFADAED.KKAVON11161YYNSGEVC
                           82 DVAVDAABKAF KGSWSTADPAIRGKALWNLAELLEAHKDTLAATESLDNGKALQLAQGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1807; 198 21; Length 518;
Pred. No. 5.9e 161;
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tive 72, Mismatches 83,
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CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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GENERAL INFORMATION:
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ORGANISM: Pichia angusta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Debe, Derek
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICHORIAL PROTFINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 ALVTGNIVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKKV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 AFTGSTATGRHIYQSAAAGLKKVTLFLGGKSPNIVFADAELKKAVQNIILGIYYNSGFV^ 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 VALVSKYLRSCGGWADKIYGNVIDTGKNHFTYSIKEPLGVCGQIIPWNFPLLMWSWKIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 27, Length 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                        TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)A
CUPRENT APPLICATION UNIBER '18/50/346,039
CUPRENT FILING DATE: 2002 02 21
NUMBER OF SEO ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                          67.8%, Score 1728.5, DB 27
64.8%; Pred. No. 1.6e-153;
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CURRENT APPLIANTION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 70612, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81;
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                                             Chen, Xianfeng
Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310, Conscivative
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                         APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
  GENERAL INFORMATION.
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                                                                                                                                                                                                                                                                                      SEO ID NO 1749
                                                                                                                                                                                                                                                                                                          LENGTH: 520
                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
FILLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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121 DSEYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDA 480
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                                                                                                                                                                                                                                                          Sequence 105395, Application US/09791537
GENERAL INFORMATION:
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62 EEAVQAADRAFSNGSW--NGIDPIDRGKALYRLAELIEQDKDVIASIETLDNGKAISSSK 119
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APPLICANT: GREENE, JONATHAN R.
TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC ACIDS AND POLYPEPTIDES,
TITLE OF INVENTION: AND USES THEREFOR
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                                                                                                                                  66.5%; Score 1695; DB 21; Length 519; 63.7%; Pred. No. 2.3e-150;
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CURRENT FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 10194
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GENERAL INFORMATION:
                                                                ; ORGANISM: Saccharomyces cerevisiae US-09-791-537-70612
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APPLICANT: SHIMER JR., GEORGE H.
APPLICANT: KESSLER, MARCO
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                                                                                                                                                        Best Local Similarity
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SEQ ID NO 70612
LENGTH: 519
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREDF
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                                                                                                                                         86 AVEAAQAAYHNG-WAQGPPEQRSKVLFKLADL.LEENAELLAOLETWDNGKSLONARGDVA 144
                                                                                                                                                                                          124 LVINYLKSSAGFADKIDGRMIDTGRTHFSYTKROPLGVGG011PWNFPLLMWAWKIAPAL 183
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4 IDMTVPTKLPNGLEYEQPTGLETNNKFVPSKONKTFEVTNPSTEEDTCHTYEGREDDVEE 6.4
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<del>- .</del>
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CURRENT APPLICATION NUMBER: 08/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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; Sequence 26771, Application US/09791537
; GENERAL INFORMATION:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
TITLE OF INVENTION. EXPRESSION OF MICRORIAL PROTEINS IN FLANTS FOR PROJUCIION OF TITLE OF INVENTION. EXPRESSION OF TITLE OF INVENTION. EXPRESSION OF TITLE OF INVENTION. EXPRESSION OF TITLE OF TAPPLICATION. WIMBER: US/60/360,039
FULD REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
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2002 02 21
NUMBER OF SEQ ID NOS: 47374
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54.8%; Pred. No. 2e-127;
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THPRE DIMENSIONAL STRUCTUPES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
                         300 VOCAGSRVYVERSIYDKFIFEFKAASESIKVGDPFDESTFQGAGFSQMQLNKILKYVDIG 459
                                                                                                                                                                                                                                                               360 KNEGATLITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMA 419
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                                                                                     241 VAFTGSTATGRHIYQSAA-AGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGE
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54 8%; Pred. No. 28-127;
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92; Mismatches 128, Indels
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
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TITLE OF INVENTION: EXPRESSION OF MICRORIAL PROTEINS IN PLANTS FOR PRODUCTION OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 RGIYLLKIJADILEKNIJDIJAAVESIJNGKSTIMAKODVGAVVGTIRYYGGWADKIJGKIT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTGRTHFSYTKRQPLGVCGQ11PWNFPLLMMAWK1APALVTGNTVVLKTAESTPLSALVV 204
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                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Recombinant Cladosporium Herbarum
                     PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                           LOCATION: (1)..(498)
OTHER INFORMATION: unsure at all Xaa locations
                                 FILE REFERENCE: 38-10(52052)
CURRENT APPLICATION NUMBER: 2002-92-21
NUMBER OF SEQ. ID NOS: 47374
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GENERAL INFORMATION:
APPLICANT: Achatz, Gernot.
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APPLICANT: Hirschwehr, Reinhold
                                                                                                                                                                                                                                                                                                                                                                                                            88;
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                                                                                                                                                                                TYPE: PRT
ORGANISM: Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117
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Unger, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                      NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                      US-60-360-039-3846
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                                                                                                                                     SEQ ID NO 3846
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                                                                                                                                                             LENGTH: 498
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                                                                                                                                                                            APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILLES AND FAMILY MEMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VEEAVQAADRAFSNGSWNGIDPIDRGKALYRLAELIEQDKDVIASIETLDNGKAIS-SSR 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 KVAFTGSTATGRHI-YQSAAAGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSG 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 KLAFTGSTEVGKSVAVDSSESNLKKITLFLGGKSAHLVFDDANIKKTLPNLVNGIFKNAG 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 HFDTAEPVKITLPNGLTYEQPTGLFINNKFMKAQDGKTYPVEDPSTENTVCEVSSATTED 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.6%; Score 1443.5; DB 21; Length 501; 54.7%; Pred. No. 1.3e-126;
Live 92; Mismatches 128; Indels 5,
                                                                                                                                                                                                                                               TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/791,537
                                                                                                           Sequence 70619, Application US/09791537
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Saccharomyces cerevisiae
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NUMBER OF SEQ ID NOS: 153055
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485 EVYHAYTEVKAVRIKL 500
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APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
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                                                                                                                                                        APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                    FILE REFERENCE: 261/210
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es 272; Conservo
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                                                                                 08-09-791-537-70619
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Lechenauer, Erich
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477 ALENYTQIKTVHYRL 491
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                                                                                                                        APPLICANT: Bionomix, Inc.
                                                                                                                                          Debe, Derek
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es 276, Conserv
                                                                  US-09-791-537-73644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 4%, Shore 1412.5; EB 10; Length 497; 54.5%; Pred. No. 1e-123; tilve 88, Mismatches 132, Indels 5;
                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 6530-021-999
                                                                                                                                                                                                                      PRIOR APPLICATION (ATA:
APPLICATION NIMBER POT/AT94/00120
FILING DATE: 02-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      US/08/612,859
                                                                                                                                     SOFTWARE: FastSEO Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           AGENT INFORms E Friebel, Thomas E Friebel, Thomas E Friebel, Thomas E
                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE
INFOPMATION FOR SEG ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 ALONYLQVKAVRAKL 494
                                                                                                 IBM Compatible
                                                                                                                                                                                      26-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                           497 amino acids
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                                                                                     Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHAFACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                        DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
OFIGINAL SOUPCE
                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                        APPLICATION NUMBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                    OPERATING SYSTEM:
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                                                                                                                                                                                                           CLASSIFICATION:
New York
                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                            FILING DATE:
                                                                                     MEDIUM TYPE:
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                                                                                                     COMPUTER:
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                                 COUNTRY:
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Matches
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 EVELVINYLKSSARFARFIRSBARFRRESPIRBESPIRBERVESQIIPWNFPILMMAWKIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 DLANSIGCLEYYAĞMADKINĞQIIDINPETLIFTEREVGVÇĞQITPMNEPLLMMSWKIĞ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 PALVTGNTVVLKTAESTPLSALYVSKYIPQASIPPGVINIVSGFSKIVVEAIINHPKIKK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 VCCAGSRYYVERSIYUKFIEEFKAASESIKVGLPFDESIF9GAQITS9MQLNKILKYVDIG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 KNEGATLITGGERLGSKRYFIKPTVPGLVKELMMIVKEFIFGPVVTVTKFKSADEVINMA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSHLPMTVPIKLPNGLEYEQPTGLFINNKFVPSKQNKTFEVINPSTEEEICHIYEGREDD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSDLFTT1ETPV----IKYEQPLGLF1NNEFVKGVEGKTFQVINPSNEKVITSVHEATEKD 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 VAETGSTATGPHTYQSAA-AGLKKVTLELGGKSPNIVEANAELKKAVQNLTLGTYYNSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.4%; Score 1412.5; DB 21; Length 497; 54.5%; Pred. No. 1e-123; Live 88, Mismatches 132, Indels 5;
                                                                                                                                                                                                                               FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
Sequence 73644, Application US/09791537
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08612853
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-02-22 NUMBER OF SEQ ID NOS: 153055
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Simon, Birgit
Unger, Andrea
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.0
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67 AADRAFSNGSWNGIDPIDRGKALYRLAELIEQDKDVIASIETLDNGKAISSSRGDVDLVI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 NYLKSSAGFADKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAWKIAPALVTG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 NTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEALTNHPKIKKVAFTGS 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 RVYVQESIYDKFVQKFKERAQKNVVGDPFAALJFQQPQVSKVQFDKIMEYIQAGKDAGAT 361
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tive 89; Mismatches 135; Indels
              TITLE OF INVENTION Recombinant Cladosporium Herbarum
TITLE OF INVENTION: Altergens
NUMBER OF SEQUENCES: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Cladosporium herbarum
DEVELOPMENTAL STAGE: Spores and vegetative hyphae
US-08-612-853-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 29,258
REFERENCE/TOCKET NUMBER: 6550-021-999
                                                                                               ADDRESSEE: Fennie & Edmonds LLF
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                           ....ск: US/08/612,853
26-FEB-1996
7N: 536
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/AT94/00120 FILING DATE: 02-MAK-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
APPLICANT: Hirschwehr, Reinhold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                          1BM Compatible
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                                                                                                                                                                                            ZIP: 10036-2711
COMPUTER READARLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212-869-9741
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                                                       NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Friebel, Thoma
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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Best Local Similarity
Matches 263; Conserval
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                                                                                                                                       New York
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                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO FRACMENT TYPE:
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                                                                                                                  STREET:
CITY: No
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Job time : 182,207 sees

466 LLIGGERLGSKGYFIKPTVEGDVKEDMETVRELFGPVVTVIKFKSADEVINMANDSEYG 4.25

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GenCore version 5.1.6
Copyright (c) 1994 - 2004 Compages Lid
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OM protein protein search, using sw model

Run on: June 24, 2003, 10:14:35 ; Search time 53 5476 Seconds

(without alignments) 2375.712 Million cell updates/sec

MSVIJALQUYLQVKAVPAKED 495

Title: US-09-830-751-2 Perfect score: 2550

Sequence: I MSHLPMTVPIKLPN3LEYEg Scoring table. BLOSUM62

Searched: 1171708 segs, 257189365 residues

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1171708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Fending\_Fatents\_AA\_New:\*

1: /cgn\_\_fyfredata/2/payHs7in\_NEW\_TOME pep \*

2: /cgn2\_fyfredata/2/payHs7in\_NEW\_TOME pep \*

3: /cgn2\_fyfredata/2/payHs7in\_NEW\_TOME pep \*

4: /cgn2\_fyfredata/2/payHs7in\_NeW\_TOME pep \*

5: /cgn2\_fyfredata/2/payHs7in\_NeW\_TOME pep \*

6: /cgn2\_fyfredata/2/payHs7in\_NeW\_TOME pep \*

7: /cgn2\_fyfredata/2/payHs1in\_NEW\_TOME pep \*

6: /cgn2\_fyfredata/2/payHs1in\_NEW\_TOME pep \*

7: /cgn2\_fyfredata/2/fyfr

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result No.	Score	Query	, Length	DB	ID	Description
1	0.55%	0.007	9.4	٠,٠	S-09-830-751-	Sequence 2, Appli
Cŧ	2538	6		ď.		Sequence 22438, A
ĸ	1728 €		1 520	¥	-10-369-493-	1749, 7
4	Ę,			9	US-10-369-493-22495	
5	۲.	56.2	4	¢	US-10-164-441-3846	
9	1274.5	50.0	519	9	US-10-219-051B-6969	
7		50.0		9	US-10-219-051B-6973	6973,
80	1254.5	49.2	53	9	-10-369-493-	
s		+ 7	. 6.17	Œ	ns-10 219 0518-6971	Sequence 5'471, AF
10	1253 5	40		ت.	US-10-219-051B-6975	Sequence 6975, Ap
11	1202	-	900	tı-	0.5-04-444-016-1065-4	
12	1252 4	49.7		ď.	HS-10-369 493 23162	23162,
13	1243 5	4 x	4 5.1h	٤.	115-10-464-4655	3555, A
14	1239.5	48.6	51	7	US-60-453-135-14871	14871,
15	1239 5	4.8	7.	7	TIS-60-453-050-14871	14871,
16	1239.5	48.6	51	7	US-60-466-412-14871	Sequence 14871, A
17	1236	α.	5.4	ۍ	US-10 369 493.5715	5715, A
18	1234.5	4.8.4		œ	065-	59042,
19	1231	48	CH (M)	r,	1026-910-646-60-80	9207,
20	1230	48.2		ď	115-09-724-676-64510	64510,
21	1230	48		ľ	US-04-724-676A-64510	64510,
C1	1226.5	48.	299	Ð	US-10-425-114-49963	Sequence 49963, A
53	1226	48	1.44	,T.	08-10-425-114-51294	51294,
54	1225.5	48.1		5	US-09-830-751-4	4
52	1224		C 813	φ.	US-10-437-953-112958	Sequence 112958,
55	1222.5	47.5	9 518	Œ)	US-10-144-779-472	4

27	1218.5	47.8	512	Н	PCT US02-32971-2	Sequence 2, Appl:
œ	1218.5	47.8	512	w	08-10-268-518-2	Sequence 2, Appli
7	1216.5	47.7	474	7	119-60-453-135-13150	Sequence 13160,
3.0	1215.5	47.7	479	7	US-60-453-050-13160	Sequence 13160,
3.1	1215.5	47.7	479	۲		Sequence 13160,
(4	1215	47.6	433	<i>ر</i> .	77 10 369 493 12932	Sequence 12932,
33	1207.5	47.4	533	ټ.	US:10-424-599:264414	Sequence 264414,
<b>*</b>	1205.5	47.4	4. X	ŭ,	PS 10 (F4-494-17129	Seguence 17129, A
35	1501	47.1	538	۵	US-19-293-865-20	sequence 20, Appl
9	1195.5	46.9	5.53	ع	1)5-10-437-963-131978	Sequence 131978,
37	1195	46.9	550	•	US-10-438-246-8835	Sequence 8835, Ap
38	1182.5	46.4	200	Œ.	US-10-219-051B-12834	Sequence 12834,
س س	S	41- 4	C	٠	8887[-8]50-8[7-6]-80	Sequence 12838,
=	11 × ≥ €	4	Ü	ď.	115-04-724-575-54517	Sequence 64517,
	1182.5	46.4	501	S	US-U9-724-676A-64517	sequence 64517,
11	1181.5	46.3	4	(پ	US-10-282-122A 46958	Sequence 46958,
₹*	11/4.5	46.1	484	٥	US-10-369-493-16430	Sequence 16430,
14	1174.5	46.1	540	9	US-10-424-599-230301	Sequence 230301,
5	1173.5	46.0	58 83 83	9	US-10-437-963-131981	Sequence 131981,

### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DVDLVINYLKSSASFADKIDSPMIGGSPHESYTKROPDSVOSQIIPWNEPLAMMAMKIA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSHLPMIVPIKLPNGLEFFQPTGLFINNKFVPSKQNKTFEVINPSTEFFICHTFFGD 60
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                                                        APPLICANT: Suthers, Patrick F
APPLICANT: Cameron, bouglas C.
TITLE OF INVENTION - Enclored of A Hydroxypropically A 1d in Borombinant
TITLE OF INVENTION: Organisms
TITLE OF INVENTION: Organisms
TITLE OF THE PREPRENCE OF 36617
CHERENT AFFILM OF WHAREF 185.092/818,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 PALVIGNIVVLKIAESIPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKK
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Best Local Similarity 100.0%, Prod No 2e-197;
Matches 49%, Conservative 0, Mismatches 0,
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: h0/151,440
PRIOR FILIN; DATE: 1999-08-30
PRIOR APPLICATION NUMBER: PCT/US00/23878
PRIOR FILING DATE: 2000-08-30
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Saccharomyces cerevisiae
                  ; Sequence 2, Application US/09830751
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver 2 1
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US-09-830-751-2
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                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                             ; Sequence 1749, Application US/10369493
; GENERAL INFORMATION:
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                                                                                                                                                                                                   APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
                       482 ONYLOVKAVRAKLD 495
                                                             505 QNYLQVKAVRAKLD 518
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US-10-369-493-1749
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301 CCAGSRVYVERSIYDKFIREFKAASESIKVGDPFDESTFQGAQTSQMQLAKILKYVDIGK 360
                                        361 NEGATLITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMAN 420
                                                           421 DSEYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDA 480
                                                                                                                                            62 BEAVQAADRAFSNGSWNGIDPIDRGKALYRLAELIEQDKDVIASIETLDNGKAISSSRGD 121
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 67/360,039
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ 1D NOS: 47374
                                                                                                                                                                                                                                                                                                                                         Sequence 22438, Application US/10369493 GENERAL INFORMATION:
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ORGANISM: Saccharomyces cerevisiae
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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APPLICANT: Gao, Yongwoi
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICPORTAL PROPERTS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 HLPMTVPIK--LPNGLEYEQPTGLFINNKFVPSKQNKTFEVINPSTEEEICHIYEGREDD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.8%; Pred. No. 1.2e-108; ive 92, Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.9%; Score 1452; DB 6;
                                                                                                                                                                                            FILE REFERENCE: 38-10(52052)B
CUPPENT APPLICATION NUMBER: US/10/369,493
                                                                                                                                                                                                                                            CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
, ORGANISM. Sacchalomyces celevisiae
US-10-369-493-22495
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 47374
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Matches 272, Conservative
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GENERAL INFORMATION:
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APPLICANT: The General Hospital Corporation doing business as Massachusetts Genera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 DTGRIHESYTKROPLGVCGOJIPWNFPLLMWAWKIAPALVTGNTVVLKTAESTPLSALYV 204
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                                                                                                                                                                                                                                                                                                                                 Length 498;
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TILLE OF INVERTION: Nucleocitide sequences involved in pain
FILE REFERENCE: Led 35693 Foreign Countries
CURHENT APPLICATION NUMBER: US/10/219,051B
PRIOR APPLICATION NUMBER: 2093-05-09
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR FILING DATE: 2001-08-14
                                                                                                                                                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                              88; Mismatches 114,
                                                                                                                                                                                                                                                                                                                              56.2%; Score 1432.5; DB 6 54.1%; Pred. No. 4.4e-107;
                                                                                                                                                                                                                                  ; LOCATION: (1). (498)
; TTHEP INFORMATION: unsure at all Xaa locations
US-10-369-493-3846
CUPPENT APPLICATION NUMBER: US/10/369,493
              CUPPENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3846
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                                                                                                                                                                            ORGANISM; Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                  268, Conservative
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 14715

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PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PALVIGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 KAVKAAQAAFQLGSPWRRMDASDRGRLLYRLADLIERDRTYLAALETLDNGKPYVISYLV 139
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                                                                                                                                                                                                                                                                                24 TSAVPAPN----QOPEVFCNQIFINNEWHDAVSKKTFPTVNPSTGEVICQVAEGNKEDVD 79
                                                                                                                                                                              DB 6, Length 519,
                                                                                                                                                                            50.0%, Score 1274.5; DB 6, Length
50.8%; Pred. No 2 8A-94;
Live 85; Mismatches 146, Indels
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TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: Lea 35693 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/219,051B
CURRENT FILING DATE: 2003.05.09
                                                                                                       DATABASE ACCESSION NUMBER: SWISS-Prof / P11884 DATABASE ENTRY DATE 2002-06-15
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PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
SEQ ID NO 6973
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PPIOP APPLICATION NUMBER: US 60
PRIOR FILING DATE: 2001-11-01
                                                                      ORGANISM: Rattus norvegicus
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                                                                                                                                                                                             Local Similarity 50.83
nes 252; Conservative
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                                                                                       PUBLICATION INFORMATION
SOFTWARE: Perl script
SEQ 1D NO 6969
LENGTH: 519
                                                                                                                                        US-10-219-051B-6969
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                                                          PRT
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APPLICANT: Chen, Xianfenq
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                121 DVDLVINYLKSSAGFADKIDGRMIDTGRTHFSYTKROPLGVGGGIIPWNFPLLMWAWKIA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 QCCCAGSRTFVQEDVYDEPVERSVARAKSRVVGNPFDSRFEQGPQVDEJQFRKIJJ3Y1RS 478
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                                                                                                                                                                                                                                                                                                                          24 TSAVPAPN-----QQPEVFCNQTFINNEWBIAVSKKTFPTVNPSTGEVICQVAEGINEEDVD 79
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                                                                                                                      Query Match
Hest Local Similarity 50.8%: Pred. No. 2.8e 94;
Matches 252, Conservative 85; Mismatches 146; Indels 14: Gaps
Matches 252, Conservative 85; Mismatches 146; Indels 14: Gaps
DATABASE ACCESSION NUMBER: SWISS-Prot / PILRHA DATABASE ENTRY DATE: 2002-06-15
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OTHER INFORMATION: unsure at all Xaa locations
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CURRENT APPLICATION NUMBER: US/10/369,493
CURPENT FILING DATE: 2003-02-28
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PRIOR FILING DATE: 2002-02-38
NUMBER OF ALING DATE: 2002-02-07
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Sleven C.
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SEQ ID NO 12695
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                                                                   US-10-219-051B-6973
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APPLICANT: The General Hospital Corporation doing business as Massachusetts General APPLICANT: The General Hospital / Bayer AG TITLE OF INVENTION: Nucleotide sequences involved in pain FILE REFERENCE: Las ASAGAS FOREIGN COUNTIES CUBRENT APPLICATION NUMBER: US/10/219,051B
                                                                                                                                                                                                                                                                                                                                                                                        300 VCCAGSRVYVEESIYDKFIEEFKAASESIKVGDPFDESTFQGAQTSQMQLNKILKYVDIG 359
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                                                                     63 EAVUAADKAFSNGS-WNGIDPIDRGKALYRLAELIEQDKDVIASIETLDNGKA-ISSSRG 120
                                                                                                   121 DVDLVINYLKSSAGFADKIDGPMIDTGRTHFSYTKPQPLGVGGQIIPWNFPLLMWAWKIA 180
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                       QQFEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVD
                                                                                                                                                                                                                                                                  181 FALVTONTVVLKTAESTFLSALYVSKYIPQAGIPFGVINIVSGFGKIVVEAITNHPKIKK
                                                                                                                                                                                                                                                                                      241 VAFTGSTATGRHIYQSA-AAGLKKVTLELGGKSPNIVFADAFLKKAVQNIILGIYYNSGE
  Indels 11, Gaps
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50 3%, Pred No. 1.46-92;
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DATABASE ENTRY DATE: 2002-06-15
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PRIOR APPLICATION NUMBER: US 60/345,382
PRIOR FILING DATE: 2001-11-01
PRIOR PRILICATION NUMBER: US 60/333,347
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
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Best Local Similarity
                       TO TOAVPAPN
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                                                                                                                                            1 VSLTAPNGHKYEQPIGLFINNEFVASKSGEKFATVNPQVCISGDARXXLYSNIRASDEEE
                    Pred. No. 1.2e-92;
88; Mismatches 151; Indels 41; Gaps
49.2%; Score 1254 5; DR 6; Tength 532; 47.0%; Pred. No. 1.2e-92;
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FILE PEFERENCE: LeA 3569 Fort-ign Countries
CUPERTA APPLICATION NUMBER: 18/10/219,051F
CUPERT FILLIOATEN 2003-05-09
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                                                                                            8 VPIKLPNGLEYEQPTGLFINNKFVPSKQNKTFEVINP---
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DATABASE ACCESSION NUMBER: SWISS-Prof / P05091
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PRIOR FILING DATE: 2001 08:14
PRIOR APPLICATION NUMBER: US 60/346,382
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS-14715
SEPTAMARE: Perl Script
SEQ ID NO 6971
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                    Best Local Similarity 47.0%
Matches 248; Conservative
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US-10-219-051B-6971
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299 VPCAGSEVETHKDQYDFVVFEMASYAESLAQGAGLIKRDQGGTLVFERIGHED 1966 408
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CURRENT FILING DATE: 2003-52-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING THE: 2002-02-21
NUMBER OF SEO ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23162, Application US/10469494 GENERAL INFORMATION:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
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Chen, Xianteng
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APPLICANT:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOUP 307
                                        121 DVDIVINYIKSSAGFAPKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAWKIA 180
                                                                                                                      PALVIGNIVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKK 240
                                                                                                                                           78 KAVKAARAAFÜLGSPWRPMPASHRGPLINRLADLIERPPTYLAALETLDNGKPYVISYLV 137
                                                                 241 VAFTGSTATGRHIYQSA-AAGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGE 259
                                                                                                                                                                                                                                            258 VAFTGSTEIGRVIQVAAGSSNLKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQ 317
                                                                                                                                                                                                                                                                                   300 VCCAGSRVYVEESIYDKFIEEFKAASESIKVGDPFDESTFQGAQTSQMQLNKILKYVDIG 359
                                                                                                                                                                                                                                                                                                              ||||||| :|| |||||:|| | 318 CCCAGSRTFVQEDIYDEFVERSVARAKSRVVGNPFDSKTEQGPQVDETQFKKILGYINTG 377
                                                                                                                                                                                                                                                                                                                                                                 360 KNEGATLITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMA 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/U9/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PRILICATION NUMBER: 60/237,768
PRIOR PRILICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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SEGTWARPE: Fast SEQ for Windows Version 4.0
SEQ ID NO 10653
LENGTH: 520
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US-09-949-016-10653
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-19(52052)B
201 PALATGNVVVMKVAEQTPLITALIYVANLIKEAGEPPGVVNTVPGFGPTAGAATASHEDVDK 260
                                                                         241 VAPTGSTATGRHIYQSA-AAGLKKVTLELGGKSPNIVPADAELKKAVONI 11.G1YYNGGE 299
                                                                                                                     300 VCCAGSRVYVEESIYDKFIEEFKAASESIKVGDPFDESTPQGAQTSQMQLNKILKYVDIG 459
                                                                                                                                                                                                                                                                           360 KNEGATLITGGERIJSSKGYFIKPTVPGDVKEDMPIVKEEIFGPVVTVTKFKSADEVINMA 419
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Similarity
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                                                                                                                                                                                       US-60-453-135-14871
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 14871
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360 KNEGATLITGGERLGSKGYFIKPTVFGDVKEDMRIVKFEIFGPVVTVTKFKSADEVINMA 419
                    420 NDSEYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVD 479
                                                                                                                    419 NHSEYGLAAGLWTENVKQAHYIADRLQAGTVWVNCYNVFDAASPFGGYKQSGLGREMGSY 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.8%; Score 1243.5; DB 6; Length 516; 47.3%, Pred. No. 8.7e-92;
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Five 92; Mismatches 155,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(516)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER-US BUJANU, 044
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3555
                                                                                                                                                                                                                                                                                                            Sequence 3555, Application US/10369493 GENERAL INFORMATION:
                                                                                                                                                              480 ALQNYLQVKAVRAKLD 495
                                                                                                                                                                                                       479 ALDNYTEVKSVWVNLE 494
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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US-10-369-493-3555
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US-10-369-493-3555
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TITLE OF INVENTION: GENETIC FOLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYGRAPIAL INFARCTION, METHOUS OF DELECTION AND USES THEREOF
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403 VVTVIKEKSADEVINMANUSEYSLAAGIHTSNINTALKVADRVNAGITWINTYNDEHHAV 462
                                                                 425 CVALTTEKTEEEALTLANDSMYGLGAALFTKRUTFAHPVAPEIEAGMVWVNSSNDSDFRI 484
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SOFTWARE: FastSEQ for Windows Version 4.0
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; GENEPAL INFORMATION:
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US-60-453-135-14871
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APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: SIENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001457
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                                                                                               CURRENT APPLICATION NUMBER: US/60/453,050 CURRENT FILING DATE: 2003-03-10 NUMBER OF SEQ ID NOS: 82762 SOFTWARE: EastSEQ for Windows Version 4.0 SEQ ID NO 14871 LENGTH: 514
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Matches 246; Conservative
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US-60-453-050-14871
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Search completed: June 24, 2003, 10:35:19 Job time : 54.5876 secs

GenCore version 5 1.6 Copyright (c) 1993 - 2003 Compugen Ltd

OM protein - protein search, using sw model

Tune 24, 2003, 10:10:05 : Search time 18:9426 Seconds (without alignments) 2512.144 Million cell updates/sec Pun on.

#\$-09-830-751-2 2550 Title. Perfect score.

MSVDALQNYLQVKAVRAKLD 495 1 MSHLPMTVPIKLPNGLEYEQ Sequence:

RLOSUM62 Gapop 10 0 , Gapext 0.5 Scoring table.

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20ຕຸກຕຸກຄຸກຄຸ

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	probable aldehyde	probable aldehöde												protein F54D8.3 (i	rf2 nuclear restor	aldehyde dehydroge	aldehyde dehydicae					aldehyde dehydroge		hypothetical prote	aldehyde dehydroge				probable aldehyde
		ID	S67286	S50576	626098	A29055	843114	S43108	T39216	148966	803564	DEHUE2	H69614	A40872	S050 40	D88449	T03983	874224	S00364	A55684	10:5:0:	814629	CR3717	T06683	JC4924	C86372	PEHTE1	S14752	JC5553	802302	T50272
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æ	Query	Match	99.5	67.8	56.9	55.4	54.9	53.4	53.4	50 n	50.0	49.2	49.1	49.1		48.5	48.3			•			47 3	47.1	•	46.6	46 4	46.3	46 3	46.1	46.0
		Score	2538	1728.5	1452	1412.5	1399	1362.5	1362	1275.5	1274.5	253.		1252.5	1240 5	1236	1232.5	1222.5	1220.5	1218.5	1216 5	1212 5	1205 5	1201	1192.5	1189	1182.5	1181.5	1179.5	7	1172.5
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# ALIGNMENTS

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A. Accession: 50720. Accession	Submitt	ed to the Protein Sequence Database, July 1996
A: Molecule type: DNA A: Residues: 1-519 - CDED- A: Cross references: BMBL.275282; PIDN CAA99705 1; GSPDB GNOODIS; MIPS-YOR374w A: Concention: 158 A: Genetics: Concentration: Catalydes Oxidation of an addebyde to an acid using NAD+ and water A: Made position: 158 C: Function: 158 C: Function: 158 C: Function: Catalydes Oxidation of an addebyde to an acid using NAD+ and water A: Made concentration: Catalydes Oxidation of an addebyde to an acid using NAD+ and water A: Made concentration: Catalydes Oxidation of an addebyde debydrogenase homology C: Reywords: NAD, Oxidoreductase elucity Aids C: Reywords: NAD, Oxidoreductase debydrogenase homology C: Reywords: Added debydrogenase (NAD+); aldehyde debydrogenase homology C: Bethamportation of A: Genetic debydrogenase homolo	A; Acces	ence number: 30/201 sion: S67286
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A,Gene: SGD:ALD7; MIPS:YOR374w A,Gene: SGD:ALD7; MIPS:YOR374w A,Gene: SGD:ALD7; MIPS:YOR374w A,Map Position: 158 C,Function: 1	C; Genet	300
Aptropass references: SGD:SGD05901; MIPS:YOR374w Aptroposition: 15R C; Function: C;	A; Gene:	SGD:ALD7; MIPS:YOR374w
C, Function:  C, Function:  A, Description: etallytes oxidation of an aldebyde to an acid using NAD+ and water A, Description: etallytes oxidation of an aldebyde dehydrogenase homology C, Keywords. NAD, oxidoreductase C, Superfamin: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology C, Keywords. NAD, oxidoreductase C, Salchydrogenase Logical Colored C, Selchydrogenase Logical C, Colored C, Selchydrogenase L,	A;Cross	references: SGD:SUUU59U1; MIPS:YOR3/4w
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A; Note: onlymes with this activity are involved in diverse actabolic pathways in v C; Superiamily: aldebyde dehydrogenase (NAD*); aldebyde dehydrogenase homology C; Keywords. NAD. E; 87:344/Ecmain: aldebyde dehydrogenase homology Alda. E; 290,324/Active site. Glu, Cys *status predicted  Query Match  Qu	A, Descr	uption: catalyzes oxidation of an aldehyde to an acid using NAD+ and water
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99.5%; Score 2538; DB 1; Length 519; Best Local Similarity 99.8%; Pred. No. 4.9e-159; Matches 493. Conservative 0, Mismatches 1, indels 0; Gaps 2 SHLEMTVPIKLFNGLEYEQPTGLFINNKFPFFVINFSFEEDICHTFEGENOV 61 [11] [11] [11] [11] [11] [11] [11] [11	F;83·34 F;290,3	/Domain: aldelyde dehydrogenase Lomology Allo. 24/Active site, Glu, Cys Estatus predicted
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62 EFAVÇAAGERAFSNOSWINTIGETIFFORALYPLAELIEQDKIVTASIELILINGKAISSSEGD [111111111111111111111111111111111111	q	SHILMTVPIKLFWGLEYEOPTGLFINWKFVFSKONKTFEVINFSTFERICHTFILLF
122 VOLVINVLKSSAGFAKTÖFNIGTETTITTITTITTITTITTITTITTITTITTITTITTITT	οy	EFAVÇAADPAPSNGSWNTIDPTIPMGKALYPLABLIBQDKIVTASTELIINGKALSSSMGD
122 VDLVINYLKSSAGFAERTIGEMITTGETHESTEREGTGWUGGLIPWNEPLLMWAWKIAP HITHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT	วุด	EEAVQAADRAFSNGSWNGIDPIDRGKALYRLAELIEQLKDVIASIETLDNGKAISSSRGD
145 VGUINYLKSSAGFALKIGEMIGGELHESYLKEG GOVEGLIGHTHILLIT	ŠĢ	VELVINYLKSSASFAFR (MRFM THIGH THESY TREFT GROSG) IPWNEPILMWAWKIAP
182 ALVIČNIVVEKTAESIELSALYVSKYIFVAAGIEGOVINIVSGEGETVVEALIRGERIEKE 11111111111111111111111111111111111	સુ	VGEVINYLKSSÄÄFÄRELOGEM LOTON HESVYRKOT STAVONALTELMMAMKTAL
205 ALTGORIVETAESTELSALIVSKYLEGAGIEFGULITITITITITITITITITITITITITITITITITITIT	i,	ALVIONIVVEKTAESITELSALYVSKY LEGAGIFFGVINIVSGFGKTVVEATITHFRIEKY
242 AFTGSTATGRHIYQSAAAGLKKVTLELGGKSPNIVFAGLFKAVGHLIGGLYHKGGEVC 	台	ALVFONTVVEKTAESTPLSALVVSKYTFQAGIFFGVINIVSGFGKIVGEATJNHFKIKKV
CASS AFFICIAL MACAGARANT KENTELET STREET AND	ŷ.	AFTGSTATSRHIYQSAAAGLKKVTLFLQGKSPNTVFATAEL, FBAVÇNI TIGIYTNSGEVT
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302 CASSEVIVEESIYDKEIBBEKAASESIKVGPEPESIFYSAÇIZMALAKILKIVLIGEN 361

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00 00 00 00 00 00 00 00 00 00 00 00 00		Db         383 BSJAKLVIGGAPHSSKGYEVKPTUFAJIVKGTDMETUKEFEUTIVSKESTVIDEVTAMAND 442           Qy         422 SEYGLAAGTHTSNINTALKVADRVNAGTVWINTYNDPHRAVPEGGENASGLGREMSVDAL 481           Db         443 SQYGLAAGTHTNDINKAVLYSKRVKAGTVWINTYNNFHONVPEGGEGOSGLGREMSEAAL 502           Qy         482 ONYLOVKAVRAKLD 495           (1   1:1
QY	482 ONYLOVKAVRAKLD 495 	KESULT 3 S60929 probable aldehyde dehydrogenase (NAD) (EC 1.2.1.3) YPLOGIW yeast (Sarcharomyces cer NyAlternate names, protein LPE9W
RESULT S50576 probabl C; Speci C; Acces R; Dietr	RESULT 2 S56576 probable aldehyde dehydrouenase (NAD) (EC 1 2 1 3) YER073w · yeast (Saccharomyces cerevi C;Species: Saccharomyces cerevisiae C;Date, 28 May-1993 #sequence_revision 31-Jan-1997 #text_change 03-Jun-2002 R;Dietrich, F.S.	
submit A;Desc: A;Refe: A;ACCEX A;MOLEC	ted to the EMBL Data Library, December 1994 ciption: The sequence of S. cerevisiae lambda clone 3612 and cosmid 9747. sence number: S50438 ssion: S50576 sule type: DNA hues: 1-520 <dhr></dhr>	
A,CLOS: A,Experior C,General A,General A,Nap. F	A ALLOS FELEFENCES - EMRI-HIVR14: NII-ganakon, FIDN-AARAANIZ i, FID-ganakon, GSFDR-GNUDO A BEPPETIMENTAL SOURCE: Strain \$288C (AB972) C.Genetics: A.Genetics: ACON-YENDTAL A.GENETICS: NIPS-YENDTAL A.GENETICS: SGD:S0000875 A.Map position: 5R C.Function:	
A, Descr A, Note C, Super C, Keyw F, 288, 3	Iption, catalyzes oxidation of an alebyde to an acid using NAD+ and water enzymes with this activity are invoived in diverse metabolic pathways in various family aldehyde dehydrogenase (NAD+); addehyde dehydrogenase (NAD+); addehyde dehydrogenase fonology ords, alcehof metabolism, NAD, exidereductase to addehyde dehydrogenase homology salchos aldehyde dehydrogenase homology salchos alcehof dehydrogenase homology.	Query Match         56.9%;         score 1452;         DB 1;         Length 500;           Hest Local Similarity         54.8%;         Pred. No. 9.80 BB;         Brid.           Matches         222;         Conservative         92;         Mismatches         128;         Brdels         4;         Gaps           Qy         * HLPMTVPIK*         LPNGLEYEGFOLEINNKEVPSKANKTFFVINESTEREICHHYEGED         1         1111 <td< td=""></td<>
Query Maches Matches	Action 1	ţ (I)
e o o o	24 SQAPLKVPITLPNGFTYEQPTGLFINGEFVASKQKKTFDVINPSNEEKITTVYKAMEDDV 83 62 EEAVQAADRAFSNGSWNGIDPIDPGKALYRLAFLIFQDKDVIASIETLDNGKAISSSFGD 121 11   1   1   1   1   1   1   1   1   1	QY
o v	143 VALVSKYLRSCGGWADK FYGNVIDTGKNIPTYSTKEPLGVGGQLIPWNFPLLMWSWKIGP 202  182 ALVJSKYLRSCGGWADK FYGKVIPTGKNIPTYSTKEPLGVGGQLIPWNFPLLMWSWKIGP 202  182 ALVJGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINTVSGFGKIVVEALTNHFKIKKV 241  183 ALVJGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINTVSGFGKIVVEALTNHFKIKKV 241  203 ALVJGNTVVLKTAESTPLSALYVSKYIPQAGIPSGFGKIVATTAGIPT 111   1   1   1   1   1   1   1   1	OF 241 VAPTCSTATCRH1-YOSAAACIJKVTI,ELGGKSPNIVPAJAELJKRAVQNI,ILGITYYNSTE 299  11.11   1   1   1   1   1   1   1   1
c a co	ACAGENTATOR TOTAL SALENCE CENTER OVER LESS SERVICES SALEGERS.  AFTGSTATGRELYGSAAAGIKKVILELDERSEN IVFALAELKRAVAN ILGITYNSGEVCE THE HILL THE	V. CANAGEM VEES HER FIRE FARENCE VORTHERS FEW OF THE TOTAL SERVICE OF THE SERVICE
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Riachatz, G., Oberkefler, H., Simon, R.; Lecheraner, E., Hoger, A., Kandler, D.; Prill submitted to the EMBL Data Library, March 1994
A.Description: Molecular characterization of allergens of Cladosporium herbarum and A.Reference number: $43108
A.Reference number: $43108
                                                                                                                                                                                                         R;Achatz, G.; Oberkofler, H.; Simon, B., Lechenauer, E.; Unger, A., Kandler, D.; Prill submitted to the SMB Data Library, March 1994
A;Doscription: Molecular characterization of alicigens of Cladospotium herbatum and A A;Reference number: S43108
                                                                                                                                                                                                      Oberkofler, H.; Simon, B., Lechenauer, B.; Unger, A., Kandler, D.; Pril
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 NIVVLKTAEQIPLGGLVAASLVKEAGFPPGVINVLSGFGKVAGAALSSHMDVDKVAFIGS 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 LITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEYG 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 TVFIKLPNGLEYEQFTGLFINNKFVFSKQNKTFEVINFSTEEEICHIYEGREDDVEEAVQ 66
                                                                                                                                                                                                                                                                                                                                                                                A, Residues, 1496 -787H5
A, Choss references EMML.X7M2LM, NID.g467624, FIRM CAAST672 1, FID.g467625
C, Superfamily: aldebyde debydrogenase (NAD+): aldebyde debydrogenase homology
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C;Species: Alternaria alternata
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 03-Jun-2002
                                                                                                                    C;Species: Cladosporium herbarum
C;Date, 19-Mar-1997 #sequence_revision 06-Jun 1997 #text_change 03 Jun-2002
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                                                                                        aldehyde dehydrogenase (NAD) (EC 1.2.1.3) - fungus (Cladosporium herbarum)
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F,56-317/Eomain alachyde dehydrogenise homology ALD
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A; Residues: 1-495 <ACH>
                                                                                                                                                                                                                                                                                                                              A; Accession: S43114
A; Molecule type: mRNA
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C.Function: 21/2; 422/1
C.Function: actalyzes the oxidation of an aldehyde to an acid using NAD+ and water
A.Boscription catalolism
A.Note: enzymes with this activity are involved in diverse metabolic pathways in various
C.Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
C.Keywords: alcohol metabolism: NAD: oxidoreductase
F:57-318/Domain: aldehyde dehydrogenase homology <ALDD>
                                                                                                                                                                       A29055
all dehydrogenase (NAD) (EC 1.2.1.7) • Emericella nidulans
clobedies: Bmericella nidulans, Aspergillus nidulans
Clobetes: Bmericella nidulans, Aspergillus nidulans
Clobetes: 30-Jun-1988 #sequence_revision 31-Jan-1997 #text_change 03-Jun-2002
Clocession: A29055
E.Pickett, M.; Gwynne, D.I., Buxton, F.P.; Elliott, R.; Davies, R.W.; Lockington, R.A.;
Gene 51, 217-226, 1987
A.Fitle: Cloning and characterization of the alda gene of Aspergillus nidulans.
A.Reference number: A29055; MUIH:87248080; FMID: N036552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEEAVQAADPAPSNISSWNITIPPIDEGKALYRLAELIEQDKLVIASIETLDNGKAISSSEG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 DLANSIGCLRYYAGWADKIHGQTIDTNPETLTYTRHEPVGVGGQIIPWNFPLLMWSWKIG 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Residues: 1.407 .prc.
A.Cross references: CR:M16197; NID:9168010; PIDN:AAA33293.1; PID:9168011
A.Experimental source: strain Glasgow FGSC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.4%; Score 1412.5; DB 1; Length 497; 54.5%; Pred. No. 3.8e-85; 1.vc 88; Mismatches 132; Indels 5;
                                                     485 EVYHAYTEVKAVRIKL 500
479 DALQNYLQVKAVRAKL 494
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Matches 270; Conservative
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A;Cross-references: EMBL:299262, PTDN-CAR16407-1, GSPDR-GN00066, SPDE-SPAC9E9.09c
A;Experimental source: strain 972h-; cosmid c9E9
                                                                                                                                                                                                                                                                                                                                       67 AADRAFSNGSWNGIDPIDRGKALYPLAELIEQDKDVIASIETLDNGKAISSSRG-DVDLV 125
                                                                                                                                                                                                                                                                                                                                                                   126 INYLKSSAGFADKIDGRMIDTGRTHFSYTKRÖPLGVGGGIIPWNFPLLMWAWKIAPALVT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 AGCLRYYGGWADKIEGKVVDTAFDSFNYI RKSLLVFAVRSSMELFILMWSWKIGFAIAT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 GNTVVLKTABSTPLSALIVSKYIPQAGIPPGVINIVSGFGKIVVEALTNHPKIKKVAFTG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GNTVVLKTAEGTPLSAYIACKLIQEAGFPPGVINVITGFCKIAGAAMSAHMDIDKIAFTG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 STATGRHIYQSAA-AGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGEVUUAU 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420 GLSAAVHTSNLTTAIEVANALRAGTVWVNSYNTLHWQI.PFGGYKESGIGRELGEAAI.DNY 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 SRVYVEESIYDKFIEEFKAASESIKVGDPFDESTFQGAQISQMQLNKILKYVDIGKNEGA 364
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A;Cross:references: EMBL:X7822/; NID:q46/614; PIDN:CAA55071.1; PID:q46/615 C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology C;Krywords: NAD; oxidoreductase P:56-317/Formain: aldehyde dehydrogenase homology <ALD>
                                                                                                                                                                                                                                7 TVPIKLPNGLEYEQPTGLFINNKFVPSKQNKTFEVINPSTEEEICHIYEGREDDVFFAVQ 66
                                                                                                                                                                                                                                                                                    3 SVKLSTPQTGEFEQPTGLFINNEFVKAVDGKTFDVINPSTEEVICSVQEATEKDVDIAVA 62
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A;Map position: 1
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
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C,Date. 03.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C;Accession: T39216
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                                                                                                                                    Length 495;
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A:Relerence number: Z21836
A:Relerence sumber: Z21836
                                                                                                                                    DB 2;
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                                                                                                                                  53.4%; Score 1362.5; DB 354.3%; Pred. No. 7.3e-82;
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                                                                                                                               Query Match
Best Local Similarity 54.3°
Matches 256; Conservative
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9 VEITVPTGKTYIOPVGLFINNOHVDSVHGGRVKVYSPSTEKLICEVADADEEDVDIAVKV 68

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Additionable dehydrogenase (NAD) (EC 1.2.1.3) 2 precursor, mitochondrial measons aldehydrogenase AHD MI
N.Alternate names: aldehydrogenase AHD MI
C.Species: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #sequence_revision 31-Jan 1997 #text change 03 Jun 2002
C.Accession: 148966; S50106; 157960
E.Chang, C.: Yoshida, A.
Gene 148, 311-336, 1994
A.Title: Cloning and characterization of the gene encoding mouse mitochondrial aldeby
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A. Cross-references. EMBL. 232545; NID:g563496
A. Cross-references. EMBL. 232545; NID:g563496
A. Note. the macLectide sequence was submitted to the EMBL Data Library. March 1994
B. Chen, M.; Achkar, C.; Gudas, L.J.
MOI. Pharmacol. 46, 88-96, 1994
A.Title: Enzymatic conversion of retinaldehyde to retinate acid by cloned murine cyto
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R;Caubin, J.; Iqlesias, T.; Bernal, J.; Munoz, A.; Marquez, G.; Barbero, J.L.; Zaball
Nucleic Acids Res. 22, 4132-4138, 1994
A;Title: Isolation of genomic DNA fragments corresponding to genes modulated in vivo
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A.Residues: 1-87,°C°,90-180,182-226,′S′,228-443,'G′,445-469,'N′,471-477,'M′,479-475,
A.Cross references: GB:S71509; NID:q560644; PIDN:AAC60691.1; PID:q560645
68 ADRAF-SNGSWNGIDPIDRGRALYRLAELIEQDRDVIASIETLDNGRAISSSRGDVDLVI 125
                                   127 NYELKSSAGFADKI DGRMI DTGKTHFSYTKKOFLAVYGOT I PWNFFLLMWAWK LAPALVTG - 1 R6
                                                                                                                                                                        129 (AFRYNSSMAUKONSQUEED) KREANTREETGVOOG HEWERELMCAMETAVANG 1883
                                                                                                                                                                                                                                                                         187 NTVVLKTAESTPLSALYVSKYTPQAGTPPRVTINTVSGPGKTVVEATTNHPKTKKVAPTUS 246
                                                                                                                                                                                                                                                                                                                                      189 NTIILKTAELTPLSAL/TTKFVPEGGFPPGVINVLSGDGERGGNAISSHMDIDKVAFTGS 248
                                                                                                                                                                                                                                                                                                                                                                                                           247 TATGRHIYQSAA-AGLKKVTLELGGKSPNIVFADAELKKAVONIII.GIYYNSGEVCCAGS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                           306 RVYVEESTYDKFTEEFKAASESTKVCDPFDESTFQGADTSOMOLNKTLKYVDTGKNFGAT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 LITGGERLGSKGYFIKPTVFGDVKEDMRIVKEELFGPVVTVTKFKSADEVINMANDSEYG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.26 LAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALGNYL 445
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A;Accession: 148966
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A;Molecule type: mRNa; DNA
A;Rcsiducs: 1-519 <RES>
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C:Complex: homotetramer
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C;Complex: homotetramer
    A; Molecule type: mRNA
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A;Genome: nuclear
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A, Note: enzymes with this activity are involved in diverse metabolic pathways in various A, Note: enzymes with this activity are involved in diverse metabolic pathways in various C, Superfamily: add-hyde dehydrogenase (NAP), add-hyde dehydrogenase homology C, Keywords: alcohol metabolism; homotetramer, liver, mitochondrion, NAD, oxidoreductase P;1-19/Domain: transit peptide (mitochondrion) #status predicted *INF.
F;23 519/Incohologist add-hyde dehydrogenase homology *ALEPO*
F;237,321/Anchive site: Clu, Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 150, 1083-1087, 1988
A;Title. Sequence of the signal peptide for rat liver mitochondrial aldehyde dehydrogena
A;Reference number: A27713; M(1):98134217; PM(D:3342060)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAVQAADRAFSNGS-WNGIDPIDPRRALYRLAELIEQDKDVIASIETLDNGKA-ISSSEG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 KAVKAARAAFQLGSPWFRMDASDPGRIJLYFLADLIEFDPTYLAALETLDNGKPYVISYLV 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 DLDMVLKCLRYYAGWAPKYHGKTIPIDGPFFSYTRHEPVGVGGIIPWNFPLLMQAWKLG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 PALVIGNIVVLKTAESIPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHFKIKK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 VAFTGSTATGRHIYQSAA--AGLKKVFLELGGKSPNIVFADAELKKAVQNIILGIYYNSG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVOCAGSPVYVERSIYDKFIERFKAASESIKVGDPFDFSTFQGAQTSQMQLNKILKYVDI 358
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                                                                                                                                                                                                                                                                                                                                        7 TVPIKLPNGLEYEOP----TGLFINNKFVPSKQNKTFEVINPSTEEFICHIYEGKELDVE 52
                                                                                                                                                                                                                                                                                                                                                                                   24 TSAVPAPN----HQPEVFCNQIFINNEWHDAVSRKTFFTVNFSTGEVICQVAEGNKEDVD 79
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                  13,
                                                                                                                                                                                                                                                         DB 1, Length 519;
                                                                                                                                                                                                                                                                                                  84; Mismatches 146; Indels
                                                                                                                                                                                                                                                                             Pred. No. 48-7h;
                                                                                                                                                                                                            F;474/Binding site: NAD (Cys) #status predicted
                                                                                                                                                                                                                                                       Score 1275.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 DALQNYLQVKAVRAKI, 494
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                                                                                                                                                                                                                                                                           51.0%;
                                                                                                                                                                                                                                                                       Best Local Similarity 51.0*
Matches 253; Conservative
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C; Function:
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A; kesidues. [7:29 -FALA
A; Cress-references: GB. M13936, NID 9202847, FIDN AAA46712.1, FID.9202848
B; Dawan, J. 9. Pallawal, R.; Kaftan, E.; Bawa, R.
Pribs Lett. 273, 215-218, 1990
A; Filte: A mitochondria; protein fraction catalyzing transport of the K(+) analog T1(
A; Feterence number: Sligns; MUH-41932184; PMID 1899808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Superfamily: aldehyde dehydrogenase (NAbr); aldehyde dehydrogenase homology
C.Keywords: alcohol metabolism: homoletramer: liver; mitochoud lon; NAbr oxidoreducta
P.1-19/Domain. transit peptide (mitochondrion) #status predicted (INP)
P.20-519/Product: aldehyde dehydrogenase (NAD+) 2 #status predicted (MAT>
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A.Note: enzymes with this activity are involved in diverse metabolic pathways in vari
                                                                                                                                                                                                                                          A.Molecule type. protein
A.Rosiduce, 3.27 470 denve.
R.Jongy J.; Weiner, H.
A.Title, Parlification and characterization of catalytically active precursor of rat
A.Futerence number S.1442, Multi eligation, PMile interes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           b. FAVGAABBAFSNGS-WMOLDPPDPBCALYFLAELFEDKLVIASIETLDNGKA-ISSSEG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DVPLVINYLKSSAGFADKIFGPMIDTGPTHESYTKPQPLGVGGGIIPWNFPLLMWAWKIA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 ANDSEYGLAAGIHTSNINTALKVADFVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSV 478
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Matches 252, Conservative
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A General GDB.ALDH2
A Cross reterences, GDB.119668, OMIM.188650
A Cross reterences, GDB.119624.2
A introp position: 19244.2-12924.2
A introp position: 19244.2-12924.3
A introperation: 2024 12874. 1477. 164, 4. 212, 4. 2077. 405; 0.5. 407. 2. 407.2)
C)Complex: homotetramer
C)Function: catalyzes the oxidation of an aldehyde to an acid using NAD+ and water
A Pathway: ethanol catalobilis activity are involved in diverse metabolic pathways in variance (NAD+), aidehyde dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Saperfamily aldebyde debyttequease (NAD+), aldebyde debydrogenase homology
C.Keywords: alechol metabolism; bomoletramer; liver; mitschondrion; NAD+ oxidoroducta
P;1-17/Domain; transit poptide (mitochondrion) *status predieted *SES.
F;18-17/Product; aldebyde debydrogenase (NAD+) 2 *status experimental *MAT+
F;75-39/Promain; aldebyde debydrogenase (NAD+)
F;211-29/Zomain; NAD-binding *status predieted *NAD+
R;Kunst, F.; Oqasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bør
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caidwell, B.; Capanno, V.; Carter, N.M.;
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C.Date: 05-Dec-1997 #sequence_revision 05 Dec 1997 #text change 20 Jun 2000
C.Accession: H69614
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F.319/Active site: Cys #status experimental
F.472/Binding site: NAD (Cys) #status predicted
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50.3%; Pred. No. 1.1e
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                                                                                aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 2 precursor, mitochondrial (validated) - human
N.Alternate names: aldehyde dehydrogenase E2; aldehyde dehydrogenase I
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A;Reference number: A23503; MUID:86055846; PMID:4065146
A;Accession: A23503
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A;Residues: 'A',19-517 (HEM>
A:Noto: the sequence shown is presumably that of the mature protein, however, the number
R;Braun, T.; Bober, E.; Singh, S.; Agarwal, D.P.; Goedde, H.W.
Nucleic Acids Res. 15, 3179, 1987
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A;Reference number: A27509; MUID.87174836, PMID.3562250
A;Accession: A27509
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A; Residues: 1-6, AMPMAA',10, P',12, VS',15, RHPGR',21,27-79, 'REGRPG',86-336,'V',338-517
A:Cross-references: EMBL Y00109; NIC-928607; Film.CAAUBL9U.1, FILH.g2e608
R:Braun, T.; Bober, E.; Singh, S.; Agarwal, D.P.; Gocdde, H.W.
FEBS Lett. 215, 233-236, 1987
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A;Accession: A26743
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A; Pesidues: 119-336, 7V, 338-517 < HSU2>
A; Molecule type: mRNA
A; Pesidues: 119-336, 7V, 338-517 < HSU2>
A; Cross-reference: GH: KNAOND; NID-94178395; PIDN.AAR59500.1; PID:9178396
A; Note: thirty-three tryptic pepides were also sequenced
B; Yoshida, A.: Ikawa, M.; Hsu, L.C.; Tani, K.
Alcohol 2, 103-106, 1985
A; Aichol 2, 103-106, 1985
A; Title: Molecular abnormality and cDNA cloning of human aldehyde dehydrogenases.
A; Reference number: 139431; MUID:85252089; PMID:4015823
A; Reference number: 139431; MUID:85252089; PMID:4015823
A; Molecule type: mRNA
A; Molecule typ
                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Genomic structure of the human mitochondrial aldehyde dehydrogenase gene.
                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence_revision 17-Nov-1995 #text_change U4-Jun-2002
C;Accession: AZ975; S00804; Az3503, A27509; A26743, I39432, I39433, I39430
Gricuits 2, C7-65, 1988
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FEBS Lett. 233, 440, 1988
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A;Accession: A29975
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A;Fostduas: 1-6, AHAY, In, FP, 13-49 FBPA-
A;Cross-references: EMH.:X65409; NID:928605
A;Note: correction to A26743

    J.; Kaiser, R.; Joernvall, H.
Biochem 153, 13-28, 1985

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A;Accession: S00804
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A; Residues: 1-517 <HSU1>
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A; Status: preliminary
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A. Ehrlich, S.D., Frmersen, P.T., Entian, K.D., Errington, T.; Fabrot, C.; Fritati, E. Mautes 30, 249-256, 1947

Alauthors: Frought, C.; Fritt, C.; Frijita, M.; Fujita, Y.; Fuma, S.; Galizza, A., Galler Lech, T., Harwood, C.F., Herbut, A., Hillert, H., Hoisapell, S.; Hosson, S.; Hollic, M.F. Koctter, P., Koningstell, G., Krögh, S., Kumano, M., Kurita, K., Lapidas, A., Ladidineis, A., Authors: Lauber, J. Lazerevic, V. Krögh, S., Kumano, M., Kurita, K., Lapidas, A., Ladidineis, N., M., Ogawa, K., Ogiwara, A., Ondaya, R., Fark, S.H., Farro, V., Foll, T. Masuda, S., Maueel, Y., M., Rado, M., Rivolta, C., Roche, B., Rose, M., Sadale, Y.; Setto, T.; Scanion, A; Authors Schleich, S.; Schlecht, R.; Scoffone, F.; Sekiyardi, V.; Erwska, A.; Serv, T., Wipat, A.; Yamanoto, H.; Yamane, F.; Sekiyardi, A.; Tanaka, T.; Terpstra, P.; Tognool, A.; Tosato, V.; Uchlyama, A. Authors, Yoshikawa, H.; Dumchin, A.; Tasaka, H.; Pamanoto, H.; Yamanoto, H.; Yasumoto, K.; Yata, K.; Yoshida, M.; Title, The complete genome sequence of the Gram-positive bacterium Bacilius subtilis. A.; Status; preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Residues: 17495 <KUN>
A)Cross references: GB.299114; GB.AL009126, NIB 92634240, PHRN:CABIRES 1, PIB 92634324
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C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homelogy
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C;Species: Homo sapiens (man)
C;Date: 27-Mar-1992 #sequence_revision 31-Jan-1997 #text_change 01-Jun-2002
C;Accessior AdAR72
R;Hsu, L.C.; Chang, W.C.
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Matches 243, Conservative
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A; Residues: 1-49
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A.Pathway: ethanol catabolism
A.Note: encymes with this activity are invelved in direcse metabolic puthways in vari
C.Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
C.Superfamily: alcohol metabolism, homotetramer, introdhondrion, NAD, oxidoreducta
F.1-20/Domain: transit peptide (mitochondrion) status predicted <INP>
F.21-51//Product: aldehyde dehydrogenase (NAD+) 5 #status predicted <AMT>
F.25-33%Domain: aldehyde dehydrogenase (NAD+) 7 MLDC.
1 Fiol. Obom 25s, 12257-122s, 1991
Agrille. Clouding and characterization of a new functional human aldehyde delydrogenas
Agreterence number: A40872; MHTD: 9128s241; PMID. 2061311
Agreession: A40872
                                                                                                                                                         A Molecule type. DNA: mkNA
A) Molecule type. DNA: HEUDA
A) Gless references GE-M67467. NIT-3737184, PITON AAA96876. L. FID-31263008
A) Note: 86-Ala and 107-Leu were also found
C) Comment: Based on similarity, this form is assumed to be mitochondrial and to have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: catalyzes oxidation of an aidehyde to an acid using NAD+ and water
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 GLAAAVETKDLDKAMYETQALQAGTVWVNTYNIVTCHTPFGGFKESGNGKELGEDGLKAY 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 REVEPLGSPWERMDASFEGFLINFLADLVEFFRVYLASLETLDNGKPFQESYALDLDEVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 NIVVMKVAEOTPLSALYLASLIKEAGFPPGVVNIITGYGPTAGAAIAOHMDVDKVAFTGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.1%, Seere 12.5.5, PP 1, Length 517, 50.6%, Fled. No. 1.3e 74;
Live 85; Mismatches 148; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                 A)General GDB:ALDHES, ALDHEX
A)General GDB:128788
A)Map position: 9Pl3-9pl3-
A)Map position: opl3-9pl3-9pl3
A)Mate: the outy insten energy before the initiator coden c)Complex: homotetramer (probably)
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Matches 248; Conservative
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Best Local S
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A.Titie, Genome sequence of the nematode C. elegans: a platform for investigating bio A.Reforence number: A75000, MIDIS 94049613; PMTD: 94041946.
A.Note: see websites genome world educated plegans/ and www sanger ac uk/Projects/C. A.Note: published errata appeared in Science 284, 45, 1999; Science 284, 2103, 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Cross references. GB.chr_HII, FIDN.AAA20615.1; FID:q529223; GBTGB.GN90021; CESP:F94
       440. ANNSKYGLAAAVPTKDLDKANYI SOALOAGTVWVNCYDVBGAOSPFGGYKI SGSGRELGE 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 LIMMAMKTAPALVTGNTVVLKTAESTPLSALYVSKYTPQAGTPFGVTNTVSGFGKTVVEAT 232
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                                                                                                                                                                                                                                                                                                                                                    Cispectos: Caenorhabditis elegans
Cibabe: 10 May-2001 #sequence_revision It May 2001 #text charge 24 May 2001
CiAecession: D88449
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                                                                                                                                                                                                                                                                                                                             protein F5408.3 [imported] - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rjanonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
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                                                                          479 DALQNYLQVKAVRAKL 494
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A; Residues: 1-544 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                            A.Molecule type: DNA
A.Residues: 1-520 -cDNA
R.Farres, J.; Guan, K.L.; Weiner, H.
Eur. J. Blothem. 180, 67-74, 1989
A.Title: Primary structures of rat and bovine liver mitochondrial aldehyde dehydrogenase
                                                               A;Title: Sequence of the precursor of boxine liver mitochondrial aldehyde dehydrogenase A;Reference number: $09030; MUID:90179198; PMID:1689984 A;Accession: $09030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٤:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DVDLVINYLKSSAGFADKIDGRMIDTGHTHFSYTKRQPLGVCGQIIPWNFPELLMWAWKIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PALVTGNTVVLKTAESTPLSALYVSKY1PQAGIPPGVINIVSGFGKIVVEAITNHPKIKK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 PALATGNYVYMKVAEQTFLTALYVANLIKEAGFPPGVVNVIPGFGTAGAATASHGGVIK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 VAFTGSTATGRHIYQSAA--AGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 EVCCAGSRVYVEESTYDKFIEEFKAASESTKVGDFFFESTFLGGAGTSGMALNKILKYVFT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 GKNEGATLITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINM 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GKEEGLKLLCGGGAAADRGYFIQPTVFGDLQDGMTIAKEEIFGPVMQILKFKSMEEVVGR 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 ANDSEYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSV 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90, Mismatches 149, Indels 13, Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                Peference number: S03564: MIID:89210865: PMID:2540003
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                                                                                                                                                                           A;Status: not compared with conceptual translation
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   R;Guan, K.; Weiner, H.
Arch. Biochem. Biophys. 277, 351-360, 1990
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R;Guan,
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393 IDORQENKILIRYTERYGVINGSATLATIGETILITIGETILESDAQUGMKIAQEEIFGDV 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 IIPWNPPLLMYAWKVGPALACGNTLVLKTAEQTPLSALYISKLLHEAGLPEGVVNVVSGF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 GKIVVEAITNHPKIKKVAFTGSTATCRHIYQSAA-AGLKKVTLELGGKSPNIVFADAELK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 GPTAGAALASHMDVDKIAFTGSTDTGKIILELAAKSNLKTVTLELGGKSPFIIMDDADVD 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 KAVQNIIIGIYYNSGEVGCAGSRVYVEESIYDKFIEEFKAASESIKVGDPFDESTFQGAQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 HAVELAHFALFENGGGGGGGSKTFVHEKYYDEFVEKAKARALKKVVGDPPFKGVEGGG 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 TEEEICHIYEGKEDDVEEAVQAADKAFSNGSWNGIDPIDKGKALYKLAELIEQDKDVIAS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 IETLDNGKAI-SSSRGDVDLVINYLKSSAGFAPKIPGPMIPTGPTHFSYTKRQPLGVCGQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 IIPWNFPLLMWAWKIAPALVTGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344 TSQMQLNKILKYVDIGKNEGATLITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPV 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 TVPADGMHRLLPGVLQRFSTAAAVERPITPSVHVNYTKLLINGNFVDSASGKTFPTLDPR 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily; aldehydə dəhydrogenasə (NAD+); aldehydə dehydrogenasə homology
F;107-370/Domain: aldehyde dehydrogenasə homology <ALD>
                                                                                                                                                                                                                                                                                                                    A;Residues: 1-549 <CUI>
A;Cross:reterences. EMEL;34 cpx; NID-g14:17.9; FIDE.AA;49:01;1, FIDE.g14:17.0; A;Experimental source: strain B73
C;Genetics:
N.Alternate names: aldehyde dehydrogenase homolog
C.Species: Zea mays (maize)
C.Dates : AcAprilana wroquene-provision .4.Aprilana min. may...unu
C.Accession: 103983
P.Cui, X.; Wise, B.P.; Schnable, P.S.
Science 272, 1334-1336, 1996
A.Title: The rf2 nuclear restorer gene of male-sterile T-cytoplasm maize.
A.Reference number: 215177; MUID:96243131; PMID:8650343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 48.3%; Snore 1232-5; DB-2; Length 549;
Best Local Similarity 48.1%; Pred. No. 2.9e-73;
Matches 244, Conservative 31, Mismatches 143, indels 23, Gaps
                                                                                                                                                                                                                                                                 A;Status: preliminary: translated from GB/EMBL/DDBJA;Molecule type: mRNA
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Search completed: Tune 24, 2003, 10:18:29 Job time: 20:9426 secs

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OM protein - protein search, using sw model

June 24, 2003, 10:02:55; Search time 9:97979 Seconds (without alignments) 2059.300 Million cell updates/sec Pur on.

Title: US-09-830-751-2
Perfect score: 2550
Sequence: 1 MSHLPMTVPIKLPNGLEYEQ.

MSVDALONYLOVKAVPAKLD 495

112892 seqs, 41476328 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing, Minimum Match 100% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ			SUMMERS	
Result		Query				
. i	Score	Match	Length	DB	QI .	Description
1	2538	99.5	519	-	DHA4_YEAST	P46367 saccharomyc
7	1695	66 5	519	<b>,-</b> ,	DHA5_YEAST	P40047 saccharomyc
3	1455	57.1	497	7	DHAL_ASPNG	
4	1452	56.9	499	7	DHA6_YEAST	
'n	1412.5	55.4	497		DHAL_EMENI	
9	1399	54.9	496		DHAL_CLAHE	P40108 cladosporiu
7	1362.5	53.4	495	7	DHAL_ALTAL	P42041 alternaria
ထ		O 05	ъ1 s.		DHAM_MOTISE	P47738 mus musc.:1::
6			515		DHAM_PAT	
0.1			500	<del></del>	DHAM_MESATI	PA1178 mesocricety
Ξ	1253.5		5.17	τ.	DHAM_HITMAN	
15	1248.5	49.0	517	۲-1	DHA5_HUMAN	P30837 homo sapien
13	1244.5	48.8	499	1	DHAS_CHICK	
14	1240.5		520	,	DHAM_BOVIN	bos tau
15	1230	48.2	499		DHA Z_HUMAN	_
16	1223 5		იი <b>⊅</b>	۲,	DHA2_PAT	Q63639 rattus norv
17	1222.5	47.9	499	۲.	DHA2_MOUSE	Q62148 mus muscula
18	1220.5		500		PHAM_HOPSE	٠,
19	1219		00,	_	CHAL_AGARI	
50	1218 5	47 B	٠. ا	-	DHA6_HITMAN	homo sa
21	1212.5	37.7	Ē,	-	DHA1_CHIOK	
C 1	1192 5	Α. α	497	_	PHAL_ENCRI	enchyti
23	1182.5	46 4	500	_	DHA1_HIIMAN	
24		46 3	ÇUÇ	-	DHA1_SHEEP	ovis
25		46.3	500	_	PHA1_PAT	P51647 rattus norv
26	1176.5	46 ]	500		PHA1_HORSE	Pis437 equus capal
27	u.	46.1	ÚO.		DHA1_MOHSE	P24549 mus musculu
83		46.1	200		DHA1_ROVIN	
29	1169.5	45.9	500	7	DHAC_RAT	
30	1155.5	45 3	501	_	PHAE_MACPP	
31		45.1	501	-	DHAE_ELEED	Q28399 elephantulu
32	1141	44.7	498	7	DHAM_LEITA	Q25417 leishmania
33		43.2	495	<del></del>	UBUM_UCTEN	P30841 octopus dof

P28037 rattus nory	P40842 ommastrephe		075891 homo sapien	P54114 saccharomyc	P71016 bacillus su	P32872 saccharomyc	P80668 escherichia	P54222 rhizobium m			P23249 vibrio chol
FTDH_RAT	C'ROM_OMMSI.	DHA2_YEAST	FTDH_HUMAN	DHA3_YEAST	DHAB_BACSU	DHAY_YEAST	FEAB_ECOLI	DHAB_RHIME	DHAR_SPIOL	ALDB_ECOLI	PHASVIBCH
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305	4.4	506	902	206	490	511	499	4 E 7	4.97	512	50.5
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			1067	1057	1034.5	1006	948.5	942.5	936	930	5 To 15

### ALIGNMENTS

ID A	NESOLI I
	reasi DHA4_YEAST STANDARD; PRT; 519 AA.
10	P45357; QU8898; 01-NOV-1995 (Rel. 32, Created)
I L	01-NOV-1997 (Re). 35, Last sequence update) 16-ort-2001 (Re) 40 Tast apportation undate)
E.	Potassium-activated aldehyde dehydrogenase, mitochondrial precursor
DE S	(EC 1.2.1.3) (K(+)-activated acetaldehyde dehydrogenase) (K(+)-ACDH).
S 0	Alak of Alak of Alak of Torkyk of 10/30. Saccharomyces cerevisiae (Baker's yeast)
9	Eukaryota, Fundi, Ascomycota, Sacchanomycotina, Saccharomycetes,
نے	Saccharomycetales, Saccharomycetaceae, Saccharomyces.
X Z	NCBI_TaxID=4932;
구	CHOUSING FROM N.A.
RA	Delius H., Rebling U., Hofmann B.;
PI.	Submitted (JUL-1994) to the EMRL/GenRank/DDBJ databases.
RN S	
χ α γ >	SEQUENCE OF 25-55. MEDITARE 01113163. DUMMAR 1080502.
Z Z	HIGH TOUR KNOWN TOUR CONTRACTOR OF THE CONTRACTO
RT	"Comparison of benzyl alcohol dehydrogenases and benzaldehyde
RT	dehydrogenases from the benzyl alcohol and mandelate pathways in
E.	Actnetobacter calcoaceticus and from the TOL-plasmid-encoded toluene
RT	pathway in Pseudomonas putida. N-terminal amino acid sequences, amino
RT	acid compositions and immunological cross-reactions.";
7 E	Blochem. J. 2/3:99-10/(1991).
ξ Q.	[2] FOURTHOR OF 25-34 AND 378-386
, <u>&gt;</u> :	MEDIINE-97295278: PubMed*9150920:
: <	Larsson T. Norbeck T. Karlsson H. Karlsson KA , Blomberg A.
£.	"Identification of two dimensional gel electrophoresis resolved yeast
£	proteins by matrix assisted lasor description ionization mass
Ħ	spectionetry.",
E,	Electrophoresis 18:418-423(1997).
z	[4]
<u>.</u>	PARTIAL SECTIONS.
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<b>5</b> {	Figure 1   Windless   Fig.   Heral House   Fig.   Mindless   Fig.   Mindless   Fig.   Mindless   Fig.   F
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FL	FEMS Microbiol Last 164 29 34 (1998)
	.: CATALYTIC ACTIVITY. An aldehyde ' NAD(.) . H(2)0 . an acid + NADH.
8	11. SUBCELLUIAE LOCATION: Mitochondrial matrix.
Ç	-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDPOGENASES FAMILY.
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	This SWISS-PROT entry is copyright. It is produced through a collaborat
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                                                                                                                                                                                                                                                                                                                                                                             62 EEAVQAADRAFSNGSWNGIDPIDRGKALYRLAELIEQDKDV1ASIETLDNGKAISSSRGD 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 AFTGSTATGPHIYQSAAAGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGFVC 301
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                                                                                                                                                                                                                                                         Length 519,
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                                                                                                                                                   NAD (APP PART) (BY SIMILARITY)
                                                                                                                      POTASSIUM-ACTIVATED ALDEHYDE
                                                                                                                                                                                                                                                                                      1; Indels
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E -> V (1N REF. 2).
E7D9944EA25F948E GFC64.
                           InterPro: IFRUGENOW, 1. PRINTER PROUTT; alded, 1. PRONTE; PSONONO, ALDERYDE_DEHYDE_CYS; 1. PROSITE; PSONONO, ALDEHYDE_DEHYDP_GLU; 1. PROSITE; PSONONO, ALDEHYDE_DEHYDP_GLU; 1. Oxidoreductase; NAD; Mitochondrion; Transit peptide. 24 MITOCHONDRION.
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                                                                                                                                                                                                                                                      Score 2538; DB 1;
Pred. No. 2.6e-158;
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01-OCT-1996 (Rel 34, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                      0; Mismatches
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Saccharomyces cerevisiae (Baker's yeast).
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           SGD: S0005901; ALD4.
InterPro: IPR002086; Aldehyde_dehydr.
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Best Local Similarity
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This SWISS PROT cutty is eapyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BABL outstand for the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for connected entitles requires a license automent (See HTTP //www ish sib elydinounce) or send an email to licenseed subject).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang X., Mann C.J., Bai Y., Ni L., Weiner H.; "Molecular cloning, characterization, and potential roles of eytosolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
-i- PATHWAY: Ethanol utilization; second step.
-i- STREFELJULAR LOCATION. Mitochondrial marrix.
-i- STREFELJULAR LOCATION.
-i- STMINAPITY: BELGNGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
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                    Wang X., Bai Y., Ni L., Weiner H.:
"Saccharomy"es cerevisiae aldehyde dehydrogenases. Identification and
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                                                                                                                                                                                                                  Dietrich F.S., Mulligan J.T., Hennessey K.M., Alten E., Araujo K., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Puncan M., Gazman E., Hartzell G., Hunicke Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Low H., Lin D., Mosedale D., Nakahara K., Namath A., Norqren R., Oetner P., et l'. Petel F.X., Roberts E., Schlemm S., Shorten T., Smith V., Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W., Smith V., Submitted (DFC:1944) to the EMRL/Abarbank/fibut databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mitochondrial aldehyde dehydrogenases in ethanol metabolism in
Saccharomyces cerevisiae.";
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ALDEHYDE DEHYDROGENASE.
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Pred, No. 2.4e-103;
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PROSITE: PS00687; ALDEHYDE_DEHYDR (LU): I.)
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MEDLINE+97212813; PubMed+9059631;
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EMBL; U18814; AAB64612.1;
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                                                                                        expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 GPALATGNTVVI.KPAETTPI.SALPASQLCQEAGTPAGVVNILPGSGRVVGERLSAHPDVK 259
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180 APALVTGNTVVLKTAESTPLSALYVSKYTPQAGTPPGVINIVSGFGKIVVEATTNHPKIK 239
                                                                                                                                                                          260 KTAFTGSTATGRHIMKVAADTVKKVTLELGGKSPNIVFALALLDKAVKNIAFGIFYNSGE 319
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                                                                                                                   240 KVAFTGSTATGPHIYQSAAAGLKKVTLELGGKSPNIVFALAELKKAVQNLILGIYYNSGE
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Connell M I , Kelly I M.;
"Physical characterization of the aldehyde-dehydrogenase-enceding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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83; Mismatches 1
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PROSITE; PSOOK87; ALDEHYDE_DEHYDR_SLU; 1.
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MEDLINE=90108705; Pubmed=2606357;
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1 MSDLFAT - ITTPNGVKYEQPLGLFIDGEFVKGAEGKIFETINPSNEKFIVAVHEATEKD 58
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"Molecular cloning, characterization, and potential notes of cytosolic and attuchoudial alabehyde dehydrogenases in ethanol metabolism in Saccharomyces cerevisiae.";
I Barterial 180 822:4370(1948).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHAG_YEAST STANDADD: PPT; 499 AA.
P54115; 902782;
D:-OTT-1996 (Rel. 34, Created)
15-70N-2002 (Rel. 41, Last anguence update)
15-70N-2002 (Rel. 41, Last annotation update)
Magnesium-activated aldehyde dehydrogenase, cytosolic (EC 1.2.1.3)
(Mg(2!) activated acetaldehyde dehydrogenase, (Mg(2+)-ACDH).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Marathe R., Messenguy F., Mowes H.-W., Mirtipati S., Moestl D., Mueller-Auer S., Namath A., Nentwich U., Oefner P., Peatson D., Petel F.X., Pobl T.M., Purnelle D., Schafer M., Scharfe M., Scharfe M., Scherens B., Schramm S., Schroeder M., Sdicu A.M., Teffelin H., Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S. V., Wamburt P., Wang Y., Wider E., Weiller H., Winnett E., The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI."; Nature 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                !- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 + an acid + NADH.
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Bussey H., Midgley M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The ALD6 gene of Saccharomyces cerevisiae encodes a cytosolic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
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SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae in 1.4 \dot{\rm M} NaCl. Evidence for osmotic induction of glycerol dissimilation via the dihydroxyacetone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.9%; Score 1452; DB 1; Length 499;
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                                                                                                                                                                                                                                                Norbeck \mathbb{R}_+ , Rlomberg A ; "Metabolic and regulatory changes associated with growth
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942AA9434302AF52 GRC64.
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PROSITE; PS00070; ALDEHYDE_CYS; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mg(2+) activated acetaldehyde dehydrogenase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-15, AND CHARACTERIZATION.
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InterPro: IPPA02086: Aldehyde_dehydr
                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 272:5544-5554(1997).
                                                                                                                                                                                                          STRAIN-ATCC 44827 / SKO2N;
MEDLINE-97190279; PubMed-9038161;
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98053564; PubMed-9392076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; NAD; Magnesium.
                                                                                                                                                                                        SEQUENCE OF 75-78 AND 481-487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U56604; AAB01219.1; -. EMBL; U39205; AAB68304.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast 13:1319-1327(1997).
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This SWISS-PROT entry is copyright It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMHL outstailton the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as iona as its content is in no way morfied and this statement is not removed. Usage by and for commercial entities requires a license apprehent (see http://www.isp.sib.et/ancenney.or send an email to licensewish sib.eh).
                                                                                                    241. VAPTGSTATGBHT-YQSAAAGILKKVFLELGBESPNIVFADAELKKAVQNITLGTYYNGGE. 299
                                                                                                                                    (40) VOCAGSRVYVEESTYDKFTEEFKAASES-TKVGDPFDESTFDGAQTSOMOLINKTLKYVDJ 458
                                                                                                                                                                                                                                                                                                  304 ICSSGSKIYVQEGIYDELLAAFKAYLETEIKVGNPFDKANFQGAITNRQQFDTIMNYIDI 363
                                                                                                                                                                                                                                                                                                                                                                          359 GKNEGATLITGGERLGSKGYFIKPTVFGDVKEDMR1VKEELFGPVVTVTKFKSADEVINM 418
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    -i- FATHWAY: Ethanol utilization; second step.
    -i- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Fungi, Ascomycota, Feriramycotina, Eurotiomycotes,
Eurotiales, Trichocomaceae, Emericella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aldehyde dehydrogenase (EC 1.2.1.3) (ALDIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emericella nidulans (Asperqillus nidulans).
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PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_CLU; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484 EVYHAYTEVKAVRIKI, 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54088 MW;
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HSSP; P05091; ICW3.
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                                                                                                                                                                                                                                                                                                                                    299
                                                                                                                                                                                        181 PALVTGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKK 240
                                                                                                                                                                                                                                                                                        177 PAVAAGNTVVLKTAQQTPLSALYAAKLIKEAPFPAGVINVISGFGRTAGAAISSHMDIDK 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 NSTDYGLAAAVHTKNVNTAIRVSNALKAGTVWINNYMMISSYQAPFGGFKQSGLGREHGSY 476
                                                                                                                        58 VDVAVAAAPAAF-FGPWFGVTPSEPGILINKLAPLMEEDLDILAAIESLDNGKAFTMAKV IIb
                                                                                                                                                                121 DVDLVINYLKSSAGFADKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAWKIA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Achatz G., Oberköfler H., Lechenduer E., Simon B., Unger A., Kandler D., Enber C., Ptillinger H., Kraft D., Breitenbach M.; Molecular cloning of major and minor allergens of Alternaria alternata and Cladosporium herbarum.";

Mol. Immunol. 32-213-227(1945)

-!- CATALYITY An ald-blyd. + H(2)0 - an acid + NALH.
-!- SUBCELLUIAR LOCATION: Cytoplasmic (Probable).
-!- SUBCELLUIAR LOCATION: THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                 41 VEEAVQAADRAFSNOSWNGIDPIDPOKALYPLAELIEGEKBVIASIFFLUNGKAISSSRG
MSHLPMTVPIKLENGLEYEQPTGLFINNKFVPSKONKTFFVINPSTREEICHIYEGREDD
                                                                                                                                                                                                                                                                                                                                  241 VAFTGSTATGRHIYOSAA-AGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
1-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Fel. 41 Last and variou update)
Aldehyde dehydrogenase (EC 1.2.1.3) (ALDBH) (Allergen Cla h 3) (Cla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycosphaerellaceae; mitosporic Mycosphaerellaceae; Cladosporium
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MEDLINE=95206305; PubMed=7898496;
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477 ALENYTQIKTVHYRL 491
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                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                    306 RVYVEESIYDKFIEEFFKAASESIKVGDPFDESTFQGAQTSQMQLNKILKYVDIGKNEGAT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 VETGGSKKGEKYFIEFITESNVTELMKIVKEETFGFVCSIAKFKIKEDAIKEGNASTYG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALQNYL 485
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                                                                                                                                                                                                                                                                                                       3 SVQLETPHSGKYBQPTGLFINNEFVKGQBGKTFDVINPSDESVITQVHEATEKDVDIAVA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 NYLKSSAGFADKILGKMIDTGKTHESYTKRQPLGVGGGITPWNFPLLMWAWKIAPALGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 NTVVLKTARSTPLSALYVSKYJPQAGIPPGVINIVSGFGKIVVRAITNHPKIKKVAFTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 NTVVLKTAEQTPLGGLVAASLVKEAGFPPGVINVISGFGKVAGAALSSHMDVDKVAFTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 TATGPHIYQSAA-AGLKKVTLFLGGKSPNIVFADAELKKAVQNI ILGIYYNSGEVGGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 KVYVQESIYDKEVQKEKERAQKNVVGDEFAADITEQGEQVSKVQEDKIMEYIQAGKDAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last Sequence update)
15-27N-2002 (Ed. 47, Last annotation update)
Aldchyde dehydrogenase (EC 1.2.1.3) (ALDDH) (Allergen Alt a 10) (Alt
                                                                                                                                                                                                                                              Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascemycota, Periromycotina, Dothidcomycetes, Pleosporales, Pleosporaceae, mitosporic Pleosporaceae, Alternaria.
                                                                                                                                                                                                                                              ćì
                                                                                                                                                                                                               Length 496;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                  Y SIMILARITY.
433706BÜEL6799ÜE CPC64;
                                                                                                                                                                                                                                              Mismatches 135,
                                                                                                                                                                                                               DB 1;
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                                                                                                                                                   BY SIMILARITY.
                                                                                                       FROSITE; PSOUGZO; ALDEHYDE_DEHYDK_CYS; 1. PROSITE; PSOUGRA7; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                                              54.9%; Score 1399;
53 8%; Pred No 4
                or send an email to livensewish-sib ch).
                                                                         Aldrhyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                    BY SI
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                                                                                                                                                                                                                                             68
                                                                                                                                 Oxidoreductase, NAD; Allergen.
Act_SlrE 263 263 B
                                                                                                                                                                             53397 MW;
                                          EMBL: X78228; CAA55072.1;
                                                                                                                                                                                                                                             263; Conservative
                                                                                    Pfam; PF00171; aldedh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                  967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 QVKAVRAKL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482 QTKTVSIRL 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=08-0203-Berlin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternaria alternata.
                                                                         [ JB07 008d ]
                                                                                                                                                                  295
495 AA;
                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCB1_TaxID=5599;
                                                            HSSP; P05091;
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P42041;
                                                                                                                                                                  ACT_SITE
SEQUENCE
                                                                                                                                                                                                               Query Match
                                                                          Interpret
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 AADRAFSNGSWNGIDPIDRGKALYRLAELIEQDKDVIASIETLDNGKAISSSRG-DVDLV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 INYLKSSAGFADKIDGPMIDTGPTHFSYTKPQPLGVCGQIIPWNFPLLMWAWKIAPALVT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 AGCLRYYGGWADKIEGKVVDTAPDSFNYI-RKSLLVFAVRSSMELPILMWSWKIGPAIAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 STATGRHIYQSAA-AGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGEVÇMAG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 SRVYVEESIYDKFIEEFKAASESIKVGDPFDESTFQGAQTSQMQLAKILKYVDIGKNEGA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 SRIYVQEEIYDKFIQPFKERAAQNAVGDPF-AATLQGPQVSQLQFDRIMGYLEGKKSGA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 TLITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEY 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 TIETGGNRKGDKGYFIEPTIFSNVTEDMKIQQEE1FGFVCTISKFKTKADVIKIGNNTTY 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 GLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALQNY 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SVKLSTPQTGEFEQPTGLFINNEFVKAVDGKTFDVINPSTEEVICSVQEATEKDVDIAVA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 TVPIKLPNGLEYEQPTGLFINNKFVPSKQNKTFEVINPSTEEEICHIYEGREDDVEEAVQ 66
                                                                                                       CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 = an acid + NADH. PATHWAY: Ethanol utilization; second step.
                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 GNTVVLKTARSTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKKVAFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Achatz G., Oberkofler H., Lechenauer E., Simon B., Unger A., Kandler D., Ebner C., Prillinger H., Kraft D., Breitenbach M.; "Molecular cloning of major and minor alletgens of Alternaria alternata and Cladosporium herbarum.";

Mol. Immunol, 32:213-227(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 495;
                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: RELONS: FO THE ALLEHYDE DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.4%; Score 1362.5; DB 1; Length 54.3%; Pred. No. 1.1e-91;
Live 84; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.

BY SIMILARITY.

bF325D778808F642 CR064;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PFOMITE: PS00070; ALDEHYDE_DEHYDR_CYS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002086; Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; NAD: Allergen.
NP_BIND 240 245 N
ACT_SITE 263 263 ACT_SITE 297 297 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53577 MW,
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X78227; CAA55071.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 485 LOVKAVRAKL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480 IQTKTVSIRI, 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P05091; 1CW3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                         Pharmacol. 46:88-96 (1994).

Pharmacol. 46:88-96 (1994).

CALALLIC ACTIVITY An addedyde - VADIC.) - H(2)O an acid - NADH.

CALALLIC ACTIVITY An addedyde - VADIC.) - H(2)O an acid - NADH.

SCHAMAY: ELHanol utilization; second step.

SUBCELLARLA LOCATION: Mitochondial matrix.

INDCTION: By retinoic acid; 3 5 fold increase.

SIMILARITY: BELONGS TO THE ALDEHYDE OBHYDRAGENSES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Caps
                                          01-FEE-1996 (kel. 33, Last sequence update)
15-JUN-2802 (kel. 41, Last annotation update)
Aldehyde dehydrogenase, mitorhondial precursor (EC 1.2.1.3) (ALDH
                                                                                                                                                                                                                                                                                                                                                              Chen M., Achkar C., Gudas L.J.;
"Enzymatic conversion of retinaldehyde to retinoic acid by cloned
murine cytosolic and mitochondrial aldehyde dehydroqenases.";
                                                                                                                                                         Mammalia, Eutheria, Rodentia, Sciuroquathi, Muridae, Murinae, Mus
                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; NAD: Acetylation; Mitochondrion; Transit poptide:
TRANSIT 1 19 MITOCHONDELON (BY SIMILARITY).
CHAIN 20 519 ALDEHYDE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Score 1275.5; DR 1; Length 519; 51.0%; Prod. No. 5 5e-76;
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146; Indels
                                                                                                                                                                                                                                                                 "Cloning and characterization of the gene encoding mouse mitochondrial aldehyde dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 AF ( (1N REF. 2),
181 MISSING (IN REF. 2),
227 I = S (IN REF. 2),
344 R = C (IN REF. 2),
370 K = N (IN REF. 2),
478 S = N (IN REF. 2),
476 D = V (IN REF. 2),
565.47 MW; 20080645.044844DA CHOSA;
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514 AA
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PROSITE: PSOOG70; ALDEHYDE DEHYDK_CYS; 1.
PROSITE; PSOOG87; ALDEHYDE DEHYDK_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002086; Aldehyde_dehydr.
                                                                                            class 2) (AHD-M1) (ALDHI) (ALDH-EZ).
PRT:
                                                                                                                                                                                                                      STRAIN-C5781,/6J;
MEDLINE: 95047445; PubMed-7958964;
                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94335908; PubMed-8058062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 ;
                             01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-2DPAGE; P47738; MOUSE.
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STANDARD;
                                                                                                         ALDH2 OR AHD1 OR AHD-1.
                                                                                                                                                                                                                                                                                                  Gene 148:331-336(1994).
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89
1181
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227
344
370
370
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                                                                                                                                                                                                                                                      ., Yoshida A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           519 AA:
                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                        NCBI_TaxID-10090;
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264
264
287
321
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181
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DHAM_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253;
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RESULT 8

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121 DVDLVINYLKSSAGFADKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAWKIA 180
                                                                                                                                                                                181 PALVIGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKK 240
                                                                                                                                                                                                                                                                                  260 VAFTGSTEVG-HLIQVAAGSSNLKRVTLFLGGKSPNIIMSDADMDWAVEQAHFALFENGG 318
                                                                                                                                                                                                                                                                                                                   299 EVCCAGSRVYVEESIYDKFIEEFKAASESIKVGDPFDESTFQGAQTSQMQLNKILKYVDI 358
                                                                                                                                                                                                                                                                                                                                       359 GKNEGATLITGGERLGSKGYPIKPTVPGDOVKEDMPIVKEEIPGPVVTVTKEKSADEVINM 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 ANDSEYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSV 478
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                                                                                                                                                 140 DEDMYTACTARYRAGWAEKYHGKIIPIEGEFFSYTKHEFVGVGGLIPWNFPELLMQAWKLG 199
                                                                                                                                                                                                                                                    241 VAFTGSTATGFHIYQSAA--AGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSG 298
Jeng J., Weiner H.;
"Purification and characterization of catalytically active precursor
of rat liver mitochondrial aldehyde dehydrogenase expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Melahai, Chindata, Chaniata, Vertubrata, Eutubeustomi.
Mammalia, Eutheria, Rodentia, Sciurograthi, Mulidae, Mulimae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Farres J., Guan R.-L., Weiner H.;
"Sequence of the signal peptide for rat live: mitochondrial aidehyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1989 (Rel. 12, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
16-Gebydusenses, mitcolondrial precursor (EC 1 2 1 3) (ALPH class 2) (ALDH1) (ALDH-E2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89210865, PubMed-7548003;
Parres J., Guan K.-L., Weiner H.;
"Primary structures of rat and bovine liver mitochondrial aldehyde
dehydrogenases deduced from cDNA sequences";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem, Biophys Res. Commun 150:1083-1087 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           519 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88134217; PubMed=3342050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91378548; PubMed-1898068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem 180.67-74(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegious (Pat)
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This SWISS-PROT entry is copyrigh. It is produced though a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation her Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and so its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 BAVOAADFAPSNGS-WN310P1DPGKAD,YFLAELTEQPRIVIASTETLDNGKA-ISSSRG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 TVPIKLPNGLEYEQP----TGLFINNKFVPSKQNKTFEVINPSTEEEICHIYEGREDDVE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 TSAVPAPN----QQPEVPCNQIFINNEWHDAVSKKTPPTVNPSTGEVICQVAEGNKEDVD 79
           DVDLVINYLKSSASFALKIDGPMIDTGPTHFSYTKPQPT;GVGG21TPWNFP1.LMWAWK!A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 PALVTGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 VAFTGSTATCHIYQSAA--AGLKKVTLELGGKSPNIVFADAELKKAVQNIILCIYYNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; NAD; Aretylation; Mirochondrion; Transit peptide.
TRANSIT 1 19 MITOCHONDKICON.
CHAIN 20 519 ALDERYDE DEHYDPGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%; Score 1274.5; DB 1; Length 519;
                                                                                                    SIMILARITY - RELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PS00070, ALDEHYDE_DEHYDR_CYS; 1. PROSITE: PS000887; ALDEHYDE_DEHYDK_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPRUU2U86; Aldehyde_dehydr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56488 MW;
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A27713; A27713.
S03564; S03564.
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HSSP; PU5091; 1CW3.
Escherichia coli.";
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HSU L.C., Tani K., Fujiyoshi T., Kurachi K., Yoshida A.; "Cloning of cDNAs for human aldehyde debydregenases 1 and 2.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Braun T., Bober E., Singh S., Adarwal D.P., Goedde H.W.
FEBS Lett, 233:440-440(1988).
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MEDLINE-86055846; PubMed-4065146;
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                                                                                                                                                                                                                 479 DALQNYLQVKAVRAKL 494
                                                                                                                                                                                                                                                                       480 YGLQAYTEVKTVTIKV 495
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                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD
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                                                                                                                                                                                                                              15-UUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase, mitochondrial (EC 1.2.1.3) (ALDH class 2)
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa: Chordata, Craniafa, Veitebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hjelmqvist L., Lundgren R., Norin A., Joernvall H., Vallee B., Klyosov A., Keung W.M.;
"Class 2 aldebyde debydrograsse. Characterization of the hamster enzyme, sensitive to daidzin and conserved within the family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
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BY SIMILARITY
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PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1
                                                                                                                                                                                                                                                                                                                                                                                      Mesocricetus auratus (Golden hamster).
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NP_BIND 245 250 NAD (A
ACT_SITE 268 268 BY SIM
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                                                                                                                                                                                                           .5-JUL-1998 (Rel. 36, Created)
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500 AA; 54334 MW;
499 YGLQAYTEVKTVTVKV 514
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                                                                                                                                                     STANDARD,
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Matches 251; Conserva
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                                                                                                                                                                                                                                                                                                                                (ALDH1) (ALDH-E2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mesocricetus
                                                                                                                                                 DHAM_MESAU
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360 GQQEGAKLLAGGGAAADRGYETQPTVFGDVRJAMTTAKEETFGFVMQTLREKTTEEVVGR 419
                                                                         419 ANDSEYGLAAGTHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSV 478
                                                                                                                MEDLINE-88256152, PabMed-2838413,
Hsu L.C., Bendel R.E., Yoshida A.;
"Genomic structure of the human mitochondrial aldebyde debydroaemase
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Isolation and sequence analysis of a full length cDNA clone coding
for human mitochondrial aldehyde dehydrogenase.";
Nucleic Acids Res. 15:3179-4179(1987).
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13-AUG-1987 (Rel. 05, Created)
13-AUG-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase, mitochondrial precursor (EC 1.2.1.3) (ALDH
class 2) (ALDH) (ALDH-E2).
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Eukaryota, Metazoa; Chordata; Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hempel J., Kaiser E., Joernvall B.; Mitochondrial aldelyde dehydrouenase from human liver. Primary structure, differences in relation to the cytosolic enzyme, and functional correlations."; Eur. J. Biochem. 153:13-28(1985).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.

CAUTION: THE CONFLICTS BETWEEN THE SEQUENCE DETERMINED IN REF I AND FEF 2 AND THAT IN PEF 3 AND 4 ARE PROHEHLY ALL DUE TO THE SEQUENCE DETERMINED IN PEF 1 THE SEQUENCE DESCRIPED IN PEF 5 AND PEP 5 AND PEP
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-!- PATHWAY: Ethanol utilization; second step.
-!- SUBUNIT: HOMOTETRAMER.
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"Mitschin Jial ald-Eyde Dehydrogenase. Hamulegy of putative turgeting
sequence to that of cartamyl phosphate synthetase I revealed by
Correlation of cDNA and protein data.";
FEBS Lett. 222:95-98(1987).
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"Molecular aknormality of an inactive aldehyde dehydrogenase variant
ocommonly found in Orientals.";
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Ni L., Zhou J., Hurley T.D., Weiner H.;
"Human liver mitochondrial aldehyde dehydrogenase: three-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 structure and the restoration of solubility and activity of chimeric
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DISEASE: A VERY HIGH INCTPRNCE OF ACUTE ALCOHOL INTOXICATION IN
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"Human aldehyde dehydrogenase isonymes and alcohel sensitivity.";
Isonymes Curr. Top. Biol Med Res 16:21 48(1987).
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                                                                                                                   SEQUENCE OF 119-517 FPOM N.A.
MEDILIDE 85252089; Dubmad-4015823,
Yoshina A., Ikawa M., HSU L., Tani K.;
"Molecular abnormality and cDNA choning of human aldehyde
Natl Arad, Sci. II.S.A 82:3771-3775(1985)
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258 VAFTGSFFTGPVTOVAAGSSNIKRVTUFLGGKSPNITINSDADMDWAVFDAHFALFFNOGO 317
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S -> A (IN REF. 2).
VKAARA -> REGRPG (IN REF. 3 AND 4).
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NAD (ADP PART) (BY SIMILARITY).
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/FTId=VAR_011302.
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A -> P (IN PEF 9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1253.5; DB Pred. No. 1.5e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId-VAR_011869.
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E -> Q (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterFro, IPF001086, Aldehyde_dehydr.
Perm: PF00111; aldedh: 1.
PROSITE, PROSITE, PROSITE; PS00687; ALDEHYDE_DEHYDE_CYS; I
PROSITE; PS00687; ALDEHYDE_DEHYDE_GUJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         M26760; AAA51694.1, -
M54931, AAA62825.1, ALT_FRAME.
                                                                                          JOINED.
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                                                                  JOINED.
                                                                                                                                                            AAA51693.1; JOINED.
                                                                                                                                                                                                                            JOINED.
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                                                                                                                                                                                                                                                                                                                                                    BC062967, AAH02967.1; -.
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                                                                                                                                                                                                                                                             AAA51693.1; CAA51693.1; CAA516
                                                                                                                                                                                                                                                                                                                                                                                     K03001; AAB59500.1;
AAA51693.1;
AAA51693.1;
                                                                                                                                                                                                                                                          M20454; AAA51693.1;
                                                                                                                                                                                          AAA51693.1;
                                                                                                                                                                                                                     AAA51693.1;
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26
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PIR; A24975; A24975.
PDB; ICW3; 10-JAN-00.
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   M20446;
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M20450;
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EMBL; M20444; AAA51693.1; JOINED. EMBL; M20445; AAA51693.1; JOINED.

EMBL, M20456; AAA51693.1; -

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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entities requires a licence are not removed.
300 VCCAGSRVYVEESIYDKFIEEFKAASESIKVGDPFDESTFQGAQTSQMQLNKILKYVDIG 359
                                                                              360 KNEGATLITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMA 419
                                                                                                                                                        420 NDSEYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVD 479
                                                                                                                                                                                             438 NNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGEY 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLARIAR LOCATION: Mitochondrial matrix.
TISSUE SPECIFICITY: LIVER, TESTIS AND IN A LESSER EXTENT IN BRAIN.
SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: ALDHS PLAY A MAJGE RGLE IN THE DELOXIFICATION GE
ALCOHOL-DERIVED ACETALDEHYDE. THEY ARE INVOLVED IN THE METABOLISM
OF CORTICOSTEROIDS, RIGGENIC AMINES, NEUROTRANSMITTERS, AND LIDID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 = an acid + NADH
                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase X. mitochondrial precursor (EC 1 2 1 3) (ALDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hsu L.C., Chang W.-C.; "Cloning and characterization of a new functional human aldehyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sherman D., Davo V., Hsu L.C., Peters T.J., Yoshida A.;
"Diverse polymorphism within a short coding region of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Ethanol utilization; second step. SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                            517 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aldehyde dehydrogenase-5 (ALDH5) gene.";
Hum. Genet. 92:477-480(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266-12257 12265(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPP002086; Aldehyde_dehydr
                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94063858; PubMed-8244338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91286241; FubMed=2061311;
                                                                                                                                                                                                                                    480 ALONYLOVKAVRAKI, 494
                                                                                                                                                                                                                                                                         498 GLQAYTEVKTVTVKV 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M63967; AAA96830.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALDH1B1 OR ALDH5 OR ALDHX.
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC.407, ALDHIBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dehydrogenase gene."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEROXIDATION.
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P30837,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 NTVVLKTAESTPLSALYVSKYTPQAGTPPGVINTVSGFCKTVVEATTNHPKTKKVAFTGS-246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 TATGRHIYQSAA--AGLKKVIDELGGKSPNIVFADAELKRAVDNIIDGIYYNSGEVGGAG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 TLITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEY 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383. KILCGGERFCERGFFIKPTVFGGVQDDMPIAKEFIFGPVQDJ FKFYK I FFVVFPANNI 92-442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 KVYRYFAGWADKWHGKTTPMHGQHFCFTKHEPVGVCGQTTPWNFFLVWGGWKLAPALATG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.25 GLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALONY 444
                                                                                                                                                                                                                                                                               9 PIKLPNGLEYEQPTGLETINNKEVPSKONKTFEVINPSTEEETCHTYEGREDDVEEAVOAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 SRVYVEESTYDKFLEEFKAASESTKVGDPFDESTFQGAQTSOMQLNKILKYVDLGKNEGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae
              Oxidoreductase, NAD; Mitochondrion; Transit poptide; Folymotphism
TRANSIT 1 17 MITOCHONDRION (FOTENTIAL).
CHAIN 18 517 ALDEHYDE DEHYDROXENASE X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT 2001 (Rel. 40, Last annotation update)
Aldehyde dehydrogenase 1A2 (EC 1.2.1.3) (Retinaldehyde specific dehydrogenase type 2) (RALDH(11)) (RALDH-2).
ALMHAZ OF PALDH2.
Gallus qallus (Chicken).
                                                                                                                                                                                                  DB 1; Length 517;
                                                             NAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                     85; Mismatches 148; Indels
                                                                                                                                                                    78AC173AA3687165 CRC64;
                                                                                                                      ZETIG VAR_002257.
L - - R (IN ALDHAIB1*3).
                                                                                                         A · V (IN ALDHAIRI*2)
                                                                                                                                                                                                                   Pred. No. 4.2e 74;
                                                                                                                                                     ZETLA VAR 002258
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                                                                                                                                                                                                  49.0%; Score 1248.5;
PROSTITE: PS00687; ALDERYDE DERYDR GLD; 1.
                                                                          POTENTIAL.
                                                                                          POTENTIAL
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Sockanathan S., Jessell T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                     57217 MW;
                                                                                                                                                                                                               50.68;
                                                                                                                                                                                                                                Matches 248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                        517
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285
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                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                    517 AA;
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                                                                            ACT_SITE
ACT_SITE
                                                                                                                                                                    SEQUENCE
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                                                            NP_BIND
                                                                                                         VARIANT
                                                                                                                                        VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 DASERGOLLDKLADLVERDFAVLATMESINSGKPFLQAFYVLILØSVIKTI.RYYASWADKI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 DPIDRGKALYRLAELIEQDKDVIASIETLDNGKA-ISSSRGDVDLVINYLKSSAGFADKI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .40 DGRMIDTGRIHFSYTKRQPLGVGGQIIPWNFPLLMWAWKIAPALVTGNTVVLKTAESTPL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 SNLKRVTLELGGKSPNI1FADADLDYAVEQAHQGVFFNQGQCCTAGSRIYVEESIYEEFV 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SALYVSKY I PQAGTPPGV (NTVSGFGK TVVEATTNHPK EKKVAFTGSTATOPHTYGSAA- 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 SALYMGALIKEAGFPPGVVNILPGFGPIVGAAIASHVGIDKIAFFGSTEVGKIIQEAAGR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 AGIKKVTLFIGGKSPNIVFADAELKKAVQNIILGIYYNSGEVCCAGSRVYVEESIYDKFI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 EEFKAASESIKVGDEFDESTFLOALTSQMQINKILKYVDIGKNEGATLITGGEFFGSRGY (7)%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 FIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADFVINMANDSEYGLAAGIHTSNINTA 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 TKIFINNEWQNSESGRVFPVYNPATGEQICFIQEADKVDTDKAVRAARLAFSLGSVWRRM 78
                                                    FINATION: PECONIZES AS SUBSTRATES FREE RETINAL AND CELLULAR PETITION: PECONIZES NOT METABOLIZE OCTANAL AND DECANAL BRILDING PROTEIN-BOUND RETINAL. DOES METABOLIZE OCTANAL AND DECANAL BRILDING, MCETALLEHYDE, ACETALLEHYDE, AND ROPANAL EFFICIENTY, (BY SIMILARITY) + H(2)0 = an acid + NADH. CATALTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 = an acid + NADH. PATHWAY. FFINACI ACID BIOSENESIS.
SUBMINIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYLOPIASANIC.
SIMILARITY: RELONGS TO THE ALDEHYDE UBHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 LKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALQNYLQVKAVRAKI, 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3, Gaps
"Motor neuton-derived retinoid signaling specifies the subtype identity of spinal motor neurons.", Cell 94:503-514(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR 1, Irength 499,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAD (ADP PART) (BY SIMILARITY).
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Pred. No. 5.5e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFam: PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDE_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDE_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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SEQUENCE
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63 EAVQAADRAFSNGS-WNGTDPTDPGKALYPLAELJEQDKDVIASIFTLDNGKA-1SSSPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 FALVESHLVVLKTAPSFESALYSKY DQASTPPTVINIVSGFGKIVVPATTNHPKTKK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 TVPIKLPNGLEYEQP----TGLFINNKFVPSKQNKTFFVINPSTEEFICHTYEGREDDVE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 TOAVPIPN----OGPEVLYNOTFINNEWHEAVSKKIFPTVNPSIGEVICHVAEGEKAEVE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CAIALYLIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 = an acid + NADH.
-!- PATHWAY: Ethanol utilization; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Gaps
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Fram, FP00717; aldedh: 1.

ProsTTE; ESGOGS7, AlloHMYDE; DEHYDE_CYS; 1.

PROSTIE: PSGOGS7, AlloHMYDE; DEHYDE_COJ; 1.

PROSTIE: PSGOGS7, AlloHMYDE; DEHYDE_COJ; 1.

Oxidoreductase; NAD; Mitochondrion; Transit peptide; 3D-structure.

MITOCHONDRION.

PROSTIEST STRUCTURE.
             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Pel. 17, Last sequence update)
15 JUN 2002 (Rel. 41, Last annotation update)
Aldebyde dehydrogenase, mitochondrial precursor (EC 1.2.1.3) (ALDH class 2) (ALDH1) (ALDH-E2).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Farres J., Guan K.L., Weiner H.;
"Primary structures of rat and bovine liver mitochondrial aldehyde
dehydrogenases deduced from cDNA sequences.";
                                                                                                                                           Eukuryota, Metuzoa) Chordata; Graniata; Vertebiata; EuteleOstomi;
Mammalia; Putheria; Cetartiodartyla; Puminantia; Pecera; Bevoidea;
                                                                                                                                                                                                                                                                                                            "Sequence of the precursor of bovine liver mitochondrial aldehyde dehydrogenase as determined from its cDNA, its gene, and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97341232; PubMcd-9195888;
Steinmetz C.G., Xie P., Weiner H., Hurley T.D.;
"Structure of mitochondrial aldehyde dehydrogenase: the genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1240 5; DB 1; Length 520;
Pred No. 1,1e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SURCELLULAR LOCATION: Mitochondrial matrix.
-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALDEHYDE DEHYDROGENASE.
NAD (ADP PART) (BY SIMILARITY).
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BY SIMILARITY.

F920RGFC05B5A65R CRC64,
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                                                                                                                                                                                                                                                                                                                                                                  Arch. Biochem. Hiophys. 277:351-360(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-PAY CPYSTALLOGRAPHY (2 65 ANGSTROMS).
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InterPro: IPR002086: Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89210855; FubMed-2540003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Blochem. 180:67-74(1989).
                                                                                                                                                                                                                                                                        MEDLINE=90179198; PubMed=1689984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        component of ethanol aversion.";
Structure 5:701-711(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56708 MW.
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44 28;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 92-520 FROM N.A.
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                                                                                                                                                                                  Bovidae; Bovinae; Bos.
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2888
322
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                                                                                                                              Bos taurus (Bovine).
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S09030; S09030.
                                                                                                                                                                                                                                                                                             Guan K., Weiner H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                 NCB1_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                 functionality.";
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ACT_SITE
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SEQUENCE
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SIANDARD;

DHAM\_ROVIN

DHAM\_BOVIN

RESULT 14 ďI us-09-830-751-2.rsp

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241 VAFTGSTATGRHIYGSAA--AGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSG 298
                                                                                      299 EVCCAGSRVYVEESIYDKFIEEFKAASBSIKVGDPFDESTFQGAQTSQMQINKILKYVDI 358
                                                                                                                                                                                    320 OCCCAGSRTFVOEDIYAEFVERSVARAKSKVVGNPFDSRIEGGPGVDETGFKKVLGYIKS 379
                                                                                                                                                                                                                               359 GKNEGATLITGGERLGSKGYFIKPTVFGDVKFDMPIVKEEIFGPVVTVTKFKSADEVINM 418
                                                                                                                                                                                                                                                                                                                                     380 GKEEGLKLLGGGGAAADRGYFIQPTVPGDLQDGMTIAKEEIFGPVMQ1LKFKSMEEVVGR 439
                                                                                                                                                                                                                                                                                                             419 ANDSEYGLAAG HTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGFEMSV 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acting as cofactors for GATA3.";
Mol. Cell. Biol. 18:6939-6950(1998)
-:- FUNTION. PERMONIZES AS SUBSTRATES FPEE RETINAL AND CELLULAR
RETINACL-BINDING PROTEIN-BROWN PETINAL. DOES METAHOLIZE OCTANAL AND
DECANAL BUT DOES NOT METABOLIZE CITRAL, BENZALDEHYDE, ACETALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND PROPANAL EFFICIENTLY (BY SIMILARITY).

AND TRAINING ACTIVITY: An aldebryde + NAD(+) + H(2)O = an acid + NADH.

PATHWAY: REIINOIC ACID BIOGENESIS.

SUPPRINT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dehydrogenase 2 expression in T-cell acute lymphoblastic leukemia by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ono Y., Fukuhara N., Yoshie O.,
"TALI and LIM-only proteins synergistically induce retinaldehyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.JUL-1999 (Rel. 38, Last Sequence update)
15.JUN-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrosenuse 1A2 (FT 1.2 1 3) (Fertinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2).
ALDHIAZ OR RALDH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: RELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
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Pfam; PF00171; aldedh; 1.
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63 EAVQAADRAFSNGS-WNGTDPTDRGRAL/PRIJAELJEQDRDVIASTETLDNGRA ISSSRG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 VAFTGSTATGFHTYQSAA-ANLIKKVILLELGGKSPINIVFADAELFRAVGNI 11/31YYNSGE 299
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NAD (ADP PART) (BY SIMILARITY).
                                                                                                                               90; Mismatches 147; Indels
                                                      FEOR5 3A47644.246B CRC64;
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Pred, No. 4.9e 73;
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                   POTENTIAL.
                                       POTENTIAL
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                                                                                           48.28
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 249
267
301
                                                    499 AA;
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267
301
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Search completed: June 24, 2003, 10:14:26 Job time : 11.9698 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Campugen Ltd
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probein search, using sw model OM protein Jame 24, 2003, To use 15 ; Search time 37 MMS2 Seronds (without alignments) 2692.168 Million cell updates/sec Fun obs

US-00-830-751-2 Title:

.. MSVDALUNYLUVKAVBAKID 495 1 MSHLPMTVPIKLPNGLEYEQ Perfect score. Sednence:

**BLOSTIM62** Scoring table:

671580 seqs, 206047115 residues Gapop 10 0 , Gapert 0 5

Searched.

Total number of hits satisfying whosen parameters

Minimum Db seq length: 0

Maximum DB seq length: 2000000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

Database :

sp\_archea:\* sp\_bacteria:\* SPTREMBL\_21:\*

sp\_unclassified:\* sp\_human:\*
sp\_invertebrate:\* sp\_vertebrate:\* sp\_bacteriap:\* sp\_organelle:\* sp\_phage:\* sp\_plant:\* sp\_todent:\* sp\_rvirus:\* sp\_mammal:\* sp\_virus:\* sp\_fungi:\* sb\_mhc:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

## SUMMARIES

NO. SCOTE NO. 1807 1 1807 1 1807 1 1808 1 18	140				
11 1807 1504 1433.5 1423.5 6 1423.5 7 1352.5 1252.5 11 1252.5 11 1252.5 12 1252.5 12 1252.5 12 1252.5 12 1252.5 12 1252.5 12 1252.5 12 1252.5	11.5.101	Match Length DR	Έ	ID	Description
2 1504 3 1442 4 1433.5 5 1423.5 6 1429.5 7 136.2 10 126.5 11 125.5 12 125.5 12 125.5 13 125.5 13 125.5 14 125.5 16 125.5 17 125.5 18 125.5 18 125.5 19 125.5 10 125.5 1	9.07	518	, 5	Q12648	Olž648 pichia angu
3 1442 141343 14235 6 14235 7 12525 10 12525 11 1252 11 12525 12505 12505 12505	59.0	474	~	Q8X01.4	Q8x014 heurospera
4 1433.5 1429.5 1429.5 1365.6 1262.5 10 1262.5 11 1252.5 12 1250.5	56.5	497	~	098303	
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	49.0	537	'n	OMXIAO	09txm0 caenorhabdi
13 1249.5	49.0	517	4	Q9PV45	Oghv45 homo sapien
14 1247.5	48.9	549	10	Q9FRX7	Q9frx7 oryza sativ
15 1246 5	48 g	549	10	Q91.1.R2	odlr2 orvza sativ
16 1244.5	48.8	519	11	090281	Q9czsl mus musculu

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5 00NJH2 13 080602 10 043774			11 Q9J172 13 Q9DEX <sup>5</sup> 15 Q9KFE2 10 Q94 <i>C</i> 57	C+C+	10 291810 13 29186 13 090046 13 091807	3 Q90Y03 Q90Y03 Q90K99 Q9UKW9 0 Q8S528
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8 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	47.9 47.9 47.9	47.4 47.7 47.7	4444 6. r 44 6. r . s s s s s s s.	447 22 47 22	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	446 3 446 2 446 0 45 9
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## ALIGNMENTS

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2 SHLPMTVPIKLPNGLEYEQPTGLFINNKFVPSKQNKTFEVINPSTFEETGHIYFG7PEDDV 61
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                                                                                                                                                                             Eukaryota, Fungi, Ascomycota, Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia
                                                                                                                                                                                                                                                                                                                                          Prilhenberg P.G., Ab G.;
Submitted (N°V-1995) to the EMBL/Genkank/ADAG databases.
-:- SIMILARITY: RELONSS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.39, Score 1807; DB 3; Length 518;
Best Local Similarity 68.29; Pred. No. 1.5e-114;
Matches 337, Conservative 72, Mismatches 83, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              518 AA; SEL33 MW; T9F7D45ge5JA5J1F CPC64;
                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 20, Last sequence update)
Aldehyde Gehydrogenase (EC 1.2.1.5).
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Pefam; PP0011; aldedbyl.
PP0817TE, PS02070, ALDEBYDP_DEBYDP_GFU; UNENOWN_1.
PP0817E; PS0687; ALDEBYDP_DEBYDP_GFU; UNKNOWN_1.
                                                                                                                                                              Pichia angusta (Yeast) (Hansenula polymorpha).
                                    518 AA
                                                                                                                                                                                                                                                                                        Thesis (1989), Unknown Institution.
                                    PPT;
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                                    PPFI.IMINAPY;
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                                                                                                                                                                                                                             242 AFTGSTATGRHIYQSAA-AGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGEV 300
                                                                                                                                                                                                                                                                                                                                                                                                       301 CCAGSRVYVEESIYDKFIEEFKAASESIKVGDPFDESTFQGAQTSQMQLNKILKYVDIGK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                      361 NEGATLITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMAN 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSEYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 EEAVQAADRAFSIGSWIGTIPPTDFGKALYPLAELTEQDKDVIASTETLDNGKAISSSFGD 121
                                                  82 DVAVDAAEKAF-KGSWSTADPAIRGKAIWNLAELLEAHKDTLAAIESLDNGKALQLAQGD 140
                                                                                                    122 VDLVINYLKSSAGFADKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAWKIAP 181
                                                                                                                                                                                                                                                                                                                                                       261 AFTGSTATGRHIMKVAADSNLKKVTLELGGKSANIVFDDADVKTAISALVAGIFYNSGEV 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schulte U., Algn V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H W., Mannhaupt G.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       German Neurospora genome project;
Submitted (JAN-2002) to the EMBL/GenBank/DDHJ databases.
EMBL: A1669991; CAD211281; -.
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR001128; Cytochrome_P450.
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01-JUN-2002 (TrEMBLrel, 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prosite: Proof71: aldedh; 1.
PROSITE: PS00070: ALDEHYDE_DEHYDR_CYS: UNKNOWN_1.
PROSITE: PS00687: ALDEHYDE_DEHYDP_GIU: NRNOWN_1.
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Matches 278, Conservative
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are also indeced during arouth in planta ".
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HSSP; P05091; 1CW3.
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                                                                                                                              4 LPMTVPIKLPNGLEYEQPTGLFINNKFVPSKQNKTFFVINPSTEEFICHIYEGREDDVEE 63
                                                                                                                                                                                          1 MSLSVQLEIPSAGKYEQPIGLFINNEWVKPVSGKFFDVINPTDESVICQVAEADEKDVDI 60
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J Riol. Them 276-6450-6458(2001)
-1- SIMILARITY: RELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY
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Eurotiales, Trichocomaceae, Emericella.
NCBL_TaxID=5072;
58.5%, Sepre 1442, PB 3, Length 497, 53.9%, Pred. No. 9 15-90; Ed. 85; Mismatches 130; Indels
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01-JUN-2001 (TTEMRLIEL, 17, Last sequence update)
01-MAP-2002 (TTEMRLIEL, 20, Last angotation update)
Aldehyde dehydrogenase ALDH15.
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PROSITE: PSCOOFR; ALDEHYDE_DEHYCK_GLU; 1.
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HSSP; P05091; 1CW3.
                                                               265; Conservative
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                                                                       5; Gaps
56.2%, Score 1433.5; DB 3; Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ethanol utilization pathway in Aspergilius nidulans.";
J Biol Chem 276-6450-6458(2001).
--- SIMILAPITY - HELOWIS TO THE ALDPHYDE DEHYDEOGENASES FAMILY.
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Burotiales; Trichocomaceae; Emericella.
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01-JUN-2001 (TrFMBLrel. 17, Last sequence update)
01-MAR-2002 (TrFMBLrel. 20, Last annotation update)
                             Pred. No. 3.4e 89; 88, Mismatches 129,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           497 AA.
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PPOSITE; PS00070; ALDEHYDE_DEHYDE_CYS; PPOSITE; PS00697; ALDEHYDE_DEHYDE_GLU;
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HSSP; P05091; 1CW3.
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                         Best_Local Similarity 55.2%;
Matches 273, Conservative 6
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                                                                                                                                    IKYEQPLGLFINNEFVKGVEGKTFGVINFSNEKVITSVHEA1EKD
                                                                                                                                                                                                                                                                                                                                  Caps
                                                  DB 3; Length 497,
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Eurotiales: Trichoromaceae; Emericella,
               9C6CFC62731A25BD CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence updatc)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                               ; Pred. No. 6.4e-89; 87; Mismatches 130
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                                                  56.1%; Score 1429.5;
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PROSITE: PS00070; ALDEHYDE_DEHYDE_CYS; 1
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61 VESAVQAADRAFSNGSWINGTOPTDROKALYRLAELTEGDROVTASTETLONGKATSSSRG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 PALVTGNTVVLKTAESTPLSALYVSKY1PQACTPGVINIVSGFGKIVVEATTNIPKTKK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 KNEGATLITGGEPLGSKGYFIKPTVFGDVKEDMRIVKFFIFGDVVTVTKFESADEVINMA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 VDVAVAAARAAF EGPWRQVI PSERGTLI NKLADLMERD I DTLAATESLD NGKAFTMAKV - 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 PVDLVINYLKSSAGFAPKTIMTPMIPTGPTHPSYTKROPLAVAGGITPWNFPLLAMMAWKIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297. CCCAGSPILVQEGIYDKEVAPEKEPAQKNKVGNPFEQDTFQSPQVSQLQEDRIMEYINHG. 356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.20 INDSEYGLAAGTHTSNINTALKVADPVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVD 4.79
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                                                                                                                                                                                                                                                     1 MSHLAMTVPTALPNGLEYEQPTGLETANKFVPSKONKTFEVTAPSTEEETCHTYEGREED.
                                                                                                                                                                                                                                                                                                                          1 MSIGLET FLELEV - - - LEYEQFIGUE LINNEFVEGYERERENDY INFSNERVTSVHENTERD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 VAPTGSTATGRHIYQSAA-AGLKKVTLELGGKSPNIVPADAFLIKKAVÇNI (631 YYNS)E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 VCCAGSKYYVEESTYDKETEEFKAASESTKVODPEDESTFYGGALTSQMUNKTLKYVDTG
                                                                                                                                                                                 Sdeg
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Submitted (SEP-1997) to the EMRL/AbenKank/DDACL databases.
-!- CATALYTIC ACTIVITY: ALDEHYDE + NAD(*) + H(2)0 — ACTD + NADH.
                                                                               score 1423.5; DB 3; Length 497;
Pred. No. 1.6e 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO THE ALDERYDE DERYDROGENASES FAMILY.
                                                                                                                                                                              141; Indels
                              54F425A3B3063B75_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NGV-1998 (TrEMBLiel 08, Last sequence apdate)
01-JUN-2001 (TrEMBLiel, 17, Last annotation apdate)
Probable aldehyde dehydroqenase (EV 1.2.1.9) (ALDAH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schinosaccharomyces pombe (Piesion yeast).
Bakaryota: Fungi: Ascomycota, Schinosaccharomycetes;
Schinosaccharomycetales; Schinosaccharomyceteses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: SECOND STEP IN ETHANOL UTILIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            504 AA
                                                                                                  55.8%; Score 1424.5;
                                                                                                                                                                              87; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
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Pfam; PF00171; aldedh; 1.
s · · 6.
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                              54168 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          477 ALENYTOIKTVHYRL 491
                                                                                                                                    54.9%;
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HSSP; P05091; 1CW3.
                                                                                                                                                                              Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                              497 AA;
                                                                                                                                        Local Similarity
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3.38
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                                     SEQUENCE
                                                                                                      Query Match
VARIANT
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ADPAF-SNISWNGTOPTIRGKALYPLARTTRUCKDVIASTETLINGKATSSSEGDVDLVT 126
                                                                                                                                                                                                       127 NYLKSSAGFADKIIGSMIDTGSPTHFSYTKMQPLJJVGQFIPWNPPLLJMWAWKIAPALJTG 186
                                                                                                                                                                                                                                                               247. TATGRITYQSAA-AGURKVTUEDGGKSPHIVPADAELKRAVQNITIGTYYNSGEVGTAGS (668
                                                                                                                                                                                                                                                                                                                                                                                  306 PVYVEESIYDKFIEEFKAASESIKVGDPPDESTFQGAQTSQMQLAKILKYVUJGKNEGAT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                             LITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADFVINMANDSFYG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 LEIGGKRHGNLGYFVEPTILSNVTEDMAVGKEEIFGFVLAVIKFKTIEEAIRRGNNSTYG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 LAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALQNYL 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 VPIKLPNGLEYEQPTGLFINNKFVPSKQNKTFEVINPSTEEEICHIYEGREDDVEEAVQA 67
                                                                                                                                                187 NIVVEKTAESTPESALYVSKYIPQAGIPPGVINIVSGEGKIVVEAITNHPKIKKVAFTGS
                                                                                                     7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SIMILARITY BELONGS TO THE ALDEHYDE DEHYDRUGENASES FAMILY EMBL; IT74468; AAC49575 1; -. HSSP; POSO91; 1CW3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Fungi, Rasidiomyotta, Ustilaginomyottos.
Ustilaginomyottidae, Ustilaginales, Ustilaginaceae, Ustilago
NAD (ADP PART) (BY SIMILARITY).
                                                                       DB 3; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rasse C.W., Lottspeich F., Steglich W., Kahmann P.;
"Two potential indole-3-acetaldehyde dehydrogenases in the
                                                                                                   84; Mismatches 141; Inders
          270 BY SIMILARITY.
304 BY SIMILARITY.
54768 MW; A778/Azirippeqces circled.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997 (TrEMBLrel, 02, Last sequence update)
01-MAR-2002 (TrEMBLrel 20, Last annotation update)
Indole-3-acetaldehyde dchydrogenase (EC 1.2.1.3).
                                                                    Score 1362, DB 3;
Pred. No. 2.5e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              497 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phytopathogenic fungus Ustilago maydis.";
Eur J. Biochem. 242.648-656(1996).
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PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
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                                                                                    53.68;
                                                                       53.48
                                                                                                   262; Conservative
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252
270
304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     489 QTKAVHINL 497
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                                                                                    Similarity
                                          503 AA;
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            ACT_SITE
ACT_SITE
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                                           SEQUENCE
                                                                       Query Match
 NP_BIND
                                                                                       Local
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                                                                                                   Matches
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185 TGNEVVLKTAESTELSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKKVAFT 244
                                                                                                                                                                                                                                                                                                                                    303
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                                                                                                                                                                                                                                                                                                                                                                                            404 GSPVYVERSTYDKPIEEFKAASESIKVADPFDESFPWADJSQMQLDKILKYVIIGKNBG 363
                                                                                                                                                                                                                                                                                                                                                                                                                           302 GSPVYVERSTYDAPMEKMTAH/VALQVGDPSANTFGGDQVSQTQYDFIMEYTESGKKD- 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 ATLIIGGERLGSKGYFIKPTVFGDVKFDMPIVKHEIFGPVVIVTKFKSADEVINMANDSE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.24. YGLAAGIHTSNINTALKVADKVNAGTVWINTYNDFHHAVPFGGFNASGLGKEMSVDALQN 483
                                                                                                                                                                                                                  .25 VINYEKSSAGFAEKIEGPMILTGPTHFSYTKPQPLGVCGQIIPWNFPLLMWAWKIAPALV 184
                                                                                                 7 TVPIKLPNGLEYEQPTGLFINNKFVPSKÖNKTFEVINPSTEEELCHIYEGKEDDVEEAVQ 66
                                                                                                                             3 TLNLDLPNGIKSTIQADLFINNKFVPALDGKTFATINPSTGKEIGQVAEASAKDVDLAVK 62
                                                                                                                                                                                                                                                                                                                                    245 GSTATGRHIYQSAAA-GLKKVTCELGGKSPNIVFADAELKKAVQNIILGIYYNSGEVCCA
                                                                                                                                                                                                                                                                                                                                                  67 AADPAFSNGSWNGIDPID-PGKAL/PLAELIEQDKDVIASIFTLDNGKAISSSPG-DVDL
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Phahditida; Phahditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The C elegans Sequencing Consortium.";
                                         TH 4: Long*h 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the nematode of elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The sequence of C. elegans cosmid F54D8."; Submitted (NoV-1994) to the FMRL/GenBank/DDBJ databases.
            497 AA; 53738 MW; BE7DA689D6A4BUC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.0%; score 1435 5; 106 4; 53.2%; Pred. No. 7.5e-82; Live 89; Mismatches 136,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99009913; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology The 7
Science 282:2012 2018(1998).
                                                       Best Local Similarity 53.2*
Matches 261; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484 YLQVKAVRAKL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 YTNIKAVHVNL 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenothabditis eleyans.
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Oxidoreductase
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               SEQUENCE
                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 RAFSNGS-WNGIDPIDPGKAL/YRLAEL/JEQDKDVIASIETLDNGKAIS-SSRGDVDLVIN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                   78 NAFRIGSEWRRMDASORGVLLNRLADIMERDRVILASLESLDNGKPYAVAYNADLPLSIK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 YLKSSAGFADKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAWKIAPALVTGN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 ATGRHIYQSAA-AGLKKVTLELGGKSPNIVFADAELKKAVQNIILGIYYNSGEVCCAGSR 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 EVGRLVMKAAAESNVKKVTLELGGKSPNIIFADADLNDSVHQANHGLFFNQGQCCCAGSR 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427 AAGIHTSNINTALKVADRVNAGTVWINTYNDFHHAVPFGGFNASGLGREMSVDALGNYLQ 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 TFVEGKIYDDFVARSKELAEKAVIGDPFDLKTTQGPQVDGKQVETILKYIAAGKKDGAQL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 ITGGERLGSKGYFIKPTVFGDVKEDMRIVKEELFGPVVTVTKFKSADEVINMANDSEYGL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 AAGVMTKDIDKALHIANATRAGSVWVNCYDVFDAAAPFGGFKUSGIGKELGEYGLFAYTE 497
                                                                                                                                                                                                                                                                                                                         12 LPNGLEYEQP -- TGLFINNKFVPSKQNKTFEVINPSTEEEICHIYEGREDDVEEAVQAAD 69
                                                                                                                                                                                                                                                                                                                                                          18 VPPGLSNMKPQYTGIFINNEFVPAKSGKTFETINPANGKVLAQVAEGDKTDVNIAVKAAQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 TVVI.KTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVVEAITNHPKIKKVAFTGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 TVVMKVAEQTPLASALHVAALTKEAGFPDGVVNIIPGYGHTAGQAISSHMDVDKVAFTGST
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarihini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                 DB 5; Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ol-mak-2002 (TrEMBLrel. 20, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
BAll3024.2 (aldehyde dehydrogenase l family, member Bl (ALDH5
ALDHX)).
                                                                                                                                                                                                                                               tch 49.5%; Score 1262.5; DB 5; Length al Similarity 50.0%; Pred, No. 1.5e-77; 244; Conservative 93; Mismatches 146; Indels
                                                   Submitted (NOV-2001) to the EMBL/GenHank/DDRJ databases.
EMBL; U12966; AAA20615.3; -.
HSSP; P05091; LCW3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL135785; CAD13246.1; -.
                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 510 AA: 55059 MW; 5995847747A023B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              517 AA.
                                                                                                                              Pfam; PFOD171; aldedh; l
PROSITE; PSOOOR70; ALDEHYDE_DEHYDE_CYS; l
PROSITE; PSOO687; ALDEHYDE_DEHYDE_GLU; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002086; Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                       "Direct Submission.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 498 VKTVTIKV 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
STRAIN-BRISTOL N2;
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                   Waterston R.;
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                                                                                                                                                                                                                                                 Query Match
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69 DRAFSNGS-WNGTDPTDRGKALYRLAELTEQDKDVTASTETLDNGKATSSSRG-DVDLVT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.4
                                                                                                                                                                                                                                                                                                                                                                  127 NYLKSSAGFADKIDGPMIDTGRTHFSYTKROPLGVCGOTTPWNFPLLMWAWKTAPALVTG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 NIVVEKTAESTPLSALYVSKY IPQAGI PPGV I NIVSGEGKI VVEA I TNIPKI KKVAFT (S. 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 TATGRHIYQSAA--AGLKKVILELGGKSPNIVFADAELFKAVONLILGLYYNSGEVOOAG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 TLITOGERLOSKOYETEFTVE-TIVKEDMETVERLIFOEVVIVIRERSKIDEVINMANDSEY 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 KLLOGGERFGEPGFFRPPPPOGVQDDMFIAKEETFGPVQPFFFFKFFEVVERANNTFY 44.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 TEVG-BLIQKAAGDSNIJKRYTIJELGGKSPSTVLADADMEHAVEGEBEALFFINMGGECEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 SPTFVEESTYNEFLERTVEKAAGHAVONIPELLIQUSPOVIPELEVILOT IQITIQUEGA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.25 GLAAGIHTSNINTALKVADRVNAGTVWINTYNDPHHAVPFGGFNASGLGREMSVDALONY 4.84
                                                                                                                                                                                                                                       28 PILNPD-IPYNQ----LFINNEWQDAVSKKTFFTVNFTTGEVIGHVAEGDRADVDRAVKAA 83
                                                                                                                                                                                                         9. PINLPNGLEYEQPIGLEINNKEVPSKONKTPEVINPSTEREICHTYEGKEDDVERAVOAA 68
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Azevedo V., Bertero M.G., Bessieres D., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Briquell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carler N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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                                                                                                                    49.3%; Score 1256.5; DB 4; Longth 517; 50.8%; Pred. No. 4.9e 77;
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                                                                                                                                                                 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lapidus A., Galleron N., Scrokin A., Ehrlich D.;
Submitted (NOV-1997) to the EMBL/GenBank/UDBJ databases.
                                                                                57249 MW; B877BD45FB770025 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLiel, 05, Last sequence update)
01-JUN-2001 (TrEMBLiel, 17, Last annotation update)
InterPro; IPR02086; Aldebyde_debydi.
Prim; PF00171; aldedh; 1.
PROSITE: PS006070; AllEHYDE_PEHYDE_CYS: UNKNOWN.).
PROSITE: PS006687; ALLEHYDE_DEHYDE_CYS: UNKNOWN.).
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                                                                                                                                                                 Matches 249; Conservative
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                                                                                                                                              Best Local Similarity
                                                                              517 AA;
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                                                                                                                         Query Match
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480 ALQNYLQVKAVRAKLD 495

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A benizot F., Devine K M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., A Frita C., Frita IF. Foulgate D., Fabrat C., Frita IF. Foulgate D., Galer D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galeron N., Ghisear P., Gaser P., Goffeau A., Galightly E.J., Grandi G. M. Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M F., Tayam M. Jones L., Andriber B., Karamata D., Kashara Y., Klactr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M., Lee S.M., Lardinois S., Lauber J., Lararevic V., Lee S.M., Lardinois S., Lauber J., Lararevic V., Lee S.M., Holsape B., Ogwara A., Oudega B., Noback M., Andriade P.P., Mizuro M., Mostl D., Nakai S., Noback M., Aparro V., Pohl T.M., Portatelle D., Fouwills S., Prescut A.M., Prescut E., Pujic P., Futneille R., Repwell S., Key M., Sadaic Y., Scholan E., Schleich S., String B.S., Soldo B., Stroklein A., Tamakokii A., Tarakai H., Takamaru K., Takahashi M., Tamakokii A., Tarakai T., Takahashi H., Takamaru K., Viari A., Manitt P., Washi P., Vassancti A., Viari A., Manitt P., Washi M., Vannior F., Viari A., Viari A., Wannior F., Viari A., Wannior F., Washi H., Pakamaru K., Viari A., Manitt P., Wannior F., Viari A., Viari A., Viari A., Wannior F., Wa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 GDVDLVINYLKSSAGFAFKTEGPMILTGPFHFSYTKRQPLGVGGTTPWNFPLLMWAWKI 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 VCCAGSRVFTHKDQYDEVVDEMASYAESLRQGAGLHKDTQ1GPLVSKEQHEPVLSY1QKG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 KNEGATLITGGERLGSKGYFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMA 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
Yoshida K., Yoshikawa H.E., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF027868; AAB84440.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR002086, Aldehyde_dehydr.
Pfam; PF00171; aldedh; 1.
PR0STTE; PS00687; ALDEHYDE_DEHYPR_GLU; 1.
COMPLETE POTCEOME: 53882 MW; 24PRC782P47034AR CPC64;
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59 LEINNEFVDAKSGKTFEFVNPANGKLLAKVABGNKLOVDIAVEAAKKAFKLGSEWFRMDA 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 PMIDTGRTHESYTKRQPLGVCGQIIPWNFPLLMWAWKIAPALVTGNTVVLKTAESTPLSA 201
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Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                         investigating biology. The C. elegans Sequencing Consortium.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NeV-1998) to the EMBL/GenBank/DDBJ databases
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Tin-Wollam A., Henkhaus J., Wohldmann P., Osborn A.;
"The sequence of C. elegans cosmid KO4F1.";
                                                                                                          ol-MAY-2000 (ITEMBLEEL 13, Created)
ULMAY 2000 (ITEMBLEEL 13, Last sequence update)
21-MAR-2002 (ITEMBLEEL 23, Last annotation update)
Hypotheifeal 58-6 KPa protein.
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Proile; ESUUTO: ALLEHRIELELEHRIFCYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDE_GLU; 1.
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479 ALDNYTEVKSVWVNLE 494
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                                                                               FRELIMINARY,
                                                                                                                                                                                             Caenorhabditis elegans.
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U9FRX7
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                                         381 KPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEYGLAAGIHTSNINTALK 440
299 VKKVTLELGGKSPNIVFADADLEFAVRQSHHALFFNUGQCCSAGSRTFVEGKIYDEFVAK 358
                            321 FKAASESIKVGDPFDESTFOGAQTSQMQLNKILKYVDIGKNEGATLITGGEKLGSKGYFL 380
                                                                                                       419 KPTIFANVNDOMKIAQEEIFGPVMIVIRFDSMEELIEKANNTIYGLAAGVVTNDLNKALQ 478
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                                                                                                                                             441 VADRVNAGTVWINTYNDFHHAVPFGGFNASGIGREMSVDALQNYIQVKAVRAKL 494
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa: Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEOUENCE 517 AA; 57238 MW; A628E448D1E8689D CRC64;
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PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE: PS00687, ALDEHYDE_DEHYDR_GLU; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 ATCHHIYOSAA-ACI KKVII FLOOF SPNIVEADAFI KKAVONI LUGIYYNSCHOOTAGK (106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 DTGKVVLELAARSNEKSVTLELGGKSPFTIMDDADVDHAVELAHFALFFNGGGCCCAGSR (35)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Būšaryota; Viridipiantae: Streptophyta; Embryophyta; Trachosphyta;
Spermatophyta; Magmoliophyta; Liliopsida; Poales: Poaceae;
Ehrhartoideae; Gryzeae; Gryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2000) to the EMBL/Adenbank/100BJ databases.
-1-SIMILARITY: BELONGS TO THE ALDERTDE DEHYDROGENASES FAMILY.
EMBL; ABOAGA37; BAR19052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.9%; Score 1247.5; DB 10; Length
49.8%; Pred. No. 1.8e-76;
"**marches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             549 AA; 59306 KW; 2B3FC2B841FB6DDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakazono M., Tsuji H.;
"Rice mitochondrial aldehydo dehydrogenase Aldh2b.";
                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. NIPPONBARE; TISSUE LEAVES OF SEEDLINGS;
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PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
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Pfam: PF00171; aldedh; 1.
                                                                                                                                                                                                                                                                                                                      P.K.T.;
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                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                       503 TEVKTVTIKV 512
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Best Local Similarity
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01-JUN-2002
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69 PRAFSNGSWNGIDPIDPGGKAL/PRIAELIEQDKDVIASIETEDNGKAIS-SSRGDVDLVIN 127
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                                                                                                                                                                                                                                                                                                                                                                                             Xu B., Xing Y., Wang Z., Zhang J., Zhu S., Hong M.,
"Cloning, characterization of cDNA encoding rice aidehyde
dehydrogenase, and analysis of its expression in male-sterile lines.";
Chih mu sheng Li Hsueh Pao 26:206-212(2000).
-i - SIMITARITY. PRIONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
EMBL; AP162665; AAF73828.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
                                                                                                                                                                                                                                                                                          Pokaryota, Viridiplantae, Streptophyta, Emboyophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enrhartoideae, Oryzeae, Oryza,
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01-MAR-2002 (TrEMBLrel, 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 9%; Score 1246.5; DB 49.8%; Pred. No. 2.1e-76;
                                                                                                                                                                 549 AA
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PROSITE; PS00070; ALDEHYDE_DEHYDE_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDE_GLU; 1.
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                                              487 VKAV 490
                                                                               536 VKAV 539
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CY 487 VKAV 490

DD 536 VKAV 539

Search completed: June 24, 2003 10
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Search completed: June 24, 2003, 10:17:08 Job time • 41 8852 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Lid.
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OM protein - protein search, using sw model

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. YGUQAYTEVKTVYVKVPQKN SÜÜ US-09-830-751-4 2625 1 MSAAATQAVPAPNQQPEVF7. Perfect score: Sednence.

Gapric 10 0 , Gaprext 0 5 RUDSHIMED Scoring table...

908470 seqs, 133250520 residues Searched

908470 Total number of hits satisfying chosen parameters.

200000000000 Minimum DB seq length a Maximum DB seq length

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

A\_Geneseq\_101002.\* Database :

.DAT:\* DAT: \* DAT: \* DAT: + DAT: \* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:\* /SIUSZ/grgdata/geneseq/geneseqp-embl/AAluun.DAT:\* DAT: \* /SIDS2/gcgdata/geneseq/geneseqp.emb1/AA2000.DAT.\* /SIDS2/gcgdatu/geneseq/geneseqp.emb1/AA2001.DAT.\* /SIDS2/gegdata/genese4/genese4Fremb1/AA2002.DAI.\* | SIDS2/gcgdata/gcneseq/gcneseqp-embl/AA.94.EAI.\*\*
| SIDS2/gcgdata/gcneseq/gcneseqp-embl/AA.94.EAI.\*\*
| SIDS2/gcgdata/gcneseq/gcneseqp-embl/AA.1984 DAT.\*\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score 2625 1929 1917 1866 1741 1741 1718	% Match Match 1100.0 73.5 73.5 73.5 66.3 66.3 65.4	%	DB 52 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	ID AAB74924 AAB449516 AAB49517 ABE61140 AAB58398 AAB68398 AAC61842 AAC61842	Description Human aldehyde deh Human ALDH5 protei Human ALDH5 protei Drosophila melanog Lung cancer associ Aldehyde-dehydroge Prostate cancer as Human aldehyde deh
10	1543	7.87.		21,	AAY67412	Novel human diagno Arabidopsis aldehy

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ALIGNMENTS

AAB74924 standard; Protein; 500 AA. RESULI 1 AAB74924

AAB74924; 

25-JUN-2001 (first entry)

Human aldehyde dehydrogenase ALDH2 protein sequence SEQ ID NO:4.

Aldehyde dehydrogenase, glycerol delydratase, 3.HF, glycerol; feedstock: 3.hydroxypropiculo acid; genetic enginesting, glucose, bacterial host, absorbable prostheric device, surgical suture; beta-lactam; acrylic acid; trifluoromethylated alcohol; diol; polyhydroxyalkonate; copolymer; lactic acid.

Homo sapiens.

W0200116346-A1.

08-MAR-2001.

30-AUG-2000; 2000WO-US23878.

99US-0151440. 30-AUG-1999,

(WISC ) WISCONSIN ALUMNI PES FOUND.

Suthers FF, Cameron DC;

WPI; 2001-315988/33. N-FSDB; AAF82082. AAM49516;

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fermenting recombinant microorganisms expressing genes for suitable
3-Hydroxypropionic acid preparation, for use e.g. as monomer, by
                                                                                                                       enzymes in the presence of glycerol or glucose -
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Claim 5; Page 32-35; 63pp; English.

Incorporation of genes encoding two enzymes makes the host organisms able to produce (3:HP) from (1). The biotechnological method of from preparing (3:HP) is potentially cheaper than chemical synthesis. The present sequence represents the human aldehyde dehydrogenase ALDH2, which recombinant microorganism in the presence of a source of glycero. (1) or glucose, where the microorganism: (1) expresses genes for non-native enzymes which catalyse the production of (3 HP) from (1); (ii) carries genetic constructions for the expression of a dycerol dehydratase (GDHT) and aldehyde dehydrogenase (ADH) capable of catalysing the production of (3 HP) from (1); or (iii) carries a genetic construct which expresses the dhab gene from Klebsiella pneumoniae and a gene for an ADH capable of catalysing the production of (3 HP) from (1); 3 HP is a monomer, and is useful e.g. in the production of absorbable prosthetic devices and surgical sutures or for incorporation into beta-lactams, production of arrival actions. The present invention describes a method for the production of 3-hydroxypropionic acid (3-HP). The method comprises fermenting a or diols, polyhydroxyalkonates and copolymers with lactic acid. is used in the exemplification of the present invention. 

500 AA; Sequence

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DKAREGRPGAFQLGSPWRRMDASHSGRLLNRLADLIERDRTYLAALETLDNGKPYVISYL 120
                                                                                                                                                                                                 61 DKAREGRPGAFQLGSPWRRMDASHSGRLLNRLADLIERDRTYLAALETLDNGKPYVISYL 120
                                                                                                                                                                                                                                                             181 GPALATGNVVVMKVAEQTPLTALYVANLIKEAGFPFGVVNIVFGFGFTAGAAIASHEDVD 240
                                                                                                                                                                                                                                                                                                                                        241 KVAFTGSTEIGRVIQVAAGSSNIKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNOG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                   241 KVAFTGSTEIGRVIQVAAGSSNIKRVTLELGGKSPNIIMSDADMDWAVEDAHFALFFNEG 300
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                                                                                                     301 QCCCAGSKTFVQEDIYDEFVVKSVAKAKSKVVGNPFDSKTEGGPQVDETQFKKILGYINT
                                                                                                                                                                                                                                      121 VDLDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTPHEPVGV@@IIPWNFPLLMQAWKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 QCCCAGSRTFVQEDIYDEFVVRSVARAKSRVVGNPFDSKTEQGPQVDETQFKKILGYINF
                                               Gaps
                                             0;
100.0%; Score 2625; DB 22, Length 500; 100.0%; Pred. No. 6e-239; Live 0; Mismatches 0; Indels 0;
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    Query Match
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AAM49516 standard; Protein; 517 AA.

RESULT 2 AAM49516

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62 KAREGREGAFOLGSPWRRMDASHSGRIJURIJAELIERDRIYIJAALETIJDNOKPYVISYJV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122. DEDMVERCERYYAGWADRYHGKTTPIDGDPPSYTRHEPVGVOGGI FWNPDI LIMGAWKLIG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel isolated genes and haplotypes of the human aldehyde dehydrogenase 5 (ALDHS) gene containing polymorphic sites. The polymorphic ALDHS variant is useful in studying the effect of the variation on the biological activity of ALDHS and on the binding affinity of candidate drugs targeting ALDHS for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2. SAAATQAVPAPUQQPEVP/NOTFINNEWHLAVSRKTFFIYNNPST/SEVI/OVAEST/KEDVD/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 SSAA - - ALPSPILINPD DYNOLFINNEWQDAVSKKTFPTVNPTTGEVIGHVAEGDRADVD - 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The products of the invention have antialcoholic activity, this sequence
                                                                                                                       ALDH5; human; polymorphism; haplotype; aldehyde dehydrogenase 5;
binding affinity; drug targeting; alcoholism; alcohol induced disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New genetic variants with polymorphisms in the aldehyde dehydrogenuse 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alcoholism and alcohol-induced disorders. Polynucleotides comprising a polymorphic gene variant or tragment may be used for therapeutic purposes. ALMHS protein isoforms may be used in assays to measure the binding affinities of one or more candidate drugs targeting the ALMHS protein. ALMHS proteins may be used to generate antibodies. Haplotyping method can be used by scientists to validate ALMHS as a candidate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             target for freating a specific condition or disease predicted to be associated with ALMS activity, and in the design of clinical trials of candidate drugs for treating a specific condition or disease predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALDHS as well as in identifying drugs targeting this protein for the treatment of disorders related to its abnormal expression or function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to be associated with ALDH5 Letivity. Information on polymorphisms on the ALDH5 gone can be applied for studying the biological function of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represents the human ALDHS protein described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ALDHS) gene, useful for studying the function of ALDHS, and for expressing ALDHS protein which is useful in screening drugs for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.5%; Score 1929; 38.23; Lonath, 527; 72.7%; Prod. No. 3.50°173; Hye. 61; Mismatches 73; Indeks 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sanchis A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Messer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 30; Page 72-74; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating ALDH5 related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENA-) GENALSSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Finkel K, Kazemi A,
                                                                                                                                                                                                                                                                                                                                             29-MAY-2001; 2001WO-US17254.
                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000; 200008-207508P.
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N-PSDH; ABA99282, ABA99283.
                                       13-MAY-2002 (first entry)
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ges 463; Conservative
                                                                                Human ALDH5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 AA;
                                                                                                                                                                                                                                                          W0200192279-A2.
                                                                                                                                                                          antial coholic.
                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                    06-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duda A,
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                                                                                                                          318 CCCAGSRTFVEESIYNEFLERTVEKAKQRKVGNPFELDTÖGGFÖVLKEUFEKVLGYIULG 377
                                                                                                                                                                          378 OKECAKLLCGGERFGERGFFIKPTVFGGVQDDMRIAKEEIFGPVQPLFKFKKIEEVVEKA 437
                                                                                                                                                                                                                          438 NNTRYGLAAAVFTRDLDKAMYFTQALQAGTVWVNTYNIVTCHTPFGGFKESGNGRELGED 497
PALATCNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGFTAGAAIASHEDVDK 241
                                                                                                 302 CCCAGSRTFVQFDIYDEFVVRSVAKAKSKVVGNPFDSKTEDGPQVDETQFKKILGYINTG 361
                                                                                                                                                   KQEGAKLLCGGGIAADPGYFIQPTVFGFVQDGMTIAKEEIFGFVMQILKFKTIE£VVGPA 421
                                                                                                                                                                                                  422 NNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGEY 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New genetic variants with polymorphisms in the aldehyde dehydrogenase 5 (ALDH5) gene, useful for studying the function of ALDH5, and for expressing ALDH5 protein which is useful in screening drugs for
                                                                                                                                                                                                                                                                                                                                                                                                                                            ALDH5, human, polymorphism, haplotype; aldehyde dehydrogenase 5;
binding affinity; drug targeting; alcoholism; alcohol-induced disorder,
                                               VAFTGSTEIGRVIQVAAGSSNLKRVTLELGGKSPN1IMSDALMDWAVEQAHFALFFNGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duda A, Finkel K, Kazemi A, Messer C,
                                                                                                                                                                                                                                                                                                                                                                                                                    Human ALDH5 protein polymorphic variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          AAM49517 standard, Protein, 517 AA
                                                                                                                                                                                                                                                                  /label= Val, Ile
Misc-difference 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Asp. Asn
                                                                                                                                                                                                                                                   482 GLQAYTEVKTVTVKVPQKN 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= Ala, Val
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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human aluchyde dehydrogenase ' (ALHE') gene containing Folymorphic sites. The polymorphic AbbHS variant is useful in studying the effect of the variation on the biological activity of ALDHS and on the binding affinity of candidate drugs targeting ALDHS for the treatment of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 RAVKAAREXFRLGSPWRRMDASERGRLLNXLADLVERDRVYLASLETLDNGKPFQESYAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEDMYEKCEKYYAGWADKYHGKIIPIDGDFFSYTRHEPVGVGGJIPWNFPLLMQAWKLG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 VAFTGSTELGEVIQVAA3SSNLKEVTLELGGKSFNLIMSFAPMFWAVPQAHFALFFNQGQ 301
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                                                                                                                                                                                                                                                                                                                                                                   protein. ALMF proteins may be used to generate and produce and protein and the proteins may be used by scientists to validate ALDH5 as a candidate target for treating a specific condition or disease predicted to be associated with ALDH5 activity, and in the design of clinical trials of candidate drugs for treating a specific condition or disease predicted to be easterned with ALDH5 activity. Information or polymorphisms on the ALDH5 as well as in identifying drugs targeting this protein for the treatment of disorders related to its abnormal expression or function or the products of the invention have antial oblicity artists sequence. The products of the invention have antial oblicity ratis sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SAAATQAVPAPNQQPEVFCNQTFINNEWHDAVSRKTFFTVNPSTGFVTCQVAEGTKEDVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alcoholism and alcoholinduced disorders. Polynucleotides comprising a perlymorphic gene variant or fragment may be used for therapeutic purposes. ALDHS protein isoforms may be used in assays to measure the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 PALATGNVVVMKVAEQTPL/TAL/YVANLIKFAGFPPGVVNIVPGFGPTAGAAIASHEDVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 PALATGNIVVMKVAEQTPLSALYLASLIKEAGEPPGVVNILTGYGFTAGAATAQHXDVDK
                                                                                                               This invention describes a novel isolated genes and haplotypes of the
                                                                                                                                                                                                                                                                                                                                                   binding affinities of one or more candidate drugs targeting the ALDH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.0%; Score 1917; DB 23; Length 517; 72.1%; Pred. No. 4.7e-172; Live 61; Mismaiches 76; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABBēğlay standard, Frotein, 520 AA
                                                          Fisclosure, Elg 3, 96pp, English.
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treating ALDH5-related diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disclosure of the invention.
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320-000AGSRIFVEDKIYDEFVERSAERAKKFIVGNRFDUNI EGGROVEDEMEKTOMIKTG-479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ROSEZ) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N PSDB; AAF18274.
                                                                                                                                                                                                                                                                                                                                                                                                      WOZ00055180-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 KAPEGRPGAPQLGSPWRRMDASHSGFLLNRLADLIERDRTYLAALETLDNGKPYVISYLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKLG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 DIPTAIKNIRYFAGWADKNHCKTIPMDCDFFTYTRHEPVCVCGQIIPWNFPILMMAWKLG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALATGNVVVMKVAEQTPLTALYVANLIKEAGFPFGVVNIVPGFGPTAGAAIASHEDVDK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 PALATGNTIVI.KPARQTSI.TALYTAQI.VKRAGFPEGVVNVVPGFG-TAGAALANHCDVDK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 CCCAGSRITYQEDIYDEFVVRSVARAKSRVVGNPFDSKTEQGPQVDFTQFKKILGYINTG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                             useful in developmental biology and in elucidating cell signalling and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 VAFTGSTEIGRVIQVAAGSSNIKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed
                                                                       Drosophila, developmental biology, cell signalling, insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.1%; Score 1866; DB 22; Length 520; 69.8%; Pred. No. 3.1e-167;
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 7212; 21pp + Sequence Listing, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABL01840-ARL16175) and the encoded proteins
                                                Drosophila melanogaster polypeptide SEQ ID No 7212.
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                                                                                                                                                                                                                                                                      Myers EW;
                                                                                                                                                                                                                                                                      Li PWD,
                                                                                                                                                                                 23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                         23-MAR:2000; 2000US 191637F;
11-JUL:2000; 2000US-0614150.
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                        26-MAR 2002 (first entry)
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                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                      Venter JC, Adams M,
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                                                                                                                                                                                                                                             (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   520 AA;
                                                                                                                                                                                                                                                                                                        N-PSDB; ABL04243
                                                                                      pharmaceutical.
                                                                                                                                   WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                        interactions -
                                                                                                                                                           27-SEP-2001.
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ABB60140,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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GIANDEGYFIQPTVEGDVQDGMTIAKEETFGDVMQILKFKTIEEV 417
                                                                                                                                                                                        4.18 VOKANNSTYOLAAAVETKOLDKANYLSQALQAJI VWVNCYDVEGAQSEEGGYKMSGSGRE 477
                                                                                                                                                                                                                                     Human, lund cancer associated protein, neuroprotective, eptostatic, cardioactive, immunomodulatory; muscular active; vulnerary; cardioactive, physical active states are associated antibheetive; appreciated; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAFIB425 AAFIB43 and peptide ABSB549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiques, useful for treatment, prevention, and diagnosis of disorders such as lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associated proteins represented in AABSB106 AABSB548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective, cytoshatic, cardioactive; and immunomodulatory; muscular active general; vulnerary; quarrointestinal general, nephrotropic, antitiatective; quecological; or antibacterial activity. The invention also includes anothedies specific for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynacicotide sequences AAP17982 - AAF18424 encode Janian Jung cameer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The proteins may be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lang cancer associated gene sequences, referred to as lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein or polynucleofide sequences. The lung cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bang cancer associated polypeptide segmence SEQ ID 746.
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                                                                                                                                                                                                                                                                                                                                                                                 478 LGEYGLQAYTEVKTVTVKVPQKN 500
                                                                                                                                                                                                                                                                                                                                                                                                                                        497 NGEYALSNYTEVKSVIVKVAOKN 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB58398 standard; Protein; 412 AA
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362 KŲEGAKLLOGG -
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A novel retro virus vector encodes human cytosolic aldehyde-
Disclosure; Fig.4; 92pp; English.
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                                                                                                                                                                                 200 GPALATGNVVVMKVARQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVD 259
                                                                                                                                                                                                                                                          241 KVAFTGSTELGRVIQVAAGSSNLKRVILELGGKSPNIIMSDADMGWAVEQAHFALFFNQG AGO
                                                                                                                                                                                                                                                                                                     DKAREGRPGAFOLGSPWRRMDASHSGRLLNRLADLIERDRTYLAALETLDNGKPYVISYL 120
                                                                                                                                              80 DKAVKAAPAAFQLGSPWPPMDASHRGPLLNPLADLIEPDPTYLAALETLDNGKPYVISYL 139
                                                                                                                                                                   121 VDLDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKL 180
                                                                                                                                                                                                                181 GPALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVD 240
                                                                                                20 LSAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVIÇQVAEGDKEDV 79
                                                                                                                                                                                                                                                                                260 KVAFTGSTEIGRVIQVAAGSSNLKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQG
                                                                           1 MSAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSKKTFFTVNFSTGEVICQVAEGDKEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potro virus, vertus, ald-hydr-delydrogenase;
glutamylcysteine-synthetase; hematopoietic cell; cyclophosphamide;
chemotherapy; transgenic animal; gene therapy; cancer therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retroviral vectors encoding human cytosolic aldehyde dehydroqenase or glutamyl cysteine syntherase oused to transform a subject's haematopoletic cells to reduce the toxic effects of cyclo phosphanide chomotherapy
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                                 Length 412,
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                             Spore 1771, DB 21,
Fred No. 2 Let158,
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                                                   7, Mishatches
                                         Fired No.
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                             6.7 F.9
9.0 F.8
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                                                                                                                                                                                                                                                                                                                                                                         380 GSKRGRSCCVVGAL 393
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                                         Best Local Similarity 90.6
Matches 339, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         selectable marker.
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         Sequence
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                                Query Match
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41 DKAPEGRPGAFQLGSPWPPMPASHSGPLLNPLADLIEPPP - TYLAALETLINGRPYVIS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 YLVDELIMVEKCERYYAGWADIKY - HGKTIPELIGIFESYTRHEFVGVGGGTFPWIFFTIMG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 FNQGQCCCAGSPTFVQEDIYDRFVVPSVAÞAKSPVVGNPFDSKTFQGPQVDFTQFKKILG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 YINTGKQEGAKLLOGGSTAADRGYFTQPTVRSDVQDGMTTAKFETFGVMQTLKFKTTFE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 VVGRANNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGR 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSAAATQAVEAPNQQEEVFCNQIFINNEWHDAVSRKTEPTVNPSTGEVICQVAEGDKEDV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 MSSSGTPDLPVLLTDLKIQYTKIFINNEWHDSVSGKKFPVFNPATEEELCQVEEGDKEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 AWKI.GPAI.ATGNVVVMKVAFQTPLTALYVANI.IKEAGFPPGVVNIVPGFGPTAGAAIASH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 EDVEKVAFTSSTELGEVIGVAAGSSNIKEVTURGGESPILIMSDADMIMAVEQAHFALE
                                                                                                                                                                                                                                                                                                                                                             4; Gaps
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dehydrogenase and/or human distangleysteine synthetase (AAP6/8673). Hematogenetic cells transfected by the vector are resistant to synthematic periodical and a means of gree thouse; that allows higher doses of toxic drugs to be used in cancer chemotherapy. The human genes may also be used as selectable markers for mammalian cell transfection and for transgenic animal breeding.
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                       Guery Match
Rest Local Similarity 65.9%; Pred. No. 2e-155;
Matches 332, Conservative 69, Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                       69, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prostate cancer-associated protein #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   477 ELGEYGLQAYTEVKTVTVKVPQKN 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497 ELGEYGFHEYTEVKTVTVKISOKN 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABC61842 standard; Protein; 512 AA
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                                                                                                                                                                                                                                 521 AA;
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                                                                                                                                                                                                                                    Sednence
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organisms such as humans or other mammals (e.g. mire, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer associated genes are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 NVVVMKVAEQTPLIALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVAFTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modulators of PC, by determining if prostate cancer-associated genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostate cancer. The nucleic acid sequences are particularly useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a prostate earest-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to methods of detecting a prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in gene therapy, as a vaccine or in antisense applications.
ABG61800-ABG61944 represent prostate cancer-associated proteins.
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                                                                                                                                                                                                                                                                                                                                                          Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; Fage 333·334; 436pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are expressed in a prostate tissue
                                                                                                                                                                                                                                                                                                  (EOSB-) FOS BIOTECHNOLOGY INC
                                                                              20010S-276791P.
20010S-276888P.
20010S-281922P.
20010S-286214P.
20010S-0847046.
                         2000US-0733742.
2001US-263957P.
0733288
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2000US.
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                                                                              16-MAR-2001;
16-MAR-2001;
06-APR-2001;
24-APR-2001;
                                                                                                                                                                                                         30-APR-2001;
                      08-DEC-2000;
24-JAN 2001;
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08-DEC-
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endometrics is by determining the amount of gene product from at least one specific gene in a patient sample and comparing with the amount of gene product in a centrol sample and comparing this with the amount of gene product in a centrol sample and comparing this with the amount of gene product in a centrol sample. A reduced level is individually to a another sample and dehydrogenase 6, gravin, phospholipase C epsilon, elastin, insulin-like growth factor binding practice. In place 2 type IV collader, transmembrane receptor binding practice. In place 2 type IV collader, subtilisin like protein PRMY or indogen type XVIII alpha 1, so that it is subtilisin. It diagnosis of endometricsis, and also the mention for the treatment of the disease. The present sequence is human abledayde.
                                379 LECGGSAMEDKGLFTRPTVFSEVTDNMRTAKEETFGFVQPTLKFKSTEEVTKRANSTAYG 4.8
                                                                                                                 428 LAAAVETKDIDKANYLSÇALJAGIVWVN:3YLVFGAJSFFGGYAMSGSGRELGEYGLGAYT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AVPAPNQQPEVECNQTETINNEWHDAVSRKTFPTVNPSTGEVTCOVAEGDKEDVDKAREGR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aldebyde dehydrogenase 6. gravin; phospholipase 6 epsilon; clastin;
insulin-like growth lactor binding protein-2; alpha-2 type IV collagen;
transmembrane receptor PTRS; collagen type XVIII alpha 1;
platelet derived growth factor receptor alpha; laminin M chain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kreft B, Winterhager E;
detecting reduced expression of specific gene products, e.g. from the fibronectin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In vitro diagnosis and monitoring of endometriosis, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.4%; Score 1718; DB-23; Length 512;
65.5%; Pred. No. 2.9e 154;
tive - 66; Mismatches 104; Indels - 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subtilisin like protein PACE4; nidogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA017364 standard; protein; 512 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human aldehyde dehydrogenase 6.
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mes 323, Conserv
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                                                                                                                                                                                                                                                                                                                                       LAAAVPTKULDKANYLSQALQAGTVWVNCYDVFGAGSFFGGYKMSGSPELGFYGGAYT 4 K7
                                    68 PGAFQLGSPWRRMDASHSGRLLNRLADLJERDRTYLAALETLDNGKPYVISYLVDLDMVL 127
139 RTLRYFAGWADKIQGKFIPT-DDNVVCFTRHEPIGVCGAITPWNFPLLMLVWKLAPALCCG
                                                                                                                                                                                                                                      FTFVQEDIYDEFVVPSVAPAKSPVVGNPFDSKTEQGFQVDETQFKKILDSYINIGKQEGAK
                                                    79 QVAFQRGSPWRRLDALSRGRLHQLADLVERDRATLAALETMDTGKPFLHAFFIDLEGCI
                                                                                     KCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVGGQIIPWNFPLLMQAWKLGPALATG
                                                                                                                                    188 NVVVMKVAEQTPLTALYVANLIKEAGFPFGVVNIVPGFGPTAGAAIASHEDVDKVAFTGS
                                                                                                                                                                                      248 TELCRVIQVAAGSSNLKRVTTELGCKSPNLIMSDADMDWAVEQAHFALPFNQGQCCGAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene therapy; forensic; food supplement, medical imaging, diagnostic, genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #6568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG06577 standard; Protein; 529 AA.
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Claim 20; SEQ ID NO 36446; InApp; English

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, belymerase chain reaction (PCE) primers. Oligomers, and for chromosome and green magning, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving devirant promein expression or biological activity the polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307
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                                                                                                                                                                                                                                                                                                           diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amano acid sequences. ABOHUHH-ARMARTZ represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                            Noté. The separate data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 PTLRYPAGWADKIGGKTIPTDNVVCFTPHFEDIGVCGATTPWNFFILMENWKLAPALCGG
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Best Local Similarity 65.5%; Pred. No. 3.1e-153;
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b; Mismatches 104;
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plant plastidic pyrivato dohydrogenase; pPCH; ATP citrile ljaso; ACL; pyrivate decarboxylase; PDC; aldehyde dehydrogenase; ALDH acctyl CoA; Latty acid; flavonoid; enzyme; phylorhemical; pyruvate decarboxylase; acetyl COA hydrolase; mitochondrial pyruvate dehydrogenase.
                                                                                                             Arabidopsis; plant plastid; acetyl CoA synthetase; E3 subunit; ACS;
Arabidopsis aldehyde dehydrogenase (ALDH)-1.
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Arabidopsis sp.

06-JAN-2000.

99WO-US14382 25-JUN-1999; 98US-0090717 26-JUN-1998;

(IOWA ) UNIV IOWA STATE RES FOUND INC.

Schnable PS, Oliver DJ, Behal R, Schnable Fatland B, Lutziger I, Wen T; Wurtele ES, Allred CC, WPI; 2000-160678/14. Nikolau BJ, Johnson JL,

N-PSDB; AAZ56973

Novel acctyl CoA synthetaso (ACS), plastidic pyruvate dehydrogenase (PDDH), ATP citrate lyase (ACL), pyruvate decarboxylase (PDC) and aldehyde dehydrogenase (ALDH) polypeptides used to alter acetyl CoA levels in plants

Examples; Fig 10B; 79pp; English.

biosynthesis of very long chain fatty acids and flavonoids. The enzymes may also be used for in vitro synthesis of acetyl CoA, which in turn can be used to produce acetyl CoA phytochemicals (plastidic ACS, ppbH, ACL, pyruvate decarboxylase, acetyl CoA pydrolase, mitochondrial pyruvate dehydrogenase and aldehyde dehydrogenase are involved in the biosynthesis The invention provides nucleic acids encoding Arabidopsis plastidic acetyl CoA synthetase (ACS), various subunits (specifically the E3 subunit) of plant plastidic pyruvate dehydrogenase (pPDH), the A and B subunits of a plant ATP citrate lyase (ACL), Arabidopsis pyruvate decarboxylase (PDC), Arabidopsis aldehyde dehydrogenase (ALDH), specifically ALDH-2 and ALDH 4. The polypeptides can be expressed by standard recombinant methodology. The ACS, pPDH, ACL, POC and ALDH polypeptides, methods and nucleic acid molecules of the invention are used to alter the level of acetyl COA in a plant or plant cell, tissues or or organs. A decrease in acetyl COA is expected to affect the 

538 AA; Sednence

62 KAREGRPGAFQLGSPWRRMDASHSGRLINRLADLIERDRTYLAALETLDNGKPYVISYLV 121 99 RAVKAARTAFIDFG-PWPKMSAYEPSPVLLPFADLVEKHSEELASLETWDNGKPYQQSLTA 157 DEDMVERCERYYAGWADKYHGKTIPIDGDFFSYTRHEFVGVCGQIIFWNFPELMQAWKEG 181 182 PALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNTVPGFGPTAGAATASHEDVDK 241 2 SAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVD 61 SAAAEEII----NPSVQVSHTQLLINGNFVDSASGKTFPTLDPRTGEVIAHVAEGDAEDIN 4; Gaps 58 8%; Score 1543; PR 21; Length 538; 61.1%; Pred, No. 1.1e-136; Indels 61; Mismatches 126; Conservative Similarit.y 300; Query Match Best Local Matches ô ò g g

or organs. A decrease in acetyl CoA is expected to affect the biosynthesis of very long chain fatty acids and flavonoids. The enzymes

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                                                                                                                                                                                                                                                  NNSTYGLAAAVETKIILIAKANYLSQALQAGTVWVN:YDVEGAQSPEGGYKMSGSGREIGEY 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis; plant plastid, acetyl CoA synthetase; Et subunit; ACS; plant plastidic pyruvate dehydrogenase; pPDH; ATF ettrate lyase; ACL; pyruvate deeraboxylase; PDC; aldehyda dehydrogenase; ALDH; acetyl CoA; tatty acid; flavonoid; enzyme; pytytochemical; pyruvate deeraboxylase; acetyl CoA hydrolase; mitochondrial pyruvate dehydrogenase.
                302 PHYSINE TROOTERY PREPARES VARIABLES STEWNSTED BY WAS TRUCKED FROM THIS TABLE
                                                                                                           338 COCASSELEVHEKVYLEEVEKSKAPALKEVVGOPEPROLEGGGG OF KOEFERVMKY EKSG
242 VAFTGSTEIGRVIQVAAGSSNIKRPTLELGGKSPNIIMSDADMDWAVEGAHFALFFNGGG
                                                                                                                                                      362 ROBGARLLCGGGTAAPRGYFTOPTVEGDVORGMITARRELFTDWMCTERFTTEDVORA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel acetyl CoA synthetase (ACS), plastidic pyruvate dehydrogenase (PDDH), ATP citrate lyase (ACL), pyruvate decarboxylase (PDC) and aldehyde dehydrogenase (ALDH) polypeptides used to alter acetyl CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schnable PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oliver DJ, Behal R, Sc
Fatland B, Lutziger L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Atabidopsis aldehyde dehydrogenase (ALDH) - 3.
                                                                                                                                                                        (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fatland B,
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY67414 standard; protein; 544 AA.
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                                                                                                                                                                                                                                                                                      61 DKAPEGRPGARQIGSPWRRMDASHSGRILNRLADLIERDRIYLAALETLDNGKPYVISYL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                              181 GPALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVD
                                                                                                                                                                                   4; Gaps
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                                                                                                                                               Length 534,
                                                                                                                                                                                 Indels
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                                                                                                                                          56.1%; Score 1473, DB 21, 59.3%; Pred. No. 4.3e-130; Itive 55; Mismatches 143;
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11-JUL-2000; 2000US-0614150.
                                                                                                                                        Query Match
Best Local Similarity 59.3%
Matches 294; Conservative
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                                                                                                            534 AA;
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                                                                        of acetyl CoA.
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                                                                                                                                                                                                                                                                                             capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genemic DNA sequences (ABLIG175-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 QLGSPWRRMDASHSGRLLNRLADLIERDRTYLAALETLDNGKPYVISYLVDLDMVLKCLR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 YYAGWADKYHGKTIPIDGDFFSYTPHRPVGVGVIGITPWNFPLLMGAWKGGPALAFGNVVV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 MKPAEQTPLTALHMAALAKFAGFPAGVINVVNSFGPTAGAAISAHPDIAKVAFTGSVEIG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.14 FIVMQAAAISNLKKVSLELGGKSFVVVFDLADIDFAVETTHEALFSNHGGSGCAGSKTYV 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The Sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pet_sequences.
                                                                                                                                                                   from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 BPDSEWPKLSPLQPTNLMNKTZALMDPDKAPLASLETQINGKPYA-FALFDVTYSTLTTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVAFTGSTEIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Gaps
                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                   Disclosure; SEQ 1D NO 13560; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.0%; Score 1470; DB 22; 57.7%; Pred. No. 1.1e-129;
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                                          Li PWD, Myers EW;
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                                          Adams M,
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                                                                                  WPI; 2001-656860/75.
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(FEKE ) PE CORP NY
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                                                                                                        N-PSDB; ABL06359
                                                                                                                                                                                           interactions
                                          Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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378. QPTVETDVISDMKIAQPETECDVVTIQKEKDVAFATKLGXSTDYGLAAAVIJTKNVNIALK. 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 LYVANLIKEAGFPGVVNIVPGFGPIAGAAIASHEDVDKVAFIGSIFIGKVIOVAAGSSN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 SHSGRIJANIJANIJEKDRTYIJAALETIJANGKPYVI SYLVIJIJMVIJKO IPYYAGMADKYBO 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 ENEGREENNEANLEEKNTULLAAVESILUNGKALSMAKVISA (ASGCIRCYGGWAUNITG) 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 IFTNNEWHDAVSKKIEPTVNFSTOEVTOOVARDOELDVORAREDERMAREDSOFWRPMINA B.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        allergens and sequences encoding them have now been isolated. The mature Clah53 allergen has mol. wt. 53 kD and is encoded by cDNA sequence AAQ86278. The allergen has been dony to aldebyde dehydrogenases. Potential epitopic subfragments were identified by computer analysis of the amino acid sequence. See AAR71492.871996 for potential B cell epitopes and AAR72615.8726.27 for patential I cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Albergens derived from Cladosporium herbarum spores—also recombinant DNA for expressing the albergens, useful for in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spores of Cladosporium herbarum are the most common funtal spores found in the air; they can cause allorqic reactions. Various Clah
                                                                                                                                                                                                                                                                                                                                                                                   Fungal spore; allergen; Clab53; allergy; aldehyde dehydrogenase.
                                                                  DB 16; Lougth 496;
                                        443 LSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGEYGLQAYTEVKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.7%; Score 1805.5; DB 16; Lengt
55.8%; Pred. No. 2.6e 114;
ative 63; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Ebner C, Hirschwehr R;
Oberkotler H, Prillinger
                                                                                                                                                                                                                                                                                                                                      Cladosporium herbarum allergen Clah54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOM-) BIOMAY PRODN & HANDELSGES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 8-9; 35pp; German.
                                                                                                                                                                                                   AAR71891 standard; Protein; 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93AT-0001725.
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                                                                                                                                                                                                                                                                                             (lirst entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                Cladosporium herbarum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ86278.
                                                                                                                                                                                                                                                                                           25-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 - AUG - 1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sednence
                                                                                                                                                                                                                                                AAR71891;
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Simon B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                          RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 SERGILINKLADI,MERDIDTLAATESI,DNGKAFTMA-KVDI,ANSIGCLRYYAGWADKIHG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 KTIPIDGDFFSYTRHEPVGYGGQIIPWNFPLLMQAWKLGPALATGNVVVMKVAEGTPUTA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 LKRVTI ELGGKSPNI IMSNADMNWAVEQAHFALFFNQGQCCCAGSRTFVQEDIYDEFVVR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 SVARAKSKVVGNPFDSKTEOGPOVDETQFKKILGYINTGKÖEGAKLLGGGGIAADKGYF1 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 OPTVFGDVQDGMTIAKEEIFGPVMQILKFKTIEEVVGRANNSTYGLAAAVFTKDLDKANY 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 IFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVDKAREGRPGAFQLGSPWRRMDA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 LFINNEFVKGVEGKTFQVINPSNEKVITSVHEATEKDVDVAVAAARAAFE--GPWRQVTP 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated with the alcohol dehydrogenase I (alcA) gene and the aldehyde dehydrogenase (aldA) gene of A. nidulans or naturally associated with the glucoanylase gene in Aspergillus niger may be used. The DNA construct may contain a promoter region in operative association with a signal peptide coding region. The promoter/signal construct is suitably provided with a flanking restriction site to allow precise coupling of the protein coding region to the signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                Sequence of aldehyde dehydrogenase (aldA) of Aspergillus nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA construct for use in filamentous fundi - comprising promoter operative in filamentous fundi to promote transcription of coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In the constructs of the invention, the promoter region naturally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pickett M, Davies R, Scazzocchio C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.0%; Score 1418.5; DB 7; 58.5%; Pred. No. 5.5e-125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 1A, 75pp, English.
                                                                                                                                                                                                                                                                                         86WO-GB00209
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                                                                                                      Filamentous fungi promoter.
                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide coding region.
                                                                                                                                                   Aspergillus nidulans.
                                                                                                                                                                                                                                                                                                                                                                                                      (ALLE-) ALLELIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1986-291664/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497 AA;
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                                                                                                                                                                                                                                                                                         14-APR-1986;
                                                                                                                                                                                                                                                                                                                                                           15-APR-1985;
                25-JUN-1991
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                                                                                                                                                                                              W08606097-A
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263 LKRVILELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQCCCAGSRIFVQEDIYDEFVVR 311
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                            443 LSQALQANTVWVNIYOVEGAQSPEGGYKMSGSGRETJSEYGLQAYTEVKTVKV 496
                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ 1D NO: 44383.
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990S-0128234.
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05-MAP-1999,

23-MAR-1999,

25-MAP-1999,

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01-APP-1999,

06-APR-1999,

16-APR-1999,

16-APR-1999,
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30-APP-1999;
30-APR-1999;
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05-MAY-1999;
06-MAY-1999;
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23-APR-1999;
23-APR-1999;
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14-MAY-1999;
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07-MAY-1999;
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Title: US-09-830-751-4

Perfect score: 2625 Sequence: 1 MSAAATQAVPAPNQÖPEVFC. YGLGAYTFVKTVTVKVPAKN SUÖ

Scoring table: BLOSUM62 Gapext 0.5

Scarched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing. Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total soure distribution

## SUMMARIES

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11	818.5	51.2	487	43"	US 09-351-224E 5		
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17	403	15.4	133	C4	US-08-794-494-2	ci	
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24	95.5	3.6	548	4	US-08-466 248-31	Sequence 31, Appl	
52	95	3.6	706	4	US-09-134-0016-4908	4908	
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## ALIGNMENTS

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                                                                                                             APPLICANT: Riccardo Dalla-Favera and APPLICANT: Alessandro Massimo Gianni TITLE OF INVENTION. A Retroviral Vector Capable of Fransducing the TITLE OF INVENTION. A Retroviral Vector Capable of Fransducing the TITLE OF INVENTION. A Retroviral of the and Here of Said TITLE OF INVENTION: Vector
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Bust Local Similarity 66.1%, Fred. No. 7.1e-178,
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1185 Avenue of the Americas
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MEDIUM TYPE: Floppy disk
COMPUTER: 1BM 330 466 DX2
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SOFTWARE: PATENTIN PG-LGS #1 24
CUERENT ARFLICATION DATA.
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                                          ; Sequence 2, Application US/09221294
; Patent No. 6268188
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: White, John P. PF678TRATTON NYMBER: 28,678 REFERENCE/COCKET NUMBER: 429 TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO. 2.
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
                                                                      317 YHQGQCCIAASRIFVEESIYDEFVRRSVERAKKYILGNPLTPGVTQGPQIDKEQYDKILD 376
                                                                                                                                                                                                                                                                                                                                                  357 YINTGKQEGAKLIQGGGGIAADAGYFIQPIVEGDVQDGMLIAKEELFGPVMQILKFKTIEE 415
                                                                                                                                                                                                                                                                                                                                                                      119 YEVOLOMVINCERYYAGWADKY -- BGKTIPIFGGFFSYTRHEPVGVGGGIIPWNFPELMG 176
                                                                                                                            177 AWKLGPALATGNVVVMKVAEQTPLTALYVANLIKEAGFPFGVVNIVPGFGPTAGAAIASH 236
                                                                                                                                                                                                                                                                            297 FNOGOCCGASSTEVGEDTYDEFVVBSVARAKSKVGNPFUSKTFGGNGVDFFGPKKTD2 NSA
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PRIOR APPLICATION NUMBER: US 60/055,779
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Matches 207; Conserva
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                                                                                                                                                                                                                                                                                         376 - ADRGYFIQPTVFGDVQDGMTTAKEETFGPVMGTLKFKTTEEVVGRANNSTYGLAAAVFT 444
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259 GSSNLKRVTLELGGKSPNTIMSDADMDWAVEGAHFALFNUGGCCCAGSKTFVDFDTYDE
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MBER: 60/152,542
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417 SVLPPEGERRAITLANDIVEGLAAGVETEUVGPALFEAGILDAGNVWINSWGVLNPASPY 476
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Genes Encoding Picric Acid Degradation
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                                                        467 GGYKMSGSGPFLGEYGLQAYTFVKTVTVKVPQ 498
                                                                                               477 RGEGOSGYGSDLGQAAIESFTKEKSIWAPLDZ 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-651-941-9
FILE REFERENCE: BC1022 US NA
CURRENT APPLICATION NUMBER: Us/09/551,941
CURRENT FILING DATE: 2000-08-31
PPIOR APPLICATION NUMBER 60/152,545
PRIOR FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                     ; Sequence 9, Application US/0965194)
; Patent No. 6355470
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APPLICANT: RAINER, RUSS
TITLE OF INVENTION: Genes E
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US-09-955-597-9

RESULT 5

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No. 5753481el L-sorbose Dehydroqenase and No. 5753481el L-s
Dehydrogenase Obtained from Gluronchacter oxydans I-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64. REGPPSAPQLOSEWPPMDASHSGPLENPLAJOLIERDETYLAALETLINGKPYVISYLVDL. 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 VEAAKAA~--ARTWQFMPPAQFTFLMFFYAALLEBHKTBLAQLQSFDMGKFTFFSLGTDL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 LATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 FTGSTEIGRVIQVAAGSSNLKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQCC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 FTGSTEVOQQIGRMA ABRUTASCELGGKSALVAFGLSSFKAVAAVVEQAMYSNQGETC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 EGAKLLGGGGI----AADMYPFIQPTVFGDVQLMTIAKEEFF0PVMQILKFKTIEEVVG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.20. FANNSTYGLAAAVETRIGGRANYLSQAGJAGGVWVN-YLVFGAGSFEGGYKMSGSGKELG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 AATQAVPAPNQQPEVPCNQTFINNEMHDAVSPKTFPTVNPSTGEVICQVARGDKEDVFKA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ALTSSVP------LVIGDOLTPSSTGATFDSINPADGSHLASVAEATAADVARA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 LAMGNAIVEKPAQLAPEVPVALGELALEAGEPPGEVNVEPGRGSVAGNALVQHPSVGKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 GAGSPTEVÖEDTYDEFVVPSVAPAKSEVVGNPFDSK1 FGGPQVDFTGFKKTLGYTNTGKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.3%; Score 926; DB 4; Length 485; Best Local Similarity 38.9%; Pred. No. 3.3e-90; Matches 194, Conservative 91; Mismatches 194; Indels
                                                                                           APPLICANT: WALTERS, DANA M
TAPLICANT: PAINED, PUSS
TITLE OF INVENTION: Genes Encoding Pictic Acid Degradation
FILE PEPERENCE: EC1022 US NA
                                                                                                                                                                                                                                                                                                                                                                                                            OPGANISM: Phodococcus Prythropolis HL PM-1
                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/955,597
CURPENT FILING DATE: 2001-09-17
                                                                                                                                                                                                                                        PPIOR APPLICATION NUMBER: 60,7152,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08513841 Patent No. 5753481
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Sequence 9, Application 98/0995597
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APPLICANT: Saito, Yoshimasa
APPLICANT: Ishii, Yoshinori
APPLICANT: Yoshida, Masaru
APPLICANT: Suzuki, Hiromi
                                                                                                                                                                                                                                                               1999-10-03
                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
                                             GENERAL INFORMATION:
APPLICANT: POUVIEW, PIEPPE E
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                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                           Patent No. 5461856
                                                                                                                                                                                                                                                                                                                                                            485
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84 HSGRILLNRLADI.IERDRTYLAALETLDNGKPYVISYLVDLDMVI.KCLRYYAGWADKYHGK 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 LKRVTLELGGKSPNTIMSPADMPWAVEQAHFALFFNQGGCCAGSRTFVQEDIYDEFVVR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 SVARAKSRVVGNPFDSKTEQGPQVDFTQFKKILGYINFGKQEGAKLLCGGGIA-ADRGYF 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 FIDGEWR--ACKDPFDRSSPAHDVPVTPIPPCTREDEDEAVAAARRAFENGS-WAGLAAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Gaps
NUMBER OF SEQUENCES: 22
COFFESPONDENCE ADDRESS:
ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
STREET. 1755 Jefferson Davis Highway, Suite 400
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.4%; Score 902; DB 1; Length 497; 39.5%; Pred. No. 1.3e-87; 1ve 98; Mismatches 186; Indels
                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 18-909-0 PCT TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1.497
IDENTIFICATION METHOD: experimentally
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 241851/1993
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/513,841
FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9304700.9
FILING DATE: 08-MAR-1993
                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
MS-POS Editor
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703-413-2220
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amino acid
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Best Local Similarity
                                                                                                                                                                                                                    OPERATING SYSTEM:
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                                                                                                         Virginia
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NORMAN F.
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                                                                                                                         COUNTRY:
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                                                                                                       STATE:
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382. TOPTVEGDVQDYMTTAKEETE/PPVMQTLIKEKTFEEVVORANNSTYSLAAAVETKFILEKAN 44.1
                                                                                         442 YESGARGATIYWAN YEVPETABSEPONYEWS APELAEN LAANTEVENTVINKPONYOO SOO SEE SELF THE THE FIRST HOLD SOO SEE SELF THE THE FIRST HOLD SOO SOO SAVEAVENANEEWANTHMAGGERTELAAFKOOMGREAALNOVLANGLAGENOVERNOVERS 493
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    34.4%; Secret 902; D8 2; Length 497;
    39.5%; Proof. No. 1, 3e 87; Prof. No. 1, 3e 87;
    1ve 98; Mismatches 186; Indels 6; Gaps

                                                                                                                                                                                                                                                                                                                                        APPLICANT: Niwa, Minco
APPLICANT: Salto, Yoshimasa
APPLICANT: Salto, Yoshimori
APPLICANT: Ishii, Yoshimori
APPLICANT: Hayashi, Masaru
APPLICANT: Hayashi, Hiromi
TITLE OF INVENTION: Method for Producing 2 Keto-L Gulonic Acid
CORRESPONDENCE: A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oblon, Spivak, McClelland, Maior & Neustadt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette - 3.50 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1755 Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD: experimentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 28612/1994
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,834
FILING DATE: 24-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS DOS
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                                                                                                                                                                                                                                                                   : Sequence 2, Application US/08696834
: Patent No. 5834263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
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TELEX: 248855 OPAT UR
INFORMALION FOR SPQ ID NO: 2:
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COMPUTER READABLE FORM:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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CLASSIFICATION:
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No. 586127251 Freethuse Poly Degense and No. 586123251
E-sorbosone Debydrogenase Obtained from Gluconobacter
exydans T-100
                                                                                                                       195 LLLAEILADAGLPKGVFNVVTGTGRTVGQAMTEHQDIDMLSFTGSTGVGKSCIHAAADSN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                       315 VVPRMEKIRVGDPFDPFTQIGAITTEAQNKIILDYJANGKAEGAKLLGGGGIVDFGKGQY 374
84 HSGPLENFLADIJEFDFTYLAALETIGNGKPYVISYLVELEMVLKGLFYYAGWALKYHGK 143
                                               76 DPAAVILKAAGGLPERRDDIAVWEVLENGKP-ISQAKGETDHCIACFEMAAGAARMLHGD 134
                                                                                                  144 TIPIDGD-FFSYTPHEPVGVGGITPWNFPFIJMQAWKLGFALATGNVVVMKVAEQTFLTA 202
                                                                                                                                                                                                  203 LYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVAFTGSTEIGRVIQVAAGSSN 262
                                                                                                                                                                                                                                                                                                    263 LERVITELGGESPUTIMSDAPMEWAVEGAHFALFENGSJONGAGSELFVQEDIYDEFVVR 311
                                                                                                                                                                                                                                                                                                                                                  255 LKKLGLELGGKNPIVVFADSNLEDAADAVAFGISFNTGQCCVSSSRLIVERSVAEKFERL 314
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1755 Jefferson Davis Highway, Suite 400
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FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
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08-MAR-1993
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SUFTWARE: MS-EUS Editor
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08942673 Patent No. 5861292
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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Ishii, Yoshinori
Yoshida, Masaru
Suzuki, Hiromi
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CORRESPONDENCE ADDRESS.
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TITLE OF INVENTION:
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US-08-942-673-2
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No. 6197562cl L sorbose Delightogenase and No. 6197562cl E-sorbosone Delightogenase Obtained from Glucomobacter oxydans I-100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 FIEGEWR--AGKEFEEPSSPAHEVPVTPIPPATFFELLEEAVAAAFKAFENGS-WAGLAAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Gaps
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1755 Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                     34.4%; Sroze 902; DB 2; Length 497; 39.5%; Pred. No. 1.3e-87; tive 98; Mismatches 186; Indels
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STRAIN: T-100
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TELEXAX: 703-412-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Ishii, Yoshinori
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APPLICANT: Suzuki, Hiromi
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 IQPTVFGDVQDGMTIAKEEIFGPVMQILKFKTIEFVVGRANNSTYGLAAAVFTKDLDKAN 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 FIDGEWR--AGKDFFDRSSPAHDVPVTRIPPCTPFDGAAAAAAAABFAFFNGS-WAGLAAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caps
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Similarity 39.5%; Pred. No. 1.3e-87;
                                             3: Diskette, 3.50 inch, 1.44 Mb storage IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98; Mismatches
                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-909-0 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION METHOD: experimentally
                                                                                                                                                                                                                                                                                       APFLICATION NUMBER. JF 24:851/1993
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                      APPLICATION NUMBER: US/09/118,317
                                                                                                                                                                                                                                   APPLICATION NUMBER: UK 9304700.9 FILLING DATE: 08-MAR-1993
                                                                                   SYSTEM: PC-DOS/MS-DOS
MS-DOS Editor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gluconobacter oxydans
                                                                                                                                                                                                       08/513,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 248855 OPAT UR INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497 amino acids
                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                       PRIOR APPLICATION DATA:
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE: 01-NO
                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN: T-100
COUNTRY: USA
                                                                                                                                                        FILING DATE
                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                   SOFTWARE:
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APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOGY
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 EEFADYLLEISPRIHEKTEHLATVESLONGKIYRETSTIIVUQAANQEKYFASVULTDEG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 SHSGKLLNKLADLIEKDRIYLAALEILDNGKFYVISYLVDLDMVLACTLKYYAGWADRYHG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 LKRVTLELGGKSPNTIMSDADMOWAVEQAHEAGEENQGGGGGGSKTFVGEDTYDEEVVR 322
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                                        435 AVTRRVRAGREWANTIMSCOPELPECHEL HELLE HEELE EE EE EE 435 AVTRRVRAGREWANTIMSCOPELPECHENGERAGERAACHEETHER 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 LETINNEFÖASUSGETLIFVSNIPANGEDLAKVARAGKKIVUKAVQAAHDAF DSWSKISK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94; Mismatches 187; Indels 14; Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/144,0010*
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING TATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/005,779
PRIOR FILING IMTE: 1997-08-14
                                                                                                                                                                                                                                        Sequence 4541, Application US/U9134001c Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Staphylococcus epidermidis US-09-134-001C-4541
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// Patent No. 6388171
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APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: GTC-007
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Best Local Similarity
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APPLICANT, Lynn Dougette Stamm et al
TITLE OF INVENTION: NHCLEIG ACTH AND AMING ACTH SEQUENCES RELATING TO STAPHYLOGGIC
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                                                                                                                                                                                                                                                                                                                                                              78 ERPELLICKTVKEYÇNPKNICLTEALTICELSAPLSVSENVHYOM---GLNHPTAAPD---- 129
                                                                                                                                                                                                                                                                                                                                                                                                                144 TIPIDGDFFSYTR-----HEPVGVGGQIIPWNFPLLMQAWKLGPALATGNVVVMKVAEQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 --ALDSFQFEEQRGDDLVVKEAIGVAGLVTPWNFPTNQTSLKLAAAFAAGSPVVLKPSEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPLIALYVANLIKEAGPPPGVVNIVPGPGPTAGAATASHEDVDKVAFTGGTFTGRVIQVA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 AGSSNERPVTERGGKSPN11MSPADMFWAVEQAHFALFFNQGQGGGASSPTFVQEDIVD 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 EPVVESVAPAKSPV-VGNPPDSKTEQGPQVDETQPKKTLGYTNTGRQPGAKTLCGG---- 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 DYLI-AVKEAFSKVKVGQPPEESTQVGFIISKKQFL@VQDYIDKGINEGAELFYGGBGKP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 -GIAADRGYFIQPTVFGDVQDGMTIAKEEIFGPVMQ1LKFKTIEEVVGRANNSTYGLAAA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432 VETKELPKANYLSGALGASTVWVNCYRVPSAGS FEGGYKMSSSSKFLSEYSLGAYIEV 489
                                                                                                                                                                                                                        24 FINNEWHOAVSRKTEPTVNPSTGEVICQVAEGDKEDVDKAPEGRPGAFOLGSPWRRMDAS 83
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                                                                                                                                                                                                                                                                     21 YINGEWVDSASGETIDVINPATEEVMGKIAKGNEEDVNKAVD---AADKVYLEFRHSSVE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 TPFAAIILAEIFDKVGVPKGVFNLVNGDGSGVGNPLSEHPKVRMMSFTGSGPTGSKIMEK
                                                                                                                                                                           34; Gaps
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                                                                                                                      Score 753; DB 4; Length 488; Pred. No. 1.1e-71;
                                                                                                                                                                      98; Mismatches 178; Indels
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: Patent No. 6380370
                           TYPE: PRT
UKGANISM: Staphylononis epidermidis
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NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4388
                                                                                                                                                                      Matches 173; Conservative
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                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                           US-09-134-001C-4246
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          LENGTH: 488
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                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 QVAAGSSNLKRVTLELGGKSPNLIMSDADMDWAVEQAHFALFFNQ-GQCCCAGSKTFVQ-312
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     APPLICANT: Crasta, Oswald R.
IIILE OF INVENTION: Compositions and Methods for Function
TITLE OF INVENTION: Bettoxification
FILE REFERENCE: 5718-111
                                                                                                                      CUPPENT APPLICATION NUMBER: US/09/351,224E
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CUPPENT APPLICATION NUMBER: "$ 2097134,0015
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NUMBER OF SEG 1D NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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PRIOR APPLICATION NUMBER: US 50/054,954
PRIOR FILING DATE: 1997-11-08
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PRIOR FILLING DATE: 1997-08-14
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Patent No. 6380370
                                                                                                                                                                                                                                                                                       ORGANISM: Exophiala spinifera
                                                                                                                                                                                                                                                                                                                                                                                                           Matches 195; Conservative
APPLICANT: Folkerts, Otto
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US-09-134-001C-4246
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Sequence 4, Application US/09155183
Patent No. 6323011
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EFIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                          75 SPWREMDASHSGRILNRLAFILIEPDPTYLAALETILINGKPYVISYLVFILMVLKGLEYYA 134
                                                                                              74 -EWERVPQPTRAEHVKLLIPLLEKNRDEIAQLYVKFQGKTLAQAY-GELDKSISF1DYMT 131
                                                                                                                                        - ----TIPIDGDFFSYTRHEPVGVGGGIIPWNFPLIMQAWKL3PALA 185
                                                                                                                                                                                                                     186 TGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVAFT 245
                                                                                                                                                                                                                                                         184 TGCSVVIKPSEETTLLTLKLAELFRASTIPAGLFQIVPGTGETVGTQLASHKDJQLJSLT 243
                                                                                                                                                                                                                                                                                                                      132 SLSMSDKGRVI,QNSIANETIQI-----INKPIGVTAGIVPWNAPII,VLMRKVIPAIV 183
                                                                                                                                                                                                                                                                                                 246 GSTEIGRVIOVAAGSSNLKRVTLELGGKSPNTIMSDADMDWAVEQAHFALFFNGGGCCCA 305
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PRIOR APPLICATION NUMBER: US 5U/U54,964
PRIOR FILING DATE: 1997-11-08
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS- 5674
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Matches 169; Conservative
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US-09-134-001C-4451
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199 PLIALYVANDIABAGEPPGVVNIVPGEGPTAGAATASHEDVDAVAFTGSTETG
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TITLE OF INVENTION: PRODUCTION OF VANILLIN
FILE REFERENCE: 20747/100
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EARLIER APPLICATION NUMBER: GR96/06187
EARLIER FILING DATE: 1996-03-23
NUMBER OF SEO ID NOS: 14
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qa	248	248 LEELGGKAPILUULPDAPLEAAVQAAAFGAYFNQGGIGMSTERLIVDAKVADAFVAQLAAK 307	307
Qy	327	327 AKSRVVGNPFDSKTEQGPQVDETQFKKILGYINIGRGEGAKLLUGGGIAADRGYFIQPTV 386	386
qu	308	308 VETTRACIPADPESVLGSTVINASAGTFIKALINNAVAKGARLVIGGQLEGSTIQPTL 364	364
Οy	387		446
qq	365	365 IDGVDASMELYREESFGEVAVVLRGESEALIGLANGSEGISAAIFSKEEGRALADR 424	424
Qy	447	447 LOAGTTUWUN YEUFIS ALSPEGGYKMSGSGRELGEYGLQAYTEVKTVTVK 495	
qq	425	425 VESGICHINGPTVHDEAUMPFGGVKSSGYGSFGGKASIEHFTQLRWYTLQ 474	
Search Job tim	complet e : 15.	Search completed: June 24, 2003, 10-31-40 Job time : 15.8469 secs	

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/ Cgnn2_6/ptodata/2/pubpaa/ICTUS_PUBCOMB.pap: *
/ Cgnn2_6/ptodata/2/pubpaa/ICTUS_PUBCOMB.pap: *
/ Cgnn2_6/ptodata/2/pubpaa/ICS09_MEM_PUB.pap: *
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/ Cgnn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pap: *
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

#### SUMMARIES

Result

Query

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Sequence 10550, A	2000	Seautifica: July 7. A	Sequence 4, Appli	Sequence 4, Appli	Sequence 21, Appl	Sequence 4, Appli	1	11,	Sequence 22, Appl	() ()	Sequence 59, Appl	() 4 ()	24,	9	Sequence 20, Appl	 	Sequence 2, Appli	Sequence 12, Appl	Sequence 736, App	Description

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; SOFTWARE: PatentIn Ver. 2
; SEQ ID NO 736
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Fatent No. US20020044941A1
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CHERENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT. Rusen et al.
HILLE OF INVENTION: Nucleic Acids. Proteins and Antibodies
FILLE REFERENCE. FAIO4
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                              y Match 67.5%; Score 1771; DR 10; Tength 412;
Local Similarity 90.6%, Fred. No. 6.9e:156;
hes 339; Conservative 7, Mismatches 2%; Indels 0
                    181 GPALATGNVVVMKVAEQTPUTALYVANLIKEAGFPPGVVNIVPGFGPTAGAATASHEDVP 240
                                                                                 ZOU GEALATONYVYMKVAEGTELTALYVANLIKEAGET EGVYNTVEGEGETAGAATASHEDVD
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GENERAL INFORMATION:
APPLICANT: HE-STUMBE
APPLICANT: HE-STUMBE
APPLICANT: KHAETZSC
APPLICANT: KHAETZSC
APPLICANT: KHEET, H
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: Publication No. US200300775H9A1
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NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 512
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APPLICANT: HE-STUMED, BERNARD
APPLICANT: KREETZSCHMAR, JOERN
APPLICANT: KREETZ, BERTHOLT
APPLICANT: WINTERHAGER, EIKE
APPLICANT: BEGLIDOR, PEDRO
APPLICANT: SCOTIL SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Onery Match 65.4%; Score 1718; DB 9; Length 512; Best Local Similarity 65.5%; Fred. No. 7.9e-151;
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CURRENT APPLICATION NUMBER: US/09/961, 403
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                             439 LTAAVETKNIJBKALKLASALESGTVWINCYNALYAQAPEGGEKMSGNGRELGEYALAEYT 498
                                                                                       4.28 LAAAVETKELDKANYLSOALQAGTVWVNCYDVEGAQSEEGGYKMSGSGFELGEYGLQAYT 487
                                                                                                                                                 (1) RVEVEEQVYSEFVRRSVEYAKKRPVGDPFDVKTEQGPQIDQKQEDKILELIESGKKEGAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 TETGRVIQVAAGSSNLKRVTLELGGKSPNLIMSDADMDWAVEQAHFALFFNQGQCCCAGS 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 RTLRYFAGWADKIQGKTIPTHDNVVCFTRHEPIGVCGAITPWNFPLLMLVWKLAPALCCG 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 KVAFTGSTEIGRVIQVAAGSSNLKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQG
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US-10-268-518-2
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; LENGTH: 512
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; Publication No. US20030100034A1
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                         Publication No. US20030108963A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
APPLICANT: Schlegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: 9136, A HUMAN ALDEHYDE DEHYDROGENASE TITLE OF INVENTION: FAMILY MEMBER AND USES THEREFOR FILE REFERENCE: MPIOL-234PIRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/329,899 PRIOR FILING DATE: 2001-10-16 NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/268,518 CURRENT FILING DATE: 2002 10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                               499 EVKTVTIKLGDKN 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 NTMVLKPAEQTPLTALYLGSLIKEAGFPPGVVNIVPGFGPTVGAAISSHPQINKIAFTGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 MGAFQLGSFWRKMDASHSGRLLNRLADLIERDRTYLAALETIDNGKPYVISYLVDLDMVL 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 66; Mismatches 104; Indels
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APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL SENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 PGAFQLGSPWPPMPASHSGFLLNPLADLIERDRTYLAALETLDNGKPYVISYLVDLDMVL 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 TEVGKLVKEAASKSNEKKVTLELGGKNIC1VCADADLEDLAVECAHUGVFFNUGQCCTAAS 318
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Best Local Similarity 65.5%; Pred. No 7 9e-151;
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                                                                                                                                                                                                                                                                        FILE REFERENCE: MRI-044
CURKENT APPLICATION NUMBER: US/10/205,823
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT PILING LATE: 2002-07-25
PRIOP FILING DATE: 2001-08-25
PRIOP FILING DATE: 2001-08-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR PILING DATE: 2001-08-25
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-19-25
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2003-03-05
NUMBER OF SRO ID NOS: 455
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                Endege, Wilson O.
Gannavarapu, Manjula
Gorbatcheva, Bella
                                                                              Hoersch, Sebastian
Kamatkar, Shubhangi
Wonsey, Angela M
Monahan, John E.
                                                                                                                                                                     Zhao, Xumei
Anderson, Dustin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         488 EVKTVTVKVPQKN 500
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                                                                                                                                                Glatt, Karen
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ORGANISM: Homo sapiens
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APPLICANT: Lutziger, Isabelle APPLICANT: Wee, Tsui-June Taui-June Tsui-June Tsui-June Taui-June Taui-June TillE PF INVENTION: Aneryl CoA Levels in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 DLDMVLKCLRYYAGWADKYHGKTTPIDGDFFSYTRHEPVGVGQIIPWNFPLLMQAWKLG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 PALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 VAFTGSTEIGRVIQVAAGSSNLKEVILELGGKSPNIIMSDADMEWAVFQAHFALFFNGGQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 CCCAGSRTFVQFP1YDEFVVRSVARAKSRVV3NPFDSKTEGGR©VDET@FKKTLGYINTG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **8 PCCAUSETEVHEKVYDEFVERSKAPALKPVVCD-PFFKOTFLIDD-TOLKDFEKVMKYTKSG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 KQEGAKELCOSGGAROVELOPETVEGOVONONGNOMITAKEETEGPVMQILKEKTIEEVVGRA 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 SAAAEEII---NPSVQVSHTQLLINGNFVDSASGKTFPTLDPRTGEVIAHVAEGDAEDIN 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 4; Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.8%; Score 1543; DB 9; Length 538; Nost Local Similarity 61.1%; Prod No. 1 5e-134; Matches 300; Conservative £1; Mismatches 12£; Indels
                                                                                                                                                                                                                                                                                                                                                           CUREENT AFFLICATION NUMBER: US/09/344,882
CHPRENT FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER - US 60,7090,717
                   ; Sequence 20, Application US/09344882
; Fatent Nc. US20920162137A1
                                                                                                                                       Behal, Robert
Schnable, Patrick S
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NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                           Ke, Jinshan
Johnson, Jerry L
Allred, Carolyn C
Fatland, Beth
                                                                              APPLICANT: Nikolau, Basil J
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                                                                                             Wurtele, Eve S
Oliver, David J
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                                                         GENERAL INFORMATION:
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US-09-344-882-20
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LENGTH: 538
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APPLICANT:
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62 KAREGRPGAFQIGSPWPPMDASHSGRIINRLADLIERDRIYLAALETIDNGKPYVISYLV 121
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APPLICANT: Men, Tsui-Junq
TITLE OF INVENTION: Materials and Methods for the Alteration of Engyme and
TITLE OF INVENTION: Acetyl CoA Levels in Plants
FILE REFERENCE: 217113
FILE REFERENCE: 217113
FILE REFERENCE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/344,882
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING NUMBER: US 60/090,717
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                  Sequence 20, Application HS/10294865
Publication No HS20040106090A1
                                                                                                       APPLICANT: Oliver, David J
APPLICANT: Schnable, Robert
APPLICANT: Schnable, Patrick S
APPLICANT: Ke, Jinshan
APPLICANT: Johnson, Jerry L
APPLICANT: Johnson, Jerry L
APPLICANT: Allred, Carolyn C
APPLICANT: Falland wart
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NUMBER OF SEQ ID NOS: 38
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                                                      GENERAL INFORMATION:
APPLICANT: Nikolau, Basii J
APPLICANT: Wurtele, Eve S
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APPLICANT: Lutziger, isabelle
APPLICANT: Wen, Tsui-June
TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Acetyl CoA Levels in Plants
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CURRENT APPLICATION NUMBER: US/U9/344,882
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/090,717
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 38
                                       Sequence 24, Application US, 209444882
Patent No. US20020162137A1
                                                                                                                                                                             Schnable, Patrick S
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Fatland, Beth
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Johnson, Jerry L
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Oliver, David J
Behal, Robert
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                                                                            GENERAL INFORMATION:
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RESULT 7
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61 DKAPEGPPGAFQLGSPWPPMDASHSGRILNPLADLIEPDRTYLAALETLDNGKPYVISYL 120
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APPLICANT: Wen, Tsui Jung
TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Acetyl CoA Levels in Plants
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CUPPENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/344,882
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PRIOR APPLICATION NUMBER- 08-60/090,717
PRIME FILING DATE: 1998-06-26
                    Sequence 24, Application US/10293865 Publication No USZ0030106090A)
                                                                                                    APPLICANT: Wurtele, Eve S
APPLICANT: Oliver, David J
APPLICANT: Behal, Robert
APPLICANT: Schnable, Patrick S
APPLICANT: Johnson, Jerry L
APPLICANT: Johnson, Jerry L
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APPLICANT: Fatland, Reth
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APPLICANT: Wurtele, Eve S
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Matches 294; Conservative
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                                                                GENERAL INFORMATION:
US-10-293-865-24
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LENGTH: 334
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83 SHSGRLLNRLADLIEPDPTYLAALETLINGKPYVISYLVDLDMVLKCLPYYAGWADKYHG 142
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                                                                                                        APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND FREATMENT OF
TITLE OF INVENTION: 19E-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CORFERT APPLICATION NYMHEP: USANYAMA47, 708
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                                                                                                                                                                                                                         CURRENT FILLING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4 0
                                 : Sequence 59, Application US/09847208 : Publication No. US20030082190A1
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Fatent No. US20926162137A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        ORGANISM: Cladosporium herbarum
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Behal, Robert
Schnable, Patrick S
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Johnson, Jerry L
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                                                                                            APPLICANT: Saxon, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                   Hest Local Similarity
Matches 262, Conserv
                                                                       GENERAL INFORMATION:
                   65-807-/$8-60-SD
                                                                                                                                                                                                                                                                                                                                                           US-09-847-208-59
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                                                                                                                                                                                                                                                                                SEQ ID NO 59
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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AFFLICANT.
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RESULT 9
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Allred, Carolyn C

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APPLICANT: Lutziger, Isabelle
PEPLICANT: Wen, TSHI-Jung
TELLE OF INVENTION: Materials and Methods for the Alteration of Engyme and
TITLE OF INVENTION: Acetyl CoA Levels in Plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 PWPRMTGFERAKLINKFADLIEENIEELAKLDAVDGGKLFQLGKYADIPATAGHFRYNAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 QVAAGSSNIKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQCCCAGSKTFVQED 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 AADROYPIQPTVFGDVQDGMIJAKEEIFGPVMQILKFKTIEEVVGRANNSTYGLAAAVFT 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 PEIKETKLFINGOFIDAASGKTFETIDPRNGEVIATIAEGDKEDVDLAVNAARYAFDHG- 73
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APPLICANT: Wen, Tsui-Jung
TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 48.8%; Score 1280; DB 9;
Best Local Similarity 53.1%; Pred, No. 3.4e-110;
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                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/344,882
CURRENT FILING DATE: 1999-06-25
                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 1999-06-25
PRIOR FILING DATE: 1999-06-25
NUMBER: US 60/090,717
NUMBER: OF COMMERCE OF CO
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Publication No. US20030106099A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Arabidopsis Thaliana
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Johnson, Jerry L
Allred, Carolyn C
Fatland, Beth
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Behal, Robert
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                                                                                                                                                                                                                                                                                                                                                                                               38
APPLICANT: Fatland, Beth
                                                                                                                                                                                               201573
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                                                                                                                                                                                                   FILE REFERENCE:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 QVAACSSNIARVILLELGCKSENTIMSPADMOWAVEDAHEALD ENGOGEORAGSRIFVUED - 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 WADKYBOKTIP-ID-GDFFSYTRHEPVGVGQTTPWNFPLLIMQAWKDGPALATGNVVVMAV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195. AEQTPL/TALYVANI,TKEAGFPP/SVVNTVPGFGPPAGAATASHEDVDKVAFTGSTETGKVT. 254.
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TITLE OF INVENTION: PUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: 146-MEDIATED ALLEKGIC DISEASES
FILE REFERENCE: UG67,002A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.8%; Score 1280; DB 9;
53.1%; Pred. No. 3.4e-110;
tive 74; Mismatches 149;
                                    CURRENT APPLICATION NUMBER: US/10/293,865
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/244,802
PRIOR FILING DATE: 1999-06-25
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CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
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                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/090,717
PRIOR FILING DATE: 1998-06-26
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ORGANISM: Alternaria alternata
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FILE REFERENCE: 217113
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Best Local Similarity
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LENGTH: 501
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Tue Jun 24 10:42:21 2003

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83 SHSGRLLINKLADLIERERTYLAALETLDNGKPYVISYLVDIJMVLKCLRYYAGWADKYHG 142
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                                                                                                                                                                                                                                                                                                                                                                                                           323 SVARAKSEVVGNPFIGSKTEGGFEVLFFGFKKTLGYINIGEQEGAKLLGGGGIAADEGYFT 382
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                                                                                                                                                                                                                                                                                    143 KTIPIDGDPPSYTPHEPVGVGGQIIPWNPPLLMGAWKLGPALATGNVVVMKVAEQTPLTA 292
                                                                                                                                                                                                                                                                                                                              138 KVVDTAPDSFNYIR-KSLLVFAVRSSMELPILMWSWKIGPAIATGNTVVI,KTAEQTPLSA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 LKRVTLELGGKSPNIIMSDADMFWAVFQAHFALEFNQGGGGGGGGGFFVQEDIYDEFVVR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 FKERAAQNAVGDPF-AATLQGPQVSQLQFDPIMGYIEEGKKSGATIETGGNRKGDKGYFI 375
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                                                                                             23 IFINNEWHUAVSRKTFPTVNFSTGEVICQVAEGDKEDVDKAREGRPGAFQLGSPWRRMDA 82
                                                                                                                              30 LFINNEFVRAVDCKTFDVINFSTEEVISSQEATEKDVDIAVAAAFKAF--NGPWAKETP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 0; Gaps
                                                      4, Gaps
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  48.3%; Score 1269, DB 9; Length 495; 52.3%; Prcd. No. 3.5e-109; ivc 77; Mismatches 145, Indels
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73.5%; Pred. No 2 3e-104;
tive 38, Mismatches 45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/US/VS/4 100 CURRENT FILING DATE. 2001-08-10 PRIOR APPLICATION NUMBER: PCT/USOO/05988 PRIOR FILING DATE: 2000-03-08 PRIOR PLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Sequence 1348, Application US/U99253UU
; Patent No. US20020151681A1
                                              Matches 248; Conservative
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SOFTWARE: PatentIn Ver. 2.0
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Query Match
Best Local Similarity
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188 NVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVAFTGS 247

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121 RTFVEBSTYNBFLERTVEKAKÇPKVGNPFELLITQQQBPÇVDKRQFERVLGYTQLGQKEGAK 180
                                                                                                                                                                                                                                                                    248 TELGBVTQVAA3SSNEKRVTLEDGGRSPNTTMSGAIMGWAVFQAHFALFFNGGGOOGAGS 307
                                                                                                                                                                                                                                             368 LLCGGCIAADPGYFIGPTVFGDVQDGMTTARPFIFGPVMQTLRFRTFFFVVGPANNSTYG 427
                                                                                                                                                                                                                                                                                                                                               428 LAAAVETKDIJDKANYI,SQALQAGTVWVNPYDVFGAQSPEGGYKMSGSOPELGEYGLQAYT 487
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1 NTVVMKVAEĢIPLSALYXASLIKEAGFPFGVVN1IIGYGFTAGAALAQHMDVDKVAFIGS 60
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TITLE OF INVENTION: FAMILY MEMBER AND USES THEREFOR
FILE REFERRICE: MPIO1-234P1RM
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PROFF FILLING DATE: 2001-10-16
NUMBER OF SEU ID NOS: 10
SOFTWARE: PASESEQ for Windows Version 4 0
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CURRENT FILING DATE: Z002-10-10
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Publication No. US20030100034A1
GENERAL INFORMATION:
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375 AADR----GYFLQPTVFGFVQDGMTIAKERIFGPVMQILKFKTIEEVVGRANNSTYGLA 429
                                                                                                                                        430 AAVETKD-LDKANYLSQALQAGTVWVN--CYDVFGAQSPFGGYKM-SGSGREL-GEYGLQ 484
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68; Mismatches 143; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: NOVEL HUMAN BNZYME FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 10448-193001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.4%; Score 1191; DB 9; Length 493; 52.3%; Pred. No. 6e-102;
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PRICK APELICATION NUMBER: UNYES, 901
PRICK FILING DATE: 2001-03-30
PRICK PILING DATE: 2001-03-30
PRICK PILING DATE: 2001-04-02
PRICK PILING DATE: 2001-04-02
PRICK PILING DATE: 2000-03-31
PRICK PILING DATE: 2000-03-31
PRICK PILING DATE: 2000-03-31
PRICK PILING DATE: 2001-05-21
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PRIOR FILING DATE. 2000-05-19
PRIOR FLLING DATE: 2001-06-15
PRIOR FLLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: PCT/US01/19319
PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/211,727
PRIOR ELLING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ); OTHER INFORMATION: consensus sequence US-10-175-696-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUPPENT FILING DATE: 2002-06-20 PRIOR APPLICATION NUMBER: 10/067,668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/266,140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-05-21
APPLICATION NUMBER: 60/205,675
FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/10175696 Publication No. US20030092658A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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258; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   US-10-175-696-21
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Best Local S
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317 DEFVVRSVARAKS-RVVGNPFDSKTE-OGPOVDETOFKKIL GYINTGKOEGAKLL/333 373
                                                                                                                                   429 AAAVFTKD-LDKANYLSQALQAGTVWVN--CYDVFGAQSPFGGYKM SGSGKEL GEYGL 484
                                                                                                                                                                                                                                                    200 ITALYVANLIKEAG — FPPGVVNIVEGFGPTAGAATASHEDVDKVAFTGFTELGFV19V 256
                                                         257 AAGSSNLKRYTLPLGGKSPN FIMSDADMOWAVEQAHFALFFNGGGCCGAGSRTFVQEDTY 416
                                                                                                                                                                             374 IAADR-----GYFIQPTVFGDVQDGMTIAKEEIFGPVMQILKFKTIFEVVGRANNSTYGL 428
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Search completed: June 24, 2003, 10:47:05 Job time: 26.1692 sees

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Genropa vorsion 5-1-6
Copyright (c) 1993 - 2003 - compugon i+d
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OM protein - protein seatah, using sw model

Pun on: June 24, 2003, Poillion ; Search time 141 017 Seyonds

(without alignments) 1780.8f: Million cell updates/ser

> Title: US-09-830-751-4 Perfect score: 2625

FELLECT SCHIPT 2727 Sequence: 1 MSAAAIQAVPAPNQQPEVPC ....YSLQAYIEVKIVIVKVPQKN 590

Scoring table: RinsmM62

Gapup 10 0 , Gapext 0.5

4569144 seqs, 644733110 residues

Searched:

Total number of hits satisfying chosen parameters: 45691

Minimum DB seq length։ 0 Maximum DB seq length։ 2000000000 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database . Per

Pending\_ParentsAA\_Masin.e.

1. /cgg2\_6/ptodata/1/paa/TSC\_COMH.pep.\*

2. /cgn2\_6/ptodata/1/paa/USO6\_COMH.pep.\*

3. /cgn2\_6/ptodata/1/paa/USO8\_COMB.pep.\*

4. /cgn2\_6/ptodata/1/paa/USO8\_COMB.pep.\*

5. /cgn2\_6/ptodata/1/paa/USO8\_COMB.pep.\*

6. /cgn2\_6/ptodata/1/paa/USO8\_COMB.pep.\*

7. /cyn2\_6/ptodata/1/paa/USO8\_COMB.pep.\*

8. /cyn2\_6/ptodata/1/paa/USO8\_COMB.pep.\*

9. /cyn2\_6/ptodata/1/paa/USO8\_COMB.pep.\*

10. /cgn2\_6/ptodata/1/paa/USO86\_COMB.pep.\*

10: /cgn2\_6/prodateA/1/paa/18080. 11: /cgn2\_6/prodateA/1/paa/1808A\_70MB.pep:\*
12: /cgn2\_6/prodateA/1/paa/1808R\_70MB.pep:\*
13: /cgn2\_6/prodateA/1/paa/1808R\_70MB.pep:\*
14: /cgn2\_6/prodateA/1/paa/18080\_20MB.pep:\*
15: /cgn2\_6/prodateA/1/paa/18090\_20MB.pep:\*

15: //git.z./pinata/1/paa/18/4/20MB.pep; \*
16: //git.z./pinata/1/paa/18/92\_10MB.pep; \*
17: //git.z./pindata/1/paa/18/93\_10MB.pep; \*
18: //git.z./pindata/1/paa/18/93\_10MB.pep; \*
19: //git.z./pindata/1/paa/18/95\_10MB.pep; \*
20: //git.z./pindata/1/paa/18/96\_10MB.pep; \*

21: /cgn\_\_6/ptodata/1/pha/18097\_comm paper - /cgn2\_6/ptodata/1/paa/18097\_comm paper - 22: /cgn2\_6/ptodata/1/paa/18099\_comm paper - 24: /cgn2\_6/ptodata/1/paa/18100\_comm paper - 25: /cgn2\_6/ptodata/1/paa/18100\_comm paper - 25: /cgn2\_6/ptodata/1/paa/18101\_comm paper - 25: /cgn2\_6/ptodata/1/paa/18101\_comm paper - 25: /cgn2\_6/ptodata/1/paa/18102\_comm paper - 25: /cgn2\_6/ptodata/1/paa/1860\_30MB.paper - 27: /cgn2\_6/ptodata/1/ptodata/1/paa/1860\_30MB.paper - 27: /cgn2\_6/ptodata/1/paa/1860\_30MB.paper - 27: /cgn2\_6/ptodata/1/ptodata/1/paa/1860\_30MB.paper - 27: /cgn2\_6/ptodata/1/ptodat

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pesult No.	Score	S Query Match	ֆ <u>Query</u> Match Length DB ID	178	dī.	Description
	26.22	6.66		7	21 08-09 791-537-77606	Sequence 77606, A
c a	2574	98 J		7	0.8+0.8+4.66+2.10pt 2	
æ	2574	98.1	515	c i	21 US 09 791-537-57517	
4	2572	98.0		-	US-09-538-092-851	
S	2572	0.86	517	= 1	US-09-791 537-74079	Sequence 74079, A
ت	2572	ر م	117	5	119 60 389 387-1747	

41 DKAPEGERFGAPQLGSFWFFMTASHSGPLINPLAGITEPEFFTYLAALFTLOMGKFYVISYL 120

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Sequence 1242, Ap Sequence 4, Appli Sequence 71773, A Sequence 56, Appli Sequence 56, Appli		rquence 1247 equence 1247 equence 1347 equence 137 equence 7407 equence 127 equence 127	o o o o o o o	3, App. 10.47, App	Sequence 1, Appl1 Sequence 126493,
US - 60 - 412 - 4 US - 08 - 366 - 21 US - 09 - 791 - 5 US - 60 - 389 - 9 US - 60 - 41 2 - 4	US-09-741-547-6 US-09-791-547-6 US-09-791-537-7 US-09-791-537-1 US-09-791-537-1 US-09-760-475-3	25.10.212.054.1245.255.05.10.212.054.1245.255.09.791.537.1961.05.09.791.537.105.05.08.612.853.12.05.08.612.853.12.05.09.791.537.7651.05.09.791.05.09.791.05.09.791.537.7651.05.09.791.05.09.09.791.05.091.05.091.	US-09-791-537 US-60-389-987 US-60-389-987 US-09-791-533 US-09-760-443 US-09-760-475 US-10-212-054	PCT-USO1-17253-3 US-09-538-092-1047 US-09-791-537-70511 US-09-614-150-7212 US-09-191-637-129281 US-60-191-637-7243 US-60-191-6449 US-60-167-217-7335 US-09-791-537-0939 US-09-791-537-0539 US-09-791-537-0539 US-09-791-537-0537-0539	US-08-748-818-2 08-69-791-537-126493
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10S-094-791-547-77bu6

Sequence 77bub, Application US/U9791537

Sequence 77bub, Application US/U9791537

Sequence 77bub, Application US/U9791537

APPLICANT: Batchenia, Inc.

APPLICANT: Dancer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILLES AND FAMILY ME

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILLES AND FAMILY ME

TITLE OF INVENTION: METHODS OF USE THEREOF

CUPPERING SEQ ID NOS: 133055

SOFTWARE: PART

ORGANISM: 516

LENGTH: 516

ORGANISM: FORCE

ORGANISM: PROD

ORGANISM
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241 KVAFTGSTEIGRVIQVAAGSSNLKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQG 300
                                                                                                                                                                360
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                                                         GPALATGNVVVMKVARQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVD 240
                                                                                                                                                                                                                                                               361 GKQEGAKLLGGGGTAADRGYFIQPTVFGDVQDGMTIAKEEIFGPVMQILKFKTIEEVVGR 420
                                                                                                                                                                                                                                                                                                                    421 ANNSTYGLAAAVFTKULDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGFFLGF 480
                                                                                                                                                                                                                                                                                                                                 301 OCCCAGSKTFVQEDIYDEFVVKSVARAKSRVVGNPFDSKTEQGPQVDETQFKKILGYINT
                                                                                                                                                                                                                                                                          APPLICANT: Lauerman et al.
TITLE OF INVENTION: Expression of a Mutant Form of Aldehyde
TITLE OF INVENTION: Dehydrogenase as an Alcohol Aversive Agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2574, DB 7, Langth 515;
Pred. No. 4.8e-257;
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60 State Street, suite 510
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FILING DATE: December 29, 1994
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                        481 YGLQAYTEVKTVTVKVPQKN 500
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08366210B GENERAL INFORMATION:
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38,872
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99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    515 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
FURRANT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001 02 22
NUMBER OF SEQ ID NOS: 15405
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Pred. No. 4.8e 257;
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GENERAL INFORMATION:
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US-09-791-537-57517
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145 PYYAGWADKYHGKTIPIIGTFFSYTKHKPVGVGGGIIPWNFPLLMGAWKLGPALATGNVV 204
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                                191 VMKVAEQTPLIALYVANLIKEAGFPFGVVNIVFGFGFTAGAATASHEDVOKVAFGSTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFRENCE: 15966-542
CURPENT APPLICATION NUMBER- US/A9/538,A92
CURRENT FILING DAID: 2000-03-29
PRIOR APPLICATION NUMBER: 5001-03-29
PRIOR FILING DAIE: 1999-04-01
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SOFTWARE: CurafatSeqFormatter Version 0.9
SEQ ID NO 851
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APPLICANT: Mansfield, Traci A.
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APPLICANT: Bionomix, Inc.
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APPLICANT: Debo, Derek
APPLICANT: Debo, Deseph
TITLE OF INVENTION: THPRE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
OURRENT FILLMONATION NUMBER: US/09/791,537
CURRENT FILLMO DATE: 2001-02-22
SOFTWARE: PALIL ONE: 133055
SOFTWARE: PALCULIN VERSION 3.0
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Pred. No. 7.8e-257;
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98.2%;
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                        421 ANNSTYGLAAAVETKDLDKANYLSQALQAGTVWVNCYDVEGAQSPFGGYKMSGSGPELGF 489
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FILE REFERENCE: 660088,465P2
                                                                                                                                                                                                                                                                                                                             APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Marinock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                             Sequence 1242, Application US/60389987 GENERAL INFORMATION:
                                                                                 481 YGLQAYTEVKTVTVKVPQKN 500
                                                                                                       497 YGLQAYTEVKTVTVKVPQKN 516
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NUMBER OF SEQ ID NOS: 3025
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                                                                                                                                                                                                                                                                                        APPLICANT: Fahy, Eoin D. APPLICANT: Zhang, Ring
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                                                                                                                                                                                                         US-60-389-987-1242
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                                                                                                                                                                                                                                                 APPLICANT: WATHOCK, DATO E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOTRODRIAL PROTEOME
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                                                                                                                                                                                                                                                                                                                                                     CURRENT ALTEGRALLER REMBER (05/07/412,418) CURRENT FILLING DATE: 2002-09-20 NUMBER OF SEQ ID NOS: 3025
                  Us-c0.412-418-1242
; Sequence 1242, Application US/60412418
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TITLE OF INVENTION: Express
TITLE OF INVENTION: Dehydro
                                                                                              APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 660088.465P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                   Zhang, Bing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                        ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-60-412-418-1242
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FILE KEFEFENCE: 7-1/210
CUPPENT APPLICATION NUMBER US/09/791,537
CUPENT FILLNS DATE: 2031-02-22
NUMBER OF SEQ ID NOS: 153055
                                  Sequence 7173, Application US/U9791537 GENERAL INFORMATION:
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Gibson, Bradford W.
                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0
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APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                               Matches 490, Conservative
                                                                 APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                  OPGANISM Homo sapiens
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               US-09-791-537-71773
                                                                                                                                                                                                                                                                                               US-09-791-537-71773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               431 AVFTKDLDKANYLSQALQAGTVWVNGYDVFGAQSPFGGYKMSGSGRELGEYGLQAYTEVK 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 APNOQPEVFCNQIFINNEWHDAVSPKTFPTVNPSTGEVICQVAEGRKERVDKAPEGPPGA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 APNOOPEVECHOIFINNEWHDAVSRKTFFIVNFSTGEVICGVAEGLKEDVOKAPEGFPGA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.9%, Score 2570, DB 7, Length 515,
99.6%; Pred. No. 1.38-256;
ive 1; Mismatches 1; Indels
          APPLICATION NUMBER: US/UB/366,210B
FILLING DATE: December 29, 1994
                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: TTI-128
                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: TRM PC compatible
OPERATING SYSTEM: PC-D/S/MS-D/S
                                                                                                                                                                                                                                                                                                                 38,872
                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NOT 4:
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
                                                                                                                                                                                                                                                                                                                                                                                                                                  515 amino acids
                                                                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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Matches 488; Conservative
NUMBER OF SEQUENCES: 4
                                                                                 Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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                                                                                                                               COMPUTER PEADABLE FORM:
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                                                                                                              ZIP: 02109 1875
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                                                               Boston
                                                                                                    USA
                                                                                                                                               MEDIUM TYPE:
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                                                                                                  COUNTRY:
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                                                                                  STATE:
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSTONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 EVAFTGSTEIGRVIQVAAGSSNLFFVTLFIGGFSPNTIMSDADMDWAVEQAHFALFFNQG 300
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APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Cary M.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2569; DB 21;
Pred. No. 1.6e 256;
3; Mismatches 7;
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ORGANISM: Homo sapieus

TYPE: PRT

US-60-412-418-56

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61 DKAREGRPGAPQLGSPWPPMDASHSGRLLNRLADLIERDRTYLAALETLDNGKPYVISYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VDLDMYLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 VOLDMYLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKL 196
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APPLICANT: Fahy, Boin D.
APPLICANT: Tang, Bing
APPLICANT: Shang, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary W.
APPLICANT: Glenn, Gary W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Tayle E.
TITLE OF INVENTION: TAKGETS FOR THERAPBUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDERAL PROTECME
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 1.6e-256;
                                                                                                                                                                                                                                                                                                           3; Mismatches
                                      CURRENT APPLICATION NUMBER 18,500,7389, 987
1919 ENT FILLING DATE: 2002.06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: PASESEO FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: AADUNG 4557
CURRENT APPLICATION NOMBER: US/60/412,418
CURPERT FILING DATE: 2002-09-20
NUMBER OF SEO ID NOS: 3025
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; GENERAL INFORMATION:
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98.08;
             FILE REFERENCE: 660088.465P2
                                                                                                                                                                                                                                                                                                        Matches 490; Conservative
                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                  LENGTH: 517
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 ANNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGE 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 LSAAATQAVPAPNQQPEVFCNQ1FINNEWHDAVSRKTFPTVNPSTGEVIGUVAEGDKEDV 76
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                                                Gaps
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97.9%; Score 2569; DB 27; Longth 517; 98.0%; Pred. No. 1.6e-256;
Live 3; Mismatches 7; Indels 0;
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CURRENT APPLICATION NUMBER: US/09/791,537
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                                              490; Conservative
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                         Best Local Similarity
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Oy 68 PGAFOLGSFWRKMDASHSGFLINFLAFFFFTVLAAFFTLINGKFYVISYIULLWVL 127   111111111111111111111111111111111111	DD 121 KCLRYYAGWALKYHGKTIPILGEDEFSYTHHEPWINGEGITHMITHITHITHITHITHITHITHITHITHITHITHITHITHI	Oy 248 TEIGRVIQVAAGSSNLKKVILELGGKSPNLIMSDADMEMAVEQAHFALFFNGGGCCAGS 307 [1111717171717171717171717171717171717	GY 3.08 ETEVGEDIYDEEVVESVARAKSRVVANPEGSKTEGARGVOFTGERKIIGSTINTGROEGAK 367 	368 LDJOGGAADRGYRIQPTVRGDVQDGMTAKEEIRGPVWQILKFKTIEEVVGRANNSTYG 	OY 4.28 LAAAVETKULKANYILSQALQAGYUWNICTDAFIQSPIGGYKRISKRIKARGYT 487  DD 421 LAAAVETKULKANYILSQALQAGYUWNICYLVEGAUSPEGYYKMSISSIAHILIITIITIITII  DD 421 LAAAVETKULKANYILSQALQAGYUWNICYLVEGAUSPEGYYKMSISSIAHILIITIITIITIITIITIITIITIITIITIITIITIITII	QY 488 EVKTVTVKVPQKN 500 	US-09-791-537-64443 Sequence 64443. Application US/09701537 GENERAL INFORMATION: APPLICANT: Debt. Detek APPLICANT: Debt. Detek APPLICANT: Debt. Object APPLICANT: Debt. Detek APPLICANT: Debt. Detek	MOSTONES OF PROTEIN PARTIES AND 7	COFFER FILLS ARE:  NUMBER OF SEQ ID NOS: 15365  SOFTWARE: PatentIn version 3.0  SEQ ID NO 64443	: TYPE: PRT :	Query Match Best Local Similarity 95.0%; Pred. No. 1.1e-249; Matches 474; Conservative 11; Mismatches 14; Indels 0; Gaps 0;	QY 2 SAAATQAVPADNQQPEVFCNQIFINNEWHDAVSFKTFFTVTVNPSTGEVICQVAEGSDKEDVD 61 	Gy 62 KAREGRESAFOLGSPWERMIASHSGPLIANFLADLIEPINFTYLAALETLONGKPYVISYLV 121 	Oy 122 DEDMYLKGERYYAGWARKYBGKTEPTORTORTORTORGANGO TEMNEPELMQAMKLOS 181 	Oy 182 PALATGNVVVMKVAEQTELFALYVANLIKEAGEFFG;VVNIVFGFGFTAGAALASHEEVDK 241 

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APPLICANT: Debe, Derck
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMHE
421 ANNSTYGLAAAVETKDLDKANYLSQALQAGTVWVNCYDVEGAQSPFGGYKMSGSGRELGE 480
                 61 DKAREGRPGAFQLGSPWPPMDASHSGRLLNRLADLIERDRTYLAALETLDNGKPYVISYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 VDLDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.5%; Score 2480; DB 21; Length 519; 94.2%; Pred. No. 2.8e-247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Mismatches 16;
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 261/210 CURRENT APPLICATION NUMBER: US/09/791,537
                                                                                                                                                                                       Sequence 130904, Application US/09791537 GENERAL INFORMATION:
                                                                  481 YGLQAYTHVKTVTVKVPQKN 500
                                                                                                  499 YGLQAYTEVKTVTVKVPQKN 518
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NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 130904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 471; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                   US-09-791-537-130904
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Search completed: June 24, 2003, 10:30:38 Job time : 183.017 secs

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Gendore version 5.1.6
Copyright (c) 1993 - 2003 (compugen 1.4
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OM protein - protein search, using sw model

Run on: June 24, 2003, 10:14:35; Search time 54:1289 Seconds

(without alignments)
2375 712 Million cell updates/sec

Title: US-09-830-751-4 Perfect score: 2625

Sequence: 1 MSAAATQAVPAPNQQPEVFC . ... YGLQAYTEVKTVTVKVPQKN 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1171708

1171708 segs, 257189465 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2(mondoun)

Maximum DB seq length: Zurenbund) Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*

1. /cgn2\_6/ptodata/2/paa/PST\_NEW\_NMR\_pap. \*
2: /cgn2\_6/ptodata/2/paa/PSG\_NEW\_NOMB\_pep. \*
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7: /cgn2\_6/ptodata/2/paa/TSG8\_NEW\_NOMB\_pep. \*
7: /cgn2\_6/ptodata/2/paa/TSG8\_NEW\_NOMB\_pep. \*

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query	Length	DB	ID	Description	
1	2625	100 0	500	יר	IIS-09-830-751-4	Sequence 4, Appli	: =
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3	2572	98.0	517	4	US-10-219-051B-6975	6975,	Αp
4	2572	98.0	520	לט	US-09-949-016-10653	10653,	Α,
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9	2546.5	97.0	514	7	US-60-453-050-14871	1487	٧
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11	1791			<b>L</b> -	HS-69-949-016-9207	3	ż
12	1790	2.89	518	Z.	US-09-724-676-64510	6451	۷,
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14	1774	9.79	501	2	724	64517,	×
15	1774	9.79	501	2	US-09-724-676A-64517	64517,	K
16	1759	57.4	500	Q	US-10-219-051B-12834	12834,	A
17	1764	474	900	٤	US-10-713-091B-1784	12838,	<
18	1756.5		516	S	US-09-724-676-64518	64518,	A
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25	1711	65.2	500	c.	US-10-214-051B-12842	7	⋖
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5715, Ap		14150, A	13160, A	65471, A	65471, A	20, Appl	51294, A	49963, A	65684, A	65684, A	59042, A	8835, Ap	264414,	196412,	9559, Ap	13161, A	13161, A	13161, A
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US-10-369-493-5715	US-50-453-135-13150	118-60-454-050-14160	115-60-466-412-14160	115-09-724-676-65471	US-09-724-676A-65471	$08 - 10 - 29 \leftarrow 865 - 20$	HS-10 425 114 51294	US-10-425-114-49963	US-09-724-676-65684	US-09-724-676A-65684	US-10-425-114-59042	US-10-438-246-8835	US-10-424-599-264414	115-10-424-599-196412	US-09-949-016-9559	US-60-453-135-13161	118-60-453-050-13161	US-60-466-412-13161
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                                                                                                                                                                 CHIPFENT AFFILINATION NUMBER HIS/HW/M30, 751 (PREMT FILING DATE: 2000.08.30 (PRICE AFFILINATION NUMBER 62/151,440 (PRICE FILING DATE: 1999-08-30 (PRICE FILING DATE: 1999-08-30 (PRICE PRICE) NUMBER: PCT/US00/23878 (PRICE PATE: 2000-08-30 (NUMBER OF SEQ ID NOS: 23 (NOS: 23))
                        Sequence 4, Application US/U9830751 GENERAL INFORMATION:
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                                                               APPLICANT: Suthers, Patrick F
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US-09-830-751-4
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APPLICANT: The General Hospital Corporation doing business as Massachusetts Genera
                     421 ANNSTYGLAAAVETKELDKANYLSGALGAGTVWVNTYEVFGAGSPFGTYKMSGSGRELGE 480
                                           121 VOLDMYLKCLKYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGJIIPWNFPLLMQAWKL 180
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TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REPERENCE: LeA 35693 FOTCHIAN COUNTRIES
CURKENT PHILICATION NUMBER: US/10/219,051B
CURKENT FILING DATE: ZUU3-05-09
PRIOR APPLICATION NUMBER: US 60/412,147
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98.28; Pred. No. 4.9e 224;
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DATABASE ENTRY DATE: 2002-06-15
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PELCE APPLICATION NUMBER: 05 662446, 482
PRIOR FILING DATE: 2001-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: BS 60/144, 447
PRIOR FILLING DATE: 2001-11-26
                                                                                                                                                                                                                                                                         ; Sequence 5975, Application 08/10219051B; GENERAL INFORMATION:
                                                                                                                481 YGLQAYTEVKTVTVKVPQKN 500
                                                                                                                                                           497 YGLQAYTEVKTVTVKVPQKN 516
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SOFTWARE: Perl script
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                                                                                                                                                                                                                                                   US-10-219-051H-6975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 517
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT. The General Hospital Corporation doing business as Massachusetts General APPLICANT: Hospital / Bayer AG
                                                              421 ANNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGE 480
                                                                                                                                                           301 OCCCAGSRTFVQED1YDEFVVRSVARAKSRVVGNPFDSKTEQGPQVDETQFKK1LGY1NT 360
                                           361 GRQEGAKILCGGGITAAFRGYFTQPTVRTDVQRGMTTAKEELFGPVMQILKEKTLEEVVGR 420
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98.2%; Pred. Nc. 4.9c.224,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Nucleotide sequences involved in pain FILE REFERENCE, LeA 35679 F-1-19n Fourtries CURENT APPLICATION UNRHER: US/10/219,051B CURENT FILING DATE: 2003.05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATABASE APPESSION NUMBER SWISS-Prot Z PU5091
DATABASE ENTRY DATE: 2002-06-15
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PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/346,382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILLING DATE: 2001-11-01
PRIOR APPLICATION NUMBER- US 60/33,347
PRIOR FILLING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
SOFTWARE: PETI SCRIPT
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6971, Application US/10219051B GENERAL INFORMATION:
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PUBLICATION INFORMATION:
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APPLICANT: CARGILL, Michele
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                                                                                          FILE REFERENCE: CL001456
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  GENERAL INFORMATION:
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LENGTH: 514
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                                                                                                                                                                                     TITLE OF INVENTION. POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF PETECTION AND USES THEREOF
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PRIOR APPLICATION NIMBER: 60/241,755
PRIOR PELLING TATE: 2000-10-20
FRICE APPLICATION NIMBER: 60/237,768
PRIOR FILING DATE: 2000-10-93
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                           FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                              ; Sequence 10653, Application US/09949016
; GENEPAL INFORMATION:
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481 YGLQAYTEVKTVTVKVPQKN 500
                  497 YGLQAYTEVKTVTVKVPQKN 516
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APPLICANT: TAKOGRÓVA, OLGA
TITLE OF INVENTION: GENETIC FOLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 DKAVKAARAAFOLGSPWRPMDASHPGFLINRLADLJERDRIYLAALETLDNGKPYVISYL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VDLDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTPHEPVGVGGGITPWNFPIJMGAWKL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.0%, Shore 2546.5, DB 7; Length 514; 97.6%; Fred. No. 9.96-222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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CHERRY APPLICATION NUMBER: US/60/453,050
CUNRENT FILING DATE: 2003-03-10
NUMBER OF SUD ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4 0
                                                                                                                               CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003:03:10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: PASTSEQ FOR Windows Version 4:0
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
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APPLICANT: IAKOUBOVA, Olqa
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYGCARDIAL INFARCTION, METHODS OF DEFECTION AND USES THEREOF
                                                                                                                                                                                                                                61 DKAREGRPGAFQLGSPWRRMDASHSGRLLNRLADLIERDRTYLAALETLDNGKPYVISYL 120
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                                                                                                         7, Indels
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                                                             97.0%; Score 2546.5; DB 7
97.6%; Pred No 9 96-222;
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Pred, No. 9.9e-222;
                                                                                                       2. Mismatches
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NUMBER OF SEQ ID NOS: 429241
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Best Local Similarity 97.6%;
                                                                                                     Matches 488; Conservative
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ORGANISM: Homo sapiens
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                                                                                   Best Local Similarity
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                   US-60-453-050-14871
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The General Hospital Corporation doing basiness as Massachusetts Genera
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                                                                                                                                                                          257 KVAPTGSTETGRVIQVAAGSSNLKRVTLFLAAKSPNLIMSDADMDWAVEQAHFALFFNGG 316
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                                                                                               137 UDLDMVLKCLRYYAGWADKYHGKTTD LDGDFFSYTRHEDVGVGGTTPWNFTJJJMOAWKL. 196
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PRIOR APPLICATION NUMBER IS 60/345, 442
PRIOR APPLICATION NUMBER: US 60/335, 347
PRIOR APPLICATION NUMBER: US 60/335, 347
PRIOR FILING DATE: 2001-11-26
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PRIOR APPLICATION NUMBER: US 60/312/147
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SOFTWARE: Perl script
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ÖY         241 KVAFTGSTELGPVLQVAAGSSNIZEVTIJELGGKSPNITMSDADMDMAVEQAHFALFFNGG 300           Db         259 KVAFTGSTEVGHLIQVAAGSSNIZEVTLELGGKSPNITMSDADMDMAVEQAHFALFFNGG 318           OY         301 QCCCAGSPTEVGEDTVDEFVVESVAPAKSPVVGNPFTGSTGGDGVDFTGFKTLGYINT 360           LI         111111111111111111111111111111111111	RESULT 10 US-10-144-779-472 Sequence 472, Application US/10144779 Sequence 472, Application US/10144779 Sequence 472, Application US/10144779 Sequence 472, Application US/10144779 TELE PERPENTION: MOUSE ORTHOLOGS OF HUMAN DISEASE GENES, TITLE OF INVENTION: DAVIDED BY THESE MOUSE GENES, TITLE OF INVENTION: DAVIDER: US/10/144,779 CURRENT AFPLICATION NUMBER: US/10/144,779 SOFTWARE: PASTSEO for Windows Version 4.0 LENGTH: 518 LENGTH: 518 TYPE: PRT ORGANISM: MUS	vuery Match Best Local Similarity 66.0%; Pred. No. 1.60-153; Matches 328; Conscrvative 77; Mismatches 92; Indels 0; Gaps 0; Qy 4 AATQAVPAPNQPEVECNQIFINNEWHDAVSKRIFPTVNPSIGEVINGVAEGDKETVDKA 63 [1:1:1:1] Db 21 ASLQILPSPTPNIETRYTRIPINNEWHOSSGRVFPVQNPATGEQVCEVQEADRVNIDKA 80 Oy 64 REGREGAEGIGSPWPRMDASHSCRILNFLANELERDETYLAALETLUNGKPVVISTIVD. 123 [1:1:1:1:1] Db 81 VOAARIAFSKASVWFRMTASPREDIEMBLICHTIMESINGSKFELOATIDL 140	DMVDKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVGGITFWNFPLDMGAMKLGFA 18 [3.1.] [] [] [] [] [] [] [] [] [] [] [] [] []	DD
QY         181 GPALATGNUVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVD         240           DD         199 GPALATGNUVVMKVAEQTPLTALYVANLIKEAGFPPGVNITVPGFGPTAGAAIASHEDVD         258           QY         241 KVAFTGSTEIGRVIQVAGSSNIKKYLLELGGKSFNIJMSDADMDAAVEDAHFALFFNUG         300           DD         259 KVAFTGSTEIGRVIQAAGSSNIKKYLLELGGKSFNIJMSDADMDAAVEDAHFALFFNUG         300           QY         361 UCCCAGSKFFVQEDIYDEEVVKSVARAKSKVQNFFDSKTEGGPQVDETQFKKILGYINT         360           PIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH	0y 481 YGLQAYTEVKTVTVVVPORN 500  1	FRIOR FILING DATE: 2001-11-91 PRIOR FILING DATE: 2001-11-91 PRIOR FILING DATE: 2001-11-96 PRIOR FILING ADTE: 2001-11-26 NUMBER OF SEQ ID NOS: 14715 SOFTWARE: Perl script SOUTH NO 6973 LEMOTH: 519 TYPE: PRT ORGANISM: Rattus norvegicus PUBLICATION INFORMATION: DATABASE AGCESSION NUMBER: SMISS-Frot / F11884	; DATABASE ENTRY DATE: 2002-06-15 US-10-219-0518-6973 Cuery Match 95.2%, Score 2509; DB 6, Length 519, Best Local Similarity 94.8%; Pred. No. 1.5e-217; Matches 474; Conservative 12; Mismatches 14; Indels 0; Gaps 0;	0.5   0.5

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118-09-724-676-64510
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND HISES THEFROF
441 SDFGLVAAVFTNDINKALMVSSAMQAGTVWINCYNALNAQSPFGGFKMSGNGREMGEFGL 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 VQAARLAFSLGSVWRRMDASERGRI,LDKLADLVERDRAVI,ATMESLNGGKPFLQAFYVDL 154
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66.2%; Pred. No. 3.1e-153;
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SOFTWARE: FastSEQ for Windows Version 4 0
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                 Sequence 9207, Application US/09949016 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
                                                484 QAYTEVKTVTVKVPOKN 500
                                                                                        501 REYSEVKTVTVKIPOKN 517
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ORGANISM: Human
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64 BECREGAPQLGSPWPRMDASHEGBLLNRLADELERFFTYLAALETTENSRPYVISYLVUL 123
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                                                  APPLICANT: Compugen LTD
TITLE OF INVENTION, Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
                                                                                                                               CURRENT APPLICATION NUMBER: US/U9/724,676.
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PALENTIN VERSION 3.2
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; GENERAL INFORMATION:
; Sequence 64510, Application US/09724676; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                              66.08;
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US-09-724-676A-64510

RESULT 12

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                                                                                          4 AATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVDKA 63
                                                                                                                             21 ASLHILPSFTPNLEIKYTKIFINNEWQNSESGRVFFVYNFATGEQVCEVQEADKADIDKA 80
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              Length 518,
                                                     Indels
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            66 0*; Pred, No 3.he-154;
11ve 76; Mismatches 93;
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67, Mismatches
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// GENEPAL INFORMATION:
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Best Local Similarity 67 0%
Matches 335; Conservative
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US-09-724-676-64517
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181 GPALATGNVVVMKVAEGTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHFDVD 240
                                                                                      181 GPALSCGNTVVVKPAEQTPLTALHVASLIKEAGFPPGVVNIVPGYGPTAGAAISSHMDID 240
                                                                                                                                241 KVAFTGSTEIGRYIQVAAGSSNLKRYTLFLAGKSPNIIMSDADMDWAVEQAHFALFFNQG 300
                                                                                                                                                                                                                    361 @GGGAGSPTFV@EDTYDFFVVPSVAPAKSPVVSNPFDSKTEGGEQVDETQPKKIEGYINT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.6%, Shore 1774, DR 5, Bost Local Similarity 67.0%; Pred. No. 9.7e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 64517, Application US/US/24676A GENERAL INPORMATION:
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US-09-724-676A-64517
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361. GRQEGSAKLIJGGGSTAAFRSYFIQPTVFGFVQDGMFFARELFGPVMQTLRFFTTEBVVGR. 420

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Search completed: June 24, 2003, 10:35:21 Job time: 56.1289 secs

GenCore version 5.1.6 Chpyright (a) 1993 - 2003 - Chmpagen Ltd.

OM protein - protein search, using sw model

June 24, 2003, 10:10:05; search time 19:10:0 Seconds (without alignments) 2512.144 Million cell updates/sec Run on.

US-09-830-751-4 Perfect score: ritle:

YRLÇAYTEVKTVTVKVPQKN SOO 1 MSAAATQAVPAPNQQPEVFC Sednence.

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283224 scqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

pirl:\* pir2:\* pir3:\* PIR\_73:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldebyde dehydroge aldebyde dehydroge rf2 nuclear restor hypóthetical prote aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehyde dehydroge aldehydo dohydrogo dehydroge dehydroge aldehyde dehydroge NADP Jependent ald aldehyde dehydroge omega.crystallin Description SUMMARIES S03564 148966 A32616 D88449 134216 983717 S14752 JC5553 JC4424 T06683 T02301 DEHUEZ **609030** 500364 A40872 DEHUE1 101/004 A556R4 10 1983 A46725 A29055 531308 1169614 Query Match Length DB . 8. 8. 6. 4. 6. 67.6 64 9 60 4 9 7 8 8 8 8 4 7 8 4 7 4 8 4 73.9 66.4 66.4 66.1 65.4 65.4 57.1 1499 1425.5 1422.5 1422.5 1338 e 1354 1325 Score 2500 2480 2434 1939 1744 1743 1736 1718 1716 1703.5 1543 1539 1537 1802 1794 1763 1587 Ņ. Pesult

aldehyde dehydroge

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	RESULT 1
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_	C; Species: Homo sapiens (man)
	C:Date: 31-Mar-1988 #sequence_revision 17-Nov-1995 #rexr_change 03-1un-2002
	C.Accession. Alustis, Sudwod, Alisous, Althous, Althous, 1394ii, 1394ii, 1494id
	Filst, L.C., Medial, F.E., Yoshida, A. Genomice 2, 57-55, 1988
	Genomics 2, 7, 9, 1900 Affille: Genomic structure of the human mitochondrial aldehyde dehydrogenase gene.
_	A. Reference number. A29575, MUID:88256152, PMID:2838413
	A. Accession: A29975
	A, MOLECULE UZPE: UNA A: Residucs : 1-515 - CHSUI>
	A.Cross.references GF.M26766, NID 4178347: PIDN AAAS1694 1: PID:4178348
	R.Braun, T., Hober, H., Singh, S., Agarwal, D.P., Goedde, H.W.
	FEBS Lett. 233, 440, 1988
	A;Reference number: S00804
	A: Accession: S00804
	A POTECUTE UP/PE: HIKNA A POTECUTE UP/PE: 116 A PDF A PDF A PDF A
	A) RESAURISE T. T. J. ANA J. D. F. J. F. BERA. A. CHESARISE A. M.
	A.V.Cos references impos Avoido. A.V.Cos references A.V.Cos A.
	R.M.C.C. COLECTION C. AZVIVA] H
	For a prochem 153 13-78 1986
	A.T. December 2. Section of the control of the cont
	A;Accession, A23503
	A;Molecule type: protein
	A) Presidance: "A', 19-517 * HEM>
	A. Note: the sequence shown is presumably that of the matter protein, however, the num
	Ribraun, T. Bobel, E., Singh, S., Agarwal, D.P., Gogdoe, H.W. Moodle Acide foot 11: 2170-1007
	NUCLEIC ACIDS RES. 13, 31/9, 1304 NUCLEIC ACIDS RES. 13, 31/9, 1304 A.THIEL TSCIBATION and SEQUENCE ANALYSIS OF A FULL LONGER CONTROL CONTROL FOR PROMISE
	Alternation and a property of the STASS No. 1 and 1990 An
	A, Accession. A27509
	A; Molecule type: mRNA
	A, Residues 1.5, 'AWFAWA', 10, 'F', 12, 'VS', 15, 'RHFGR', 11, 27-79, 'FEGREG', 86-336, 'V', 338-5
	A; Cross-reierences: EMEL: 101109; NID: 92860/; FIDN: CAA68290: 1: FID: 928608
	Fiblann, I.; Forder, F. Singli, S.; Agaiwai, D.F.; Goedde, H.W. Frre fret old one of 1007
	A.TIII) John F. Evident for a signal nebtide at the amino-terminal and of buman mitochondri
	A. Reference mander A25743, Mail: 27213491, PM   3582651
	A, Accession, A26743
	A;Molecule type: mRNA
	A:Residues: 1.6,'AWPAWA',10,'P',12,'VS',16,'PHPGE',21,17-79,'REGRPG',86-336,'V',338-5
	Appress retereboxs. EMEL.X004.09. NID-924605
	A.Note, this sequence is fevised in reletrace 800804 at the relationship in a received to the relationship in a relationship in the relationship in a relationship in a relationship in the relationship in a relationship in the
	A, Title, Cloning of conas for human aldebyde dehydrogenases ; and 2.
	A; Poforodice number 139432, MUID: 85216574; PMID 298744

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A; Accession: A27713
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A)Molecule type: mRNA
Molecule type: mRNA
A)Molecule type: mIsidentified as aldehyde dehydrogenase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Pathway: ethanol ratabolism
A Note enzymes with this activity are involved in diverse metabolic pathways in various
C Superfamily: aldehyde dehydrogenase (NAP+): aldehyde dehydrogenase homology
C Keywords: alcohol metabolism; homoleteramer; liver; mitochondrion; NAD; oxidoreductase
F;18-17/Domain: transit peptide (mitochondrion) #status predicted <SIG>
F;18-517/Product: aldehyde dehydrogenase (NAD+) 2 #status oxperimental <MAT>
F;23-33/Ponmain: Aldehyde dehydrogenase homology <ALDD>
F;21-29/Domain: NAD binding #status predicted <NAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AjCross-references: GDR-119668; OMIM-100650
AjMap position: 12924.2-12924.2
AjIntrons: 3873: 7373: 12073: 14772: 18473. 22773. 25573. G0(7). G1(7), 41673. 426,2) S9
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                                                                                                                                                                                                                                                A;Title: Molecular abnormality and cDNA cloning of human aldehyde dehydrogenases.
A;Reference number: 139431; MUID:85252089; PMID:4015823
A;Accession: 139433
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                       A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: 386-517 < HSU2>
A;Cross-references: 68-K03001, NID-917A345; PLIN:AAE595uc.i; PlU:q1/8396
A;Cross-references: 68-K03001, NID-917A345; PLIN:AAE595uc.i; PlU:q1/8396
A;Note: thirty-three tryptic peptides were also sequenced
B;Yoshida, A.; Ikawa, M.; Hsu, L.C.; Tani, K.
Alcohol 2, 103-106, 1985
                                                                                                                                                                                                                                                                                                                                     A;Status. preliminary, translated from GE/EMBL/DUBJ
A;Molecule type: mRNA
A;Rolecule type: mRNA
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A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mNID:87279033; PMID:3610592
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7; Indels
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2; Mismatches
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A; Accession: 139432
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aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 2 precursor, mitochoudrial rat
Cispecies: Rattus norregious (Norway rat)
Cisace. 28-Feb 1999 *sequence_revision 31 Jan 1997 *text_change 04 Jun 2002
Cisacession: 805564, A2771; 812093; 817492
RiFarres, J.; Guan, K.L.; Weiner, R.
Bur, J. Blochem, 180, 6774, 1989
Bur, J. Blochem, 180, 6774, 1989
Artille: Primary structures of rat and bovine liver mitochondrial aldehyde dehydrogen
A.keiterene number, 803564; MOID:89210865; PMID:2540004
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A)Experimental source: strain Spraque Dawley: liver
B)Farres, J.; Guan, K.L.; Weiner, H.
B)Farres, J.; Guan, K.L.; Weiner, H.
B)Farres, J.; Guan, K.L.; Mollor, H.
B)Farres, J.; Guan, K.L.; Mollor, H.
B)Farres, J.; Guan, K.L.; Mollor, H.
B)Farres, J.; Guan, M.
B)Farres, J.; Guan, M.
B)Farres, J.; Mollor, M.
B)Farres, M.

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A;Rosalducs: 129 47878
A;Crosalducs: 129 47878
A;Crosaltercurcas: CB:M19030; NID:q202847; FIBN:AAA40719.1; FID:q202848
B;Diwan, J.J.; Paliwal, R.; Kaffan, E.; Bawa, R.
R;Diwan, J.J.; Paliwal, R.; Kaffan, E.; Bawa, R.
A;Tille: A mitochondrial protein fraction catalyzing transport of the K(+) analog T1(
A;Reference number: $12903; M010:91032184; PM10:1699808
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A.Tille. Purification and characterization of catalytically active precursor of rafil A.Reference number: $17492; MUID:91378548; PMID:1898068
A.Recession: $17492
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A.Note: enzymes with this activity are involved in diverse metabolic pathways in variation and energy of this activity and elebyde debyde debyde debyde debyde debyde debyde debyde debyde for the state of the s
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361 GKOEGAKLLCGGGTAADRGYF1OPTVFGDVQDGMTTAKEETFGPVMQTLKFKTTEEVVGR 420
                                                                                                                                                                                    377 GKQEGAKLLCGGGIAADRGYFIQPTVFGDVQDGMTIAKEEIFGFVMQILKFKTIEEVVGR 446
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94.8%; Pred. No. 4.4c 185;
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A;Residues: 327-340 <DIW>
R;Jeng, J.; Weiner, H.
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A; Residues: 1-519 <FAR>
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A; Description: ratalyzes the oxidation of an aldehyde to an and using NAD- and water
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C. Species: Adam musculus (house monse)
C. Date (02.101-1906 dehydrogenase AND-MI
C. Species: Mus musculus (house monse)
C. Date (02.101-1906 dehydrogenase AND-MI
C. Species: Mus musculus (house monse)
C. Date (02.101-1906 dehydrogenase AND-MI
C. Date (02.101-1906 dehydrogenase AND-MI
C. Accession: 18966; Schiob, 177960
R. Chocession: 18966; Mujlu 9564745; PMIC 745894
A.TILLE: Cloning and characterization of the gene encoding mouse mitochondrial aldehyde
A.Status: translated from GB/EMBL/DGBJ
A.Status: translated from GB/EMBL/DGBJ
A.Status: translated from GB/EMBL/DGBJ
A.Status: The Bernal. J.: Muno2, A.: Marquez, G.: Barbero, J.L.; Zaballos,
Nucleic Acids Res. 22, 4132-4138, 1994
R.Caubin, J.: Iqfesias, T.: Bernal. J.: Muno2, A.: Marquez, G.: Barbero, J.L.; Zaballos,
Nucleic Acids Res. 22, 4132-4138, 1994
A.TILLE: Isolation of genomic DNA fragments corresponding to genes modulated in vivo by
A.Residues: 1.50102; MUID:95023181; PMID:1937138
A.Status: Preliminary: nucleic acid sequence ont shown; translation not shown
A.Molecule type: DNA
A.Residues: 472-6740; MUID:95023181; PMID:49040; Luiring the during multiple Alection with the middle type: MUID: Planmacol. 46, 88-96, 1994
A.TILLE: Encyments conversion of the MID:4445908; PMID:445908; PMID:4445908; PMID:44459
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Introns. 40/3, 75/3, 122/3, 149/2, 126/3, LDV.s, 257/3, 302/1, 354/3, 418/3, 471/1,
                                                                                                                                                                                                                                                                        24. KVAFTGSIELGPVIQVAAGSSNLKPVTLFLGGKSPNIIMSDALMEWAVEQAHFALFFNQG 300
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                                                      79 INAVKAAQAAFQLGSPWFRMDASDPGFLLYFLAFLIFFUFLYLAALEGLUNGKPYVISYL 138
                                                                                                                     VDLDMVLKCLRYYAGWADKYHGKTIFIDGDFFSYTRHEFVGVCGQIIFWNFPLLMQAWKL 180
                                                                                                                                               181 GPALATGNVVVMKVAEQTPLTALYVANLIKEAGFFPGVVNIVFGFGFTAGAAIASHEDVD 240
                                                                                                                                                                                                                                                                                                                                                                                                 319 QCCCAGSRTFVQEDVYDEFVERSVARAKSKVVGNPFDSRTEUGPQVDETQFKKILGYIKS 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKQEGAKLLCGGGIAADRGYFIQPTVFGDVQDGMTIAKEEIFGPVMQILKFKTIEEVVGR 420
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A Introda, 40/3, 75/3, 1
C;Complex, homotetramer
C;Function:
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C,Superfamily: aldehyde dehydrogenase (NAD); aldehyde dehydrogenase homology C; Keywords: alcohol metabolism; homoletiamer; liver, mituchondrion, NAD, oxidoreducta F,1:197Domain. transit peptide (mitochondrion) #status predicted <INF> F,2:0:519/Frodret, aldehyde dehydrogenase (NAC); z #status predicted <MAT* F;7:341/Domain: aldehyde dehydrogenase homology <ALDP* F:27:341/Domain: aldehyde dehydrogenase homology <ALDP* F:287,321/Active site: Glu, Cys #status predicted
A;Pathway: ethanol catabolism
A;Note: enzymes with this activity are involved in diverse metabolic pathways in vari
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arch. Blochem. Blophys. 277, 351-350, 1990
A;Title: Sequence of the precursor of bovine liver mitochondrial aldehyde dehydrogena
A;Feterence number: Suguso; MUID:49179198; PMID:1889984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Primary structures of rat and bovine liver mitochondrial aldehyde dehydrogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 VDLDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKL 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 KVAFTGSTEVGHLIQVAAGSSNLKPVTLELGGKSPNI IMSDADMDWAVEQAHFALFFNQG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 QCCCAGSRIFVQEDIYDEFVVRSVARAKSRVVGNPFDSKTEQGPQVDETQFKKILGYINT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RATI OKQESAKLI JOGGATAADBOVETOPTVPATIVQI KMITTAKET FISEVMQTI KEKITT BEVVGE 1420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGFVICQVAEGDKEDV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 LSAAATSAVPAPNHQPEVPCNQIFINNEWHDAVSPKTFPTVNPSTGEVICQVABGNKEDV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 2 precursor, mitochondrial - bovine
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C.barte: 30 Jun 1992 #sequence_revision 31 Jan 1997 #text_change 03 Jun 2002
C.Accession: Spartn; Stafer5; P00543
R.Guan, K.; Weiner, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GPALATGNVVVMKVAEOTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                     94 5%; Scorp 2480; DR 1; Length 519; 94.2%; Pred. No. 1.2e·183;
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A, Accession: $03565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Mismatches
                                                                                                                                                                                                                                                                                                            F;474/Binding site: NAD (Cys) #status predicted
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Eur. J. Biochem. 180, 67-74, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                              nilarity 94.2%;
Conservative 1
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A. Pescription, catalyzes the oxidation of an aldehyde to an acid using NAD+ and water A.Pathway, chlanol oddabolism.
A.Pathway, chlanol oddabolism activity are involved in diverse metabolic pathways in vari S.Noter: enzymes with this activity are involved in diverse metabolic pathways in vari C.Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase (none) og S.Esywords, alcohol metabolism, homed etramer. Liver, mitochondrion, NAD, exidoredue ta F.58.72/Domain: aldehyde dehydrogenase homology <ALDD+.
E.288.762/Domain: alchydrogenase homology <ALDD+.
E.288.762/Active site: Glu, Cys #status predicted
A,Title, Mitochandrial aidehyde dehydroaenase from horse liver, Correlations of the s
A;Reference number: $00364; MUID:88166730; PMID:4350012
A;Accession: $00364
A;Molecule type, protein
A;Molecule type, protein
A;Residues: 1-500 <00H
A;Note, amino terminal residue is uncertain; l ser and l Lou were also found; forms b
C;Complex: homoretramer

    Biol. Chem. 265, 12257-12265, 1991
    A;Title: Cloning and characterization of a new functional human aldehyde dehydrogenas
A;Reference number: A40872; MULE:91286241; PMID:2061311

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RAVKAARAAFQLGSPWREMDASDRGRILDNELADIJERDRTYLAALETIDNGKPYVISYLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGUIIPWNFPLLMOAWKLG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 PALATGNVVVMKVAEQTPLTALYVANLIKEAGEPPGVVNIVPGFGFTAGAATASHEDVDK 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 NNSKYGLAAAVFTKDLDKANYLSQALQAGTVWTNCYDVFGAQSPF017KMSGN0RELGEY 4B0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 SAAATQAVPAPNQQPEVECNQTFINNEWHDAVSRKTFFTVNH9STGEVICQVAEGGEREDVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAAATOAVPAPNOOPEVFYNG1F1NNEWHDAVSKKTFPTVNPSTGEVICOVAAGDKEDVD 60
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C;Species: 27-Mar 1992 #sequence_revision 81 Jan 1997 #text_change 63 Jun 2002
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Akosiduse: 1-517 etsp:
A:Gross-references: GB:M6.967; NID:q497H4; PIDN:AAA96840.1; FID:q1264008
A;Note: 86-Ala and 107-Leu were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2434; DB 1; Length 500;
Fred, No. 3.9e 180;
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Matches 462, Conseivative
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R:Hsu, L.C.; Chang, W.C.
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                                                                                                    Historiem, Biophys. Res. Commun. 189, 420-434, 1992
A.Title: Purification and characterization of bovine brain gamma-aminobutyraldehyde dehy A.Reference number: P00543; MUID:93080596; PMID:1440496
A.Roccession: P00543; MUID:93080596; PMID:1440496
A.Roccession: P00543; MUID:93080596; PMID:1440496
A.Roccure type: Protein
A.Roccure type: Protein
A.Residues: 22-34 *LEE.
A.Roccure type: Brain
C.Compon: This enzyme may be responsible for gamma aminobutyraidehyde dehydrogenase act
C.Compon: This enzyme may be responsible for gamma aminobutyraidehyde dehydrogenase act
C.Compon: A.Roccure theorem of an aldehyde to an acid using NAD: and water
A.Pathway. ethanol catabolism
A.Roccure enzymes with this activity are involved in diverse metabolic pathways in various
C.Superfamily: aldehyde dehydrogenase (NAD:): aldehyde dehydrogenase homology
C.Reywords: alcohol metabolism; homotetramer; liver; mitochondrion; NAD; oxidoreduriase
F.1-27/Domain: transit peptide (mitochondrion) #status predicted *SIG>
F.28 *322/Active site Glu, Cys #status predicted
F.78 *332/Active site Glu, Cys #status predicted
F.78 *Bidding site: NAD (Cys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 LDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKLGP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 LDMVLKCLRYYAGWADKYHGKTIPIDGDYFSYTRHEPVGVCGQIIPWNFPLLMQAWKIGP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 ALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 CCAGSRTFVQEDIYDEFVVRSVARAKSRVVGNPFDSKTFQGPQVDETQFKKILGYINTGK 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 CCAGSRIFVQEDIYAEFVERSVARAKSRVVANPFNSRTEQAPQVNFTQFKKVLGYIKSGK 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 QEGAKLLGGGGIAADRGYFIQPTVFGDVQDGMTIAKEEIFGPVMQILKFKTIEEVVGRAN 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 FEGLELL GGGAAADEGYFIOPTVFGOLODGMTIAKEEIFGPVMQILKFESMEEVVGRAN 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 SAATQAVPTPNQQPEVLYNQIFINNEWHDAVSKKTFPTVNPSTGDVICHVAEGDKADVDR 81
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Pred, No 2 90-180;
                                                                                          Biochem. Biophys. Res. Commun. 189, 450-454, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Mismatches
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91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.88
Matches 457; Conservative
A; Pesidues 92-F20 FFAPS
A; Experimental source: liver
R; Lee, J.E.; Cho, Y.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
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C.Comment. Based on similarity, this form is assumed to be mitochondial and to have pic Genetics.
Asgenetics.
Asgenetics.
Asgenetics.
Asgenetics.
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By 128788
Ashap position: 9p13-9p13
Ashap in the only introduced by the initiator moden
C.Complex: homotetrament (probably)
C.Function: astalyses exidation of an algebyge to an acid using Nate and water
Aspersificion: astalyses exidation of an algebyge to an acid using Nate and water
Aspersferior: astalyses exidation of an algebyge dehydrogenase homology
C.Reywords: alcolod metabolism, benefetianed: Tver, mitochendianion, NAt, exidered
E.1-20/Domain: transit peptide (mitochendian) #status predicted and acid wars
F.1-21/Froduct. aldehyde dehydrogenase (NADP)
F.25-319/Active site: Glu, Cys #status predicted
F.25-319/Active site: Glu, Cys #status predicted
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S14629
aldehyde dehydrogenase (NAP) (EC 1 2.1.3) 1, cytosolic - chicken
c)Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 21-Nov-1993 #sequence_revision 31-lan-1947 #text_change 0:-lun-zuuz
C;Date: 21-Nov-1993 #sequence_revision 31-lan-1947 #text_change 0:-lun-zuuz
C;Date: 21-Nov-1993 #sequence_resion = S14629
R;Cobbout, R.
Submitted to the EMBL Data Library, April 1991
A;Description: High levels of aldehyde dehydrogenase transcripts in the undifferentiated
A;Reference number: S14629
A;Accession: S14629
A;Accession: S14629
A;Accession: S14629
A;Accession: S14629
A;Coss-references EMRL X58869, NID 963032, PIDA,CAA41679.1; PHz 963033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 KAKEGRPGAPQIGSSPWPPMDASHSGRLLNRLADIGIERDRTYLAALETIDNSKPYVISYLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 VAFIGSTELGEVIÇVAAGSSNLKRVILELGGKSPNIIMSGAGMGWAVBQAHFALFFNGGG KOI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQEGAKLLOGGGIAADPGYF1QPTVFGDVQDXMTAKEEIFGPVMQTLKFKT/EEVVGPA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 DLDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEFVGVGGQIIFWNFPLLMQAWKLG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 PALATGNVVVMKVAEQTPLTALYVANLIKEAGFPFGVVNIVPGFGFTAGAAIASHEDVDK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422 NNSTYGLAAAVFIKDLEKANYLSQALQAGIVWVNCYDVFGAQSFFGGYKMSGSGKELGEY 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 SSAA--ALPSPILNPDIPYNQLFINNEWQDAVSKKTFFTVNPTTGEVIGHVAEGDRADVD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 GGGAGSKIEVQEDIYDEFVVRSVARAKSKVVGNPFDSKTEQGPQVDETQFKKILGYINTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61; Mismatches
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A Pathway: Athanol catabolism
A:Note: encymes with this activity are involved in diverse metabolise pathways in vari
C.Suberfamily, aidehyde dehydrogenase (NAD-), aidehyde dehydrogenase homology
C.Keywords: alcohol metabolism, cytosol, homotetramer, liver, NAD, oxidoreductase
F.57-331/Chomain: aldehyde dehydrogenase homology -ALULO-
F.277,311/Active site: Glu, Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rizhao, D.; McCaffory, P.; Tvins, K.J.; Neve, R.L.; Hogan, P.; Chin, W.W.; Draeger, U Eur. J. Fig.ham. 240, 15-22, 1996
A; Title: Molecular identification of a major retinoic-acid-synthesizing enzyme, a ret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain C3H/He; cell type embryonal carcinoma; cell line P19 te
                                                                                       A; Description: catalyses the exidation of an aldebyde to an acid using NAD+ and water
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 AVKAAPKAFELGSPWPTMDASEPGPLUNKLADLVERDPLTLATMEAIDGGKLFSTAYLMD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 LDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEFVGVCGOIIFWNFFLLMQAWKLGP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 ALATGNVVVMKVAB©TFLTALYVANLIKEAGFFFGVVNIVFGFSFTAGAATASHEDVDKV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.1. CIASSPIPVEEPIYDEPVPPSIEPAKPYID3DPD POVQQOQULKEQFQKILDDIESGK 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (*** QEGAKLLUNGGSTAADFGYFTQFTVFGTVVGNYQGSMTTAKEETFGYVMQTLKFKTTEEVVGPAN 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47] KEGAKLENGGSPWGNKGYFTUPTVPSNVTOOMPIAKEETEGPVQQIMKEKTIDPVIKPAN 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AAATGAVFAFRQQFEVFCNQIFINNEWHDAVSEKIFFTVNFSTGEVICQVAEGOKELVOK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 APVLPALPEPLKULKIKYTKIFINNEWHUSVSGKKFEVFNPANEEKICEVAEGDKADIDK 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 ALCCGNIVVVKPARQTPLSALYMGSLIKEAGEPPGVVNIVPGFGPTAGAALSHHMDIDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.4. AFTGSTEIGFVIQVAAGSSNIXKPVTLEIGGKSPNIIMSDADMOWAVEGAHFALFFNGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.3. OCAGSPIEVQED IYDEEVVESVARAKSRVVQNDEDSKTEQGEQVOPTQEKR 103Y ENTOK
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                                                                                                                                                                                                                                                                                                                                                            t8.6%, Score 1802, DB 1, Scoret 509,
67.3%, fred. No. 2.7e-131;
tive 67, Mismatches 96, Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aldehydc dehydrogenase (NAD) (EC 1.2.1.3) 2 - mouse N:Alternate names: retinaldehyde-specific dehydrogenase C;Species: Mus musculus (house mouse)
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A;Accession: S74224
                                                                                                                                                                                                                                                                                                     F,464/Binding site. NAD (Cys) #status predicted
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CySuperfamily: aldehyde dehydrog
CyKeywords: NAD; exideredustase
                                                                                                                                                                                                                                                                                                                                                                                            Hest Local Similarity 67.33
Matches 335, Conservative
A, Experimental source: retina C;Complex: homotetramer
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A;Residues: 1-499 <2HA>
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                                                          C; Function:
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A;Molecule type: DNA
A;Residues: 1:501 c48372
A;Residues: 1:501 c48372
A;Cross-reterences: GB:W1994; NID:g178370; PIDN:AAA51692.1; PID:g178372
A;Cross-reterences: GB:W1994; NID:g178370; PIDN:AAA51692.1; PID:g178372
B;Yoshida, A.; Hsu, L.C.; Yanaqawa, Y.
Adv. Exp. Med. Biol. 3289, 374-44, 1993
A;Title: Biological role of human cytosolic aldehydr dehydrogenase 1. hormonal response, A;Reference number: 151846; MUID:9326303; PMID:8493914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Title: Molecular abnormality and cDNA cloning of human aldehyde dehydrogenases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 DMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKLGPA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 LATGNVVMKVAEQTPLFALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111 | 11:1 | 1:111 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:302 | TAGSRIFVEESIYEEFVKRSVERAKRIVGSPEDPT1EQGEQUIDKKQYNKVLELIQSGVA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 REGRPGAFQLGSPWRRMDASHSGRLLNRLAPLIEPDRTYLAALETLDNGKFYVISYLVDL, 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 FTGSTEIGRVIQVAAGSSNLKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQCC 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 AATGAVPAPNQQPEVFCNOIFINNEWHDAVSRKIFPIVNPSIGEVICOVAEGDKEDVDKA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ASLQLLPSPTPNLEIKYTKIFINNEWQNSESGRVFPVCNFATGEQVCEVQEADKVJIDKA 61
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A; Status: preliminary; translated from GB/EMH;/DDBJ
A; Molecule type: DNA
A; Residues: 1-6 - YOS1>
A; Residues: 1-6 - YOS1>
A; Residues: R: SK1235; NID: 9301399, FIDN AAD; 3927 1, FID 942F1625; R; YOShida, A: 1 kawa M: Hsu, E.C.; Tani, K.
Alcohol 2, 103-106, 1985
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F)57-321/Domain: aldehyde dehydrogenase homology <alibbations and the second contract of t
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A;Accession: A33371
                                                   F:193-273/Domain: NAD binding fatatus predicted (NAD)
F:267,301/Active site: Glu, Cys #status predicted
F:454/Binding site: NAD (Cys) #status predicted
                                                                                                                                                                                                                                                                                   Score 1794; DB 2;
Pred. No. 1.1e-130;
                                                                                                                                                                                                                                           68.3%; Scc. 66.0%; Pred. No. 1...
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Best Local Similarity 66.09
Matches 328; Conservative
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A; McLeuslin 1994; McRodin 1997; translated from GB/EMBL/DDBJ
A; McLeuslin 1995; mrwn
A; Molecule type: mrwn
A; Molecule type: mrwn
A; McSiduus; Dreilminary; translated from GB/EMBL/DDBJ
A; McSiduus; Dreilminary; Lipsky, J.J.
B; Gorden, Bjophys, Res. Commun. 236, 527-541, 1997
B; Rathmann, E.C.; Lipsky, J.J.
B; Commun. 236, 527-541, 1997
A; Title: Cloning of a cDNA encoding a constitutively expressed rat liver cytosolic all A; Reference number: JC5553, MUID:97382470; PMID:9440474
A; Reference number: JC5553, MUID:97382470; PMID:9440474
A; Residuce: Juver mrNA
A; Molecule type: mrNA
A; Molec
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A;Molecule type: protein
A;Residues: 2.50; EBMs
R;Aqarwal, D.P.; Cohn, P.; Goedde, H.W.; Hempel, J.
Bnzyme 42, 47-52, 1994
A;Tille: A.dehyde dehydrogenase from human crythnecytes: structural relationship to t
A;Reference number: A61010; MUID:89477753; PMID:2776714
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A.Reference number: 139431; MUID:R5252089; PMID:4015823
A.Accession: 139431
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A;Map position: 9421-9421
C;Complex: homotetramer
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QY         3.01 QCCC3ACSETEVGELTYDEEVVESVARAKSEVVGNEDDSKIEGGEQUDEIOFKKILGYINI 360           LD         3.01 QCCC3ACSETEVGEVERSVERAKKYVLGNELIGTUREQYEKILGCYINI 360           QY         3.61 GKOEGAKLLCGGGIAADRGYPTOPTVFGDVOGMTIAKEETFGPVWOLLKFKTIEEVVGR 4.20           QY         3.61 GKOEGAKLLCGGGIAADRGYPTOPTVFGDVOGMTIAKEETFGPWOLLKFKTIEEVVGR 4.20           PC         1.1.1111.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1	RESULT 11  Global DC 2009-1904  Clobate DC 2009-1904  Exthmann, B.C.: Lipsky, J.J.  Bicken Highlys hest convenient of Freely Highlyship extraphysic (% Tun-2002)  Clobate DC 2005-23  Richmann, B.C.: Lipsky, J.J.  Accession: DC553  Richmann, B.C.: Lipsky, J.J.  Alitie: Clouding of a book library expressed fat liver cytusolic all Accession. JC553  Alitie: Clouding of a book library accession of a wide variety of alder account of the man and accession. JC553  Alitie: Clouding of a book library accession of a wide variety of alder account of a mide variety of alder accompanie. This critical delay deptydrogenase (NAD+): aldehyde achydrogenase homology clowery match and the accession of a wide variety of alder clouding and accession of a wide variety of alder clouding and deptydrogenase homology. ALC.  Keywords: oxidoreductase  Clouding and and accession of a wide variety of alder clouding and accession acce	QY         121 VDLDMVLKCLKYYAGWALKYHEKTIPIDGDFFSYTEHEFVGYGGOLIPWNFPLLMGAWKL 180           Db         (1   1   1   1   1   1   1   1   1   1
Db	0y 481 YGLQAYTEVKTVTVKVPOKN 500	Ouery Match  6.6%: Fred. No. 2.7e-128;  Best Local Similarity 66.6%: Fred. No. 2.7e-128;  Matches 333: Conservative 67; Mismatches 100; Indels 0; Gaps 0;    MSAATQAVPAPNQOPEVECNQIPINNEWHDAVSPKTFPTVNPSTGEVICQVAEGDKEDV 60     MSSSAMPDVPAPLTNLOFKYTKINNEWHDAVSKKKPPVFNPATERILCEVEEGCKEDV 60     Li :

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R;Bhat, P.V.; Labrecque, J.; Boutin, J.M.; Lavroix, A.; Yoshida, A.
Gene lbb, 304-306, 1995
A.fitle: Cloning of a cDNA encoding rat aldebyde debydrogenase with high artivity for
A.Keterence number: JC4524, MUID:90125208; PMID:8543180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Posidues: 2-19;80-84;86;88-91;96-99;10] 108;110 [21;205-209;213-215;218-219;222;224
A;Experimental source: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E.Z/Modified site, acetylated amino end (Ser) (in mature form) #status predicted
      301 QCCCAGSRTFVQEDIYDEFVVRSVARAKSRVVGNPFDSRTEGGFQVDFIQFRKILIGYINT 460
                                                              (d) QCCVAASKIEVEESSYPEE-VARSVERARRYVLGINGUPGINGUPGIDAEGHDALIBLIES (60)
                                                                                                                         GRQEGAKLLGGGGIAAD/RGYFIQPTVFGDVD/MMTIAKFFIFGDVMDILKFKTIEEVVGR 420
                                                                                                                                                                                 361 GKKEGAKLESSASSEMGNEGEF VQFTVE SNV HJEMKTAKEETFGFVQOTMNFKSVDDVTKR 420
                                                                                                                                                                                                                                            4.21 ANNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAUSFFGGYKMSGSGRELGE 4.80
                                                                                                                                                                                                                                                                        361 GROEGAKLLDSGGIAADPCYFIQPTVPCIPVQDCMTIARPPIPCDVMQII REKTIFPVVGF 4.20
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C;Superfamily: aldehyde dehydroqenase (MAD); aldehyde dehydroqenase hameloqy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date. 08 Feb-1996 #sequence_revision 19 Apr 1996 #text_change 03 Jun 2002
C;Accession: JC4524; Pc4119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24. PVAFTOSTEIGEVIOVAAGSSNIKRVTIJELGGKSPNIIMSDADMDWAVEDAHFALFENGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;kesidues: 1-501 <BHA>
A;Cross-references: GB:L42009; NID:q1256958; PIDN:AAA96657.1; PID:q974168
A,Accession. PC4119
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F;2-501/Product: aldehyde dehydrogenase *status predicted -MAT -
F;59-323/Domain: aldehyde dehydrogenase homology -ALDD>
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65.8%; Pred. No. 9,6e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aldehyde dehydrogenase [MAD(F)] (EC 1.2.1.5) - rat
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A;Residues: 1-501 <BHA>
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                                                                                                                                                                                                                                                                                                                                                                              Gene 101, 261-265, 1991
A:Title: Isolation and characterization of a cytosolic aldehyde dehydrogenase-encoding c
A:Reference number: JQ1004; MUID:91276281; PMID:2055490
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A.Pathway; exidation of retinaldehyde to retinoic acid
A.Pathway; exidation of retinaldehyde to retinoic acid
C.Superfamily: aldehyde dehydrogenase involved in discesse metabolism cytosol; humoretramer; liver; NAD;
F.S-20,Produrt; aldehyde dehydrogenase (NAP-) 1 *status predicted *MAT>
F.S9-3370main: aldehyde dehydrogenase (NAP-) 1 *status predicted *MAT>
F.Z4Modilied site, actefylated amino and (Sar) (in mature form) *status predicted
F.Z4Modilied site, actefylated amino and (Sar) (in mature form) *status predicted
F.Z4Modilied site, actefylated amino and (Sar) (in mature form) *status predicted
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Development 12, 693-702, 1931
A.Title: Aldebyde dehydrogenase is a positional marker in the retina.
A.Reference number: A60126, MUID:92037178; PMID:1935685
A.Molecule type: protein
A.Residues: 23-49, XX,52:,Y,141 150, XX,152-156,211, XX,214-218, X,1220-230,309 320,3
A.Reprimental source: embryonic mouse retina
A.Genetics
A.Gene: Aidhl; Ahd-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GPALSCGNTVVVKPAEQTPLTALHLASLIKEAGFPPGVVNIVPGYGPTAGAAISSHMDVD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 KVAFTGSTEIGKVIQVAAGSSNIKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNGG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSSPAQPRVPAPLADLKIQHTKIFINNEWHNSVSGKKFPVLNPATEEVICHVEFGDKADV 60
                                                                                                                                                                                                                                                              C.Species: Mus musculus (house mouse)
C.Date: 23-Nov-1991 #sequence_revision 41-Jan-1997 #text_change 03-Jun-2002
C.Accession: JQ1004; A33248; A60126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GPALATGNVVVMKVAEQTPL/TAL/YVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                      aldehyde dehydrogenase (NAD) (EC 1.2.1.3) I precursor, cytosolic - mouse N;Alternate names: aldehyde dehydrogenase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues: 1.22 <RG2.
A,Cross_references: GB:M74571; NTD:g191805; PIDN:AAA37203.1; PID:g191806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-reference: GR:M74570; NID-g191803; PIDN AAA37202.1; FID-g191804
A;Experimental source: liver
A;Accession: A33248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69, Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 8e 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;456/Binding site: NAD (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1744;
481 YGLQAYTEVKTVTVKVPQKN 500
                               66 48:
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                                                                                                                                                                                                                                                                                                                                                         R;Rongnoparut, P.; Weaver, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-501 <RON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Map position: 19
C:Complex: homotetramer
C:Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JQ1004
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A;Cross-references: GB:U07919; NID:g995897; PIDN:AAA79036.1; PID:g544482 C;Comment: This isozyme is found at highest levels in saliva, stomach, and kidney and C;Genetics:
A,Gene: GDB:ALDH6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Map position: 15q26-15q26
A.Introns: 34/9 68/8; 115/3; 159/1; 179/3; 222/3; 260/3; 235/1; 466/3; 461/3; 464/2;
C)Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: catalyzes oxidation of an aldehyde to an acid using NAD+ and water A;Note: enzymes with this activity are involved in diverse metabolic pathways in vari
                                                                                                                                                                                                                                                                                                                                                                  A; Title: Molecular cloning, genomic organization, and chromosomal localization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 TEVGKLVKBAASKSNLKKVTLELGGKNPC1VCADADLDLAVECAHUGVFFNUGQCCTAAS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 PGAFÇLGSPWREMDASHSOFLLNRLADLIEFDETYLAALETLDNGKFYVISYLVDLDMVL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 RVFVEEQVYSEFVRRSVEYAKKRPVGDPFDVKTEQGPQIDQKQFDKILELIESGKKEGAK 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLCGGGIAADRGYFIQPTVFGDVQDGMTIAKEEIFGPVMQILKFKTIEEVVGRANNSTYG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGEYGLQAYT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydlogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVDKAREGR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 ALPRPIRNLEVKFTKIFINNEWHESKSGKKFATCNPSTREQICEVEEGDKPDVDKAVEAA 78
                                                                                                                                                                                                                        C.Species: Homo sapiens (man)
C.Date, 03-Mar 1995 #sequence_revision 31-Jan-1997 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 NIMVLKPABQIFFLIALYLGSLIKEAGFPPGVVNIVPGFGFFVGAAISSHPQINKIAFTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 KCLRYYAGWADKYHGKTIPIDGDFFSYTPHEPVGVGGQIIPWNFPLLMQAWKLGPALATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 NVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVAFTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEIGRVIQVAAGSSNLKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQCCCAGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                    aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 6 precursor, salivary - human
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                                                                                                                                                                                                                                                                                                                                                                                          A,Reference number: A55684; MUID:95213025; PMID:7698756
A,Accession: A55684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: NAD; oxidoreductase; saliva
C; Reywords: NAD; oxidoreductase; saliva
F; 70-334/Domain: aldehyde dehydr.genase hemology ALDD>
F; 280,314/Active site: Glu, Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ed. No. 8.4e-125;
Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                            C;Accession: A55684
R;Hsu, L C; Chang, W.C.; Hiraoka, L; Hsieh, C I;
Genomics 24, 333-341, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:467/Binding site: NAD (Cys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references GDB·364103; OMIM:600463
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                                        481 GFHEYTEVKTVTVKISOKN 499
           482 GLQAYTEVKTVTVKVPQKN 500
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                                                                                                                                                                                                                                                                                                                                                                     aldehyde dehydrogenasc (NAD) (EC 1.2.1.3) 1, cytosolic - horse c) Species: Equus caballus (domestic horse)
C;Species: Equus caballus (domestic horse)
C;Species: Equus caballus (domestic horse)
C;Accession: S02302
R;von Bahr-Lindstroem, H.; Hempel, J.; Joernvall, H.
Eur. J. Biochem. 141, 37-42, 1984
A;Title: The cytoplasmic isoenzyme of horse liver aldehyde dehydrogenase. Relationship the Reference number: S02302; MUID:84208025; PMID:6723662
A;Accession: S02302
A;Mocession: S02302
A;Mocele type: protein
A;Pesidues in the regions 1-16 and 443-475 were positioned by homology with the huckpesitucs. I 500 :vyn.
A;Note: residues in the regions 1-16 and 443-475 were positioned by monology with the huckpesitucs. Homotetramer
C;Complex: homotetramer; liver; NAD;F;Se3-22,Domain: aldehyde dehydrogenase homology
C;Reywords acetylated amino end, alcohol metabolism; cycosol; homotetramer; liver; NAD;F;Se3-32,Domain: aldehyde dehydrogenase homology
C;Reywords acetylated amino end (Ser) (probably acetylated) #status experimental
F;268,302/Active site: NAD (Cys) #status predicted
F;455/Binding site: NAD (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                      421 ANNITYGLAAGVETKDLDRAITVSSALQAGVVWVNCYMILSAQCPFGGFKMSGNGRELGE 480
ANNSTYGLAAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGE 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DLGGCLKTLPYCAGWADKIQGPTIPSDGNFFTYTRHEPVGVCGQILPWNFPLLMFLWKIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAREGRPGAFQLGSPWRRMDASHSGRLLNRLADLIERDRTYLAALETLDNGKPYVISYLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KAVAAARQAFQIGSPWRTMDASERGRLLYKLADLVERDRLILATMESMNGGKLFSNAYLM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 VAFTGSTEIGRVIQVAAGSSNLKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQ 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCVAASRI.FVEESIYDEFVRRSVERAKKYVI.GNPLTPGVSQGPQIDKEQYDKILDLIESG 360
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66.1%; Pred. No. 3.3e-126;
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481 HGLYEYTELKTVAMKISQKN 500
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198 247 258 307

Search completed: June 24, 2003, 10:18:30 Job time: 20.1339 secs

# Genfore version 5 1 6 Copyright (c) 1993 - 2003 Gempugen Ltd

OM protein - protein search, using sw model

Fun on. Sune 24, 2003, 10.02 5%; Search time 10.07% Seconds

(without alignments)
2059.300 Million ceil updates/sec

Perfect score: 2625 Sequence: 1 MSAAATQAVPAPNQQPEVFC . YGLQAY1EVK1V1VKVPQKN 500

Scoring table: BLOSUM62 Gapop 10 0 , Gapext 0.5 Total number of hits satisfying chosen parameters: 112892

112892 seqs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMAPTES

		æ				
Result		Query				
NO.	Soore	Match	Length	DB.	ID	Description
-	2572	0.86	517		DHAM HUMAN	P05091 homo sapien
C1	2503		500	-	DHAM MESAU	DROE
m	2500	95.2	519	<b>—</b>	DHAM_RAT	P11884 rattus norv
4	2480		519	_	DHAM_MOITSE	P47738 mus musculu
5	2436		520	Н	DHAM_BOVIN	bos (
9	2434		500	<del></del>	DHAM_HORSE	P12762 equus cabal
7	1929		517	П	DHA5_HUMAN	837
80	1802		509	_	DHA1_CHICK	gallu
6	1795		499	-	DHA2_RAT	rattus
10	1794	68.3	499	-1	DHA2_MOUSE	mus m
11	1790		499	-	PHA2_HITMAN	094788 home sapien
12	1771		499	-1	DHAS_CHICK	gallu
13	1769		200		DHA1_HIMAN	P00352 homo sapien
14	1758	67.0	200	_	DHA1_SHEEP	ovis
15	1752		005	_	DHA1_MOTISE	P24549 mus museulu
16	1752		500	1	DHA1_RAT	P51647 rattus norv
17	1751		200		DHA1_BOVIN	P48644 bos taurus
18	1736		ÖÖS	_	DHA1_HORSE	P15437 equus cabal
19	1718		512		PHA6_HIMAN	P47895 homo sapien
20	1711	65.2	200		DHAC_RAT	
123	1706		10.		CHAE_MACPF	_
리	1697	54. b	501	-1	CHAE_ELEED	Q28399 elephantulu
23	158		407	<b>,</b>	PHAL_ENCRU	Q27540 enchytracus
24	1526 5	ת מ	रा ट च	_	OFOM_OWMSI,	P.0842 ommastrephe
C.	1499		44 0.	_	CROM_OCTRO	P30841 octopus dof
56	1425.5		497	_	DHAL_EMENT	POR157 emericella
27	1422.5		.17	_	DHAY_YEAST	P32872 sacetaromye
28	1353.5	51.6	497	7	DHAL_ASPNG	P41751 aspergillus
29	1305.5		496	7	DHAL_CLAHE	
30	1269		495	-	DHAL_ALTAI.	_
31	1258	47.9	200	-	DHAL_AGABI	
35	1235.5	47.1	613	_	DHA4_YEAST	367.8
33	1199.5	45.7	498	_	DHAM_LETTA	Q25417 leishmania

	075891 homo sapie	P28037 rattus nor	P54115 saccharomy	P47771 saccharomyc	P54114 saccharomy	P71016 bacillus s	F28237 beta vulga	P17202 spinacia	P42757 atriplex h	P17445 escherichia	P24883 escherichia
DHA5_YEAST	FTPH_HIMAN	PTOH_PAT	DHA6_YEAST	DHA2_YEAST	DHA3_YEAST	DHAB_BACSU	DHAB_BETVU	DHAB_SPIOL	DHAB_ATRHO	DHAB_ECOLI	PHAL_ECOLT
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MEDLINE-88256152; PubMed-2838413;
Hsu L.C., Bendel R.E., Yoshida A.;
"Genomic structure of the human mitochondria! aldehyd⊖ dehydrogenase
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MEDLINE-87174836, PuLMed-3562250;
MEDLINE-87174836, FuLMed-3562250;
Mischarton and sequence analysis of a full length cDNA clone coding for human mitochondrial aldehyde dehydrogenase.";
Nucleic Acids Pes. 15:3179-3179(1987).
                                                      posnal, goaras, 13. Created)
13.AnG-1987 (Rel 0s, Greated)
15.JNN-1990 (Rel. 13. Last sequence update)
15.JNN-2090 (Rel. 41. Last annotation update)
Ald-tyde deby (Rel. 41. Last annotation update)
class 2) (ALDHI) (ALDH-E2).
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Evidence for a signal peptide at the amino terminal end of human
miterbondrial aldebyd-debydh.genase.";
FEBS Lett. 215:233-236(1987).
                                                                                                                                                                                                                                                                                                        Homo Sapiens (Human).
Bukaryasa, Metakaa, Charlata, Vartebrata, Buteleostomi;
Mammalia, Eutheria, Pramates, Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Liver;
MEDLINE-B005846, PubMed-4005346,
Hempel J., Kaiser R., Joernvall H.;
Mitcchondrial aldehyde dehydrogenase from human liver. Primary
"Mitcchondrial aldehyde dehydrogenase from human liver. Primary
structure, differences in relation to the cytosolic enzyme, and
functional correlations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reaus T., Bater E., Singh S., Agarwai D.P., Goedde H.W.,
FEBS Lett. 233:440 440(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Sobmitted (FER-2001) to the EMRL/OsenBank/PDRJ databases.
[7]
                             517 AA.
                                    PRT;
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                                STANDARD;
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PEVISIONS TO N-TERMINUS.
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SEQUENCE OF 18-517
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                                                                                                                                                                                                                                                                                                                                                                                                                      NCB1_TaxID=9606;
                                                                                                                                                                                                                                                                              ALDH2 OR ALDM.
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                                DHAM_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene."
DHAM_HUMAN
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this SWISS-PPOT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMR. Outstailon the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/
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-1- SINGLE AMINO ACID EXCHANGE.
-1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
-1- CAUTION. THE CONFLICTS RETWERN HE SEQUENCE DETERMINED IN REF. 1
-1- CAUTION. THE CONFLICTS RETWERN HE SEQUENCE DETERMINED IN REF. 1
FRAMSSHIFT OK SEQUENCING ERRORS AS DESCPIBED IN REF. 5 AND REF. 6.
THE SEQUENCE DESCRIBED IN REF. 9 DIFFERS FROM THAT SHOWN DUE TO TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 = an acid + NADH.
-i- PATHWAY: Ethanol utilization; second step.
-i- SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hempel J., Hoeoeg J.-O., Joernvall H.; Mitochondrial aldehyde dehydronese. Homology of putative targeting sequence to that of carbamyl phosphate synthetase I revealed by correlation of carbamyl phosphate synthetase I revealed by FEBS Lett. 222:95-98(1987).
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M. L., Zhou J., Hurley T.D., Weiner H.; drougenase: three-dimensional "Human liver mitochondrial aldehyde dehydrogenase: three-dimensional structure and the restoration of solubility and activity of chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Mitochondrial matrix.

--- SUBCELLULAR LOCATION: Mitochondrial matrix.

--- DISBASE: A VERY HIGH INCIDENCE OF ACUTE ALCOHOL INTOXICATION IN ORIENTALS AND SOUTH AMERICAN INDIANS, AS COMPARED TO CAUCASIANS, ORIENTALS AND SOUTH AMERICAN INDIANT CALLY IMPAIRED ALDH CAN BE DIRECTLY ATTRIBUTED TO AN ENZYMATICALLY IMPAIRED ALDH ISOZYME. THE INACTIVE VARIANT (ALLELE 2 OR ALDH2*2) IS DUE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Voshida A., Huang I.-Y., Ikawa M.;
"Molecular abnormality of an inactive aldehyde dehydrogenase variant
commonly found in Orientals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION OF ORIGIN OF CONFLICTS BETWEEN REF. 2 AND DNA SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agarwal D.P., Goedde H.W.; "Human aldehyde dehydrogenase isozymes and alcohol sensitivity."; sozymes Curr. Top. Biol. Med. Res. 16:21-48(1987).
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VaříanT LYS-496.
Provoradovsky A., Tsai S.J., Goldfarb L., Peterson P., Long J.C.,
Novoradovsky A., Tsai S.J., Goldfarb L., Peterson P., Long J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Micchondrial aldehyde dehydrogenase polymorphism in Asian and "Micchondrian populations: detection of new ALDH2 alleles."; Alcohol. Clin. Exp. Res. 19:1105-1110(1995).
                                                                                Hsu L.C., Tani K., Fuilyoshi T., Kurachi K., Yoshida A.;
"Cloning of cDNAs for human aldehyde dehydfogeneses l and 2.";
proc. Natl. Acad. Sci. U.S.A. 82:3771-3775(1985).
                                                                                                                                                                                                                                              SEQUENCE OF 119-517 FROM N A MEDINE-85252089; Pubmed-4015823; Arbida A., Ikawa M., Hsu L.C., Tani K.; Molecular abnormality and cDNA cloning of human aldehyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Natl. Acad. Sci. U.S.A. 81:258-261(1984)
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                                                                    MEDLINE=85216574; PubMed=2987944;
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SEQUENCE OF 119-517 FROM N A
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121 УБЕБМУБКСБКҮҮАСМАРКҮНСКТІРІБСБЕКУТКНЕРУСУСТОТІРМИЕРІДМОАМКІ. 180
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                                                                                                                                                                                                                                                                                                                                                               REGPRIGRELLSAAATOAVP · AMPAMAPPLVSREHPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                * K (IN ALDH2*2; DKASTIC REDUCTION
                                                                                                                                                                                                                    PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS: 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU: 1.
Oxldoreductase, NAD: Mitochondrion; Transit poptide; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                       A (IN REF. 3).
S -> A (IN REF. 2).
VKAARA -> FERREG (IN REF. 4 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 517;
                                                                                                                                                                                                                                                               ALDENYDE DENYDROGENASE.
NAD (ADP PART) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                         REGPRE -> ARAPP (IN REF. 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                           E8F74D44D285A00E CRC64;
                                                                                                                                                                                                                                                                                                 . V (IN DBSNP:1062136).
                                                                                                                                                                                                                                                                                                                                                                                                  A -> K (IN REF. 9).
A -> K (IN REF. 9).
A -> P (IN REF. 9).
E -> O (IN REF. 1).
AL -> SP (IN REF. 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 8.76-190;
                                                                                                                                                                                                                                                                                                                                            OF ENZYME ACTIVITY).
                                                                                                                                                                                                                                                                                                                    . K (IN ALDH2*1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                   /FTId VAR_002248.
                                                                                                                                                                                                                                                                                                                           /FT1d VAR_011402.
                                                                                                                                                                                                                                                                                                           /FTIG VAR_011869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                            MITCORONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.0%; Score 2572;
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                             IPR002086; Aldehyde_dehydr.
                                                                                                                                                    M26760; AAA51694.1; -...FRAME.
M54931; AAA62825.1; ALT_FRAME.
                                                                    JOINED.
                                                                                   JOINED.
                                                                                           AAA51693.1; JOINED.
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AAA51693.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                56381 MW;
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                                                                                                                                    AAB02967.1;
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                                                                                                                                              AAB59500.1;
                                                                    AAA51693.1;
                                                                                                      AAA51693.1;
                                                                                                             AAA51693.1;
                                                                                                                    CAA28990.1;
                                                                                                                              CAA68290.1;
                                                                                    AAA51693.1;
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                   EMBL; MZU456; AAA51693.1;
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Pfam; PF00171; aldedh;
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es 491; Conservà
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517 AA;
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                                                       M20447;
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                                     M20445;
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class 2) (ALDH1) (ALDH-E2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 KAPBGRPGAFQLGSPWPRMFASHSGRLLNPLAFFLEROFFYLAALETLENGKFYVLSYLV 121
GPALATGNVVVMKVAEQTPL/FAL/YVANLIKEAGFFPGVVNIVFGFGFTAGAAIASHEDVD 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1902 (Rel. 41, Last annotation update)
Aldehyde dehyddrogenase, mitochondrial (EC 1.2.1.3) (ALDH class 2)
(ALDH1) (ALDH-E2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesocricetus auratus (Golden hamster).
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Eutelenstomi;
Mammalia, Eutheria, Rodentia, Schurognathi, Muridae, Ciluetinae;
Mesocricetus.
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"Class 2 aldehide delidingeriase. Characterization of the humster
enzyme, sensitive to daidzin and conserved within the family of
multiple forms.";
FEBS Lett. 416:99-102(1997)
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PROSITE, PS00070; ALDEHYDE_DEHYDE_CYS: 1
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122 DEDMYEKTERYYAGWARKYHGKTIPIEGDFPSYTRHEPVGVGGQIIPWNFPLEMGAWKLG 181
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-!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 = an acid + NADH.
-!- PATHWAY: Ethinol utilization; second step.
                                                                                                                                                                                                                                                      182 PALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Bureleoscomi;
Manmalia; Eutheria; Kodentia; Sciulognathi, Muridae; Murinae; Rattus.
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Parres J., Guan K.-L., Wehner H.;
Parres J., Guan K.-L., Wehner H.;
Parres y structures of rat and bowne liver mitochondrial aldehyde
dehydrogenases deduced from cDNA sequences.";
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01-0CT-1989 (Rel. 12, Last sequence update)
15 JUN 2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase, mitochondrial precursor (EC 1.2.1.3) (ALDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biophys Res Commun 150:1083-1087(1988).
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MEDIINE-H8144217; Pubmed- 4442050;
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                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GPALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGFTAGAAIASHEDVD 240
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PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU: 1.
Oxidoreductase; NAD; Acetylation; Mitochondrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                          SUBCELLULAR LOCATION: Mitochondrial matrix.
SIMILARITY: BELÖNGS TO THE ALLOHYDE DEHYDROGENASES FAMILY.
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756748202F133E5 CR664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interPro; IPR002086; Aldehyde_dehydr.
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Matches 474; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519
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HSSP; P05091; 1CW3.
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PIR; S03564; S03564.
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287
321
519 AA:
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ACT_SITE
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Pharmacol. 46:88-96 (1994).

CATALYTIC ACTIVITY: An aldebyde + ND(+) + H(2)O an acid + NDH.

PATHWAY: Ethanol utilization; sereoud step.

SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

INDUCTION. By retinoic acid; 4°5 fold increase.

SIMILARITY: HELONGS TO THE ALDEHYDE DEHYDEWERNASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                            01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldebyde debydrogenase, mitochondrial precursor (EC 1.2.1.4) (ALDH
class 2) (AHD-MI) (ALDHI) (ALDH E2).
                                                                                                                                                                                                                                                                                                                                                         Chen M., Achkar C., Gudas L.J.;
"Enzymatic conversion of retinaldebyde to retinoic acid by cloned
murine cytosolic and mitochondrial aldebyde debydrogenases.";
                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eureleostomi,
Mammalia, Eutheria, Rodentia, Sciuroquathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSTIE: PS00070; ALDEHYDE_DEHYDE_CYS; 1.
PROSTIE: PS00687; ALDEHYDE_DEHYDE_GLU; 1.
Oxidoreductase: NAD: Acetylation: Mitochondrion; Transif peptide.
TRANSIT 1 NITOCHONDRION (BY SIMILARITY).
CHAIN 20 519 ALDEHYDE DEHYDE
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NAD (ADP PART) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                 "Cloning and characterization of the gene encoding mouse mitochondrial aldehyde dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200806F6 4048F4DA CRC64;
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AE > C (IN REF. 2).

MISSING (IN REF. 2).

1 | S (IN REF. 2).

R > G (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K ·> N (IN REF. 2).
S ·> M (IN REF. 2).
D -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.5%; Score 2480; DB 1
94.2%; Pred, No. le-182;
 519 AA
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Pfam; PF00171; aldedh; 1.
                                                                                                                                                                                                                                                                                                                                           MEDLINE-94335908; PubMed 8058062;
                                                                                                                                                                                                                                   MEDLINE 95047445; PubMed-7958964;
                                01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56537 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U07235; AAA64636.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-2DPAGE; P47738; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S71509; AAC60691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
 STANDARD:
                                                                                                            ALDH2 OR AHD1 OR AHD-1.
                                                                                                                                                                                                                                                                                                Gene 148:331-336(1994).
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269
2287
321
89
89
181
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                                                                                                                                                                                                                                                    Chang C., Yoshida A.;
                                                                                                                              (Wonse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P05091; 1CW3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    519 AA;
                                                                                                                                                                       NCB1_TaxID-10090;
                                                                                                                                                                                                                      STRAIN-C57HL/6J;
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20
264
287
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88
181
                                                                                                                            Mus musculus
DHAM_MOUSE
P47738;
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NP_BIND
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421 ANNSTYGLAAAVETKDLDKANYLSQALQAGIVWVNGYEVEGAQSPEGGYKMSGSGRELGE 4HU
                                                                 61 DKAREGRPGAFQLGSPWRRMDASHSGRLLNPLADLIEPNPTYLAALETLINGKPYVISYL 120
                                                                                                                                  .21 VDLDMVLKCLKYYAGWADKYHGKTIPIFGDFFSYIFHGFPVGVGVGTTIPWNFPLLMQAWKL 180
                                                                                                                                                                                                    181 GPALATGNVVVMKVAFQTPLTAL/VANLIKEAGFPPGVVNIVPGFGPTAGAATASHEDVD 240
                                                                                                                                                                                                                      241 KVAFIGSTELGEVLQVAAGSSNLKEVTLELGGKSPNIIMSDADMFWAVEQAHFALFFNQG 300
                                                                                                                                                                                                                                                                                       OPTEAGSELEVGEDIYDEFVVESVARAKSEVVGNPFDSKTEQGPQVDETQFKKILGYINT 360
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                                                                                                                                                                                                                                                                                                                                                                                                             361 GKQEGAKLIZDSSITAALPRSYFILPPTVPSDVQFSMTIAKEELPSPVMJILKFKTLEEVVGK 420
                                                                                                                                                                                                                                                                                                                                                                                                                               19 LSAAATSAVPAPHQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGNKEDV 78
1 MSAAATQAVPAPNQQPEVFCNGIFINNEWHDAVSKKTFFTVNFSTGEVICQVAEGDKEDV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Last Sequence update)
1-7170-20702 (Rel. 41, Last annafation schate)
Aldehyde dehydrogenase, mitochondrial precursor (EC 1.2.1.3) (ALDH
class 2) (ALDH:) (ALDH-E2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Farres J., Guan K.L., Weiner H.; Prinary Structures of rat and bovine liver mitochondrial aldehyde dehydrogenases deduced from cDNA sequences."; Eur. J. Blochem 180:67-74(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Puminantia; Perora; Roynoidoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence of the precursor of boying liver mitochondrial ald-hyde dehydrogenase as determined from its cDNA, its gene, and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steinmetz c G , Xia P , Wainer H , Hurley T P ;
"Structure of mitochondrial aldehyde dehydrogenase: the genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      520 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                functionality.";
Arch. Biochem. Biophys, 277:351-350(1990)
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MEDLINE-97341232; Pubmed-9195888;
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MEDLINE=89210865; PubMed=2540003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499 YGLQAYTEVKTVTVKVPQKN 518
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P20000;
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63. AREGRPGAFOLGSPWRRMDASHSGRLLNRLADLLEPDRTYLAALETLDNGKPYVISYLVD 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 LDMVLKCLRYYAGWADKYHGKTIPILGDFFSYTRHEFVGVGGIIFWNFFLLMGAWKLGP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142. IJUMVLKGLRYYASWALKYHSKTIPILGDYESYTRHEPVGVGGGIIPWNFPLLMQAWKLGP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183. ALATGNVVVMKVAEQTFLIALYVANLIKEAGFFFGVVNIVFGFGFFAGAAJASHEDVDKV-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243. AFTGSTELGEVIQVAAGSSNEKKVTLELGGKSFNLIMSDADMDWAVEQAHFALFFNQGQC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 QEGAKLLCGGGIAADRGYFIQPTVFGDVQDGMTIAKEEIFGPVMQILKFKTIFFVVGRAN 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 SAATGAVETENQQEEVLYNQIFINNEWHDAVSKKTFFFTVNFSTGDVICHVAEGDKADVDR 81
303 GCAGSRTEVORDIYDREVVESVARAKSPVVGNPFDSKTEGGPGVDFTGEKKTLGYINTGK
                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PSO0070: ALDEHYDE_DEHYDE_CVS; 1.
FROSITE, ESGNER7, ALDEHYDE_INHYDE_GLU; 1.
Oxidoreductase; NAD; Mitochondrion; Transit peptide; 3D-structure.
TRANSIT 1 21 MITOCHONDRION.
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15-37N-22002 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase, mitochondrial (EC 1.2.1.3) (ALDH class 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
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Pfam; PF00171; aldedh; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56708 MW;
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                                                                                                                                                                                                                                                                                                            PDB; 1A4Z; 08-APP-98.
                                                                                                                                                                                                                                                                           1AG8; 08-OCT-97
                                                                                                                                                                                                        $03565; $03565.
$09030; $09030
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520 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Matches 457,
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      REPRETATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 CCCAGSRTFVQEDIYDEFVVRSVARAKSRVVGNPFDSKTEQGPQVDFTQFKKILGYINTG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 KQEGAKLLCGGGIAAFMGYFIQPIVMGMYLIAKEELPGPVMQILKPKTIEEVVGRA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNSTYGI.AAAVETKDLDKANYI.SQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGEY 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVD 61
                                                                                                                                                    Eur. J. Biochem. 172:527-533(1988).
-!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 = an acid + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 PALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 VAFTGSTEIGRVIQVAAGSSNEKPVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                   "Mitochondrial aldehyde dehydrogenase from horse liver, Correlations
             Bukaryota, Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria, Perissodactyla; Equidae; Equis.
                                                                                                                                                                                                           1. SUBCELLULAR LOCATION: Mitochondrial matrix.
1. SIMILARITY: BFLANGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                             MEDLINE-88166730: PubMed-1350012;
Johansson J., von Bahr-Lindstrom H., Jeck R., Woenckhaus C.,
                                                                                                                                                                                                                                                                                                                                NAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                        92.7%; Score 2434; DB 1; Length 500; 92.6%; Pred. No. 3.2e 179;
                                                                                                                                 of the same species variants for both the cytosolic and the mitochondrial forms of an enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                  A -> L.; 7P45344A73343747474524 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                    !- PATHWAY: Ethanol utilization; second step.
                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Mismatches
                                                                                                                                                                                                                                                           InterPro; IPR002086; Aldehyde_dehydr.
Pfam; PF00171; aldedh; ALDEHYDE_DEHYDR_CYS; IPR051TE; PS00070; ALDEHYDE_DEHYDR_CYS; IPR051TE; PS00687; ALDEHYDE_DEHYDR_GLU; IOXidoreductase; NAD; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                482 GLQAYTEVKTVTVKVPQKN 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 GLQAYTEVKTVTIKVPOKN 499
                                                                                                                                                                                                                                                                                                                                                                                              500 AA: 54166 MW;
                                                                                                                                                                                               SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   462; Conservative
                                                                                                                                                                                                                                                                                                                                  250
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Equus caballus (Horse)
                                                                                                                                                                                                                                    PIR; S00364; S00364.
                                                                                                                                                                                                                                                   HSSP; P05091; 1CW3.
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                                      NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                             268
                                                                                                                                                                                                                                                                                                                                                        302
                                                                                                       Inernvall H.;
                                                                   SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               this SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAIALLIC ACTIVILY: An aldehyde + NAD(+) + H(2)0 an acid + NADH. PATHWAY: Ethanol utilization; second step. SUBGNIT: HOWOTETRAMER (BY SIMILARITY). SUBCELLULAR LOCATION: Mitochonfrial matrix. TISSUE SPECIFICITY: LIVER, TESTIS AND IN A LESSER EXTENT IN BRAIN. SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORTION: ALDRE PLAY A MAJOR ROLE IN THE DEPOXIETCATION OF ALCOHOL-DERIVED ACETALDEHYDE. THEY ARE INVOLVED IN THE METAHOLISM OF CORTICOSTEROIDS, HIGGENIC AMINES, NEUROTRANSMITTERS, AND LIPID
                                                                                                                                                         Aldehyde dehydrogenase X, mitochondrial precursor (EC 1.2.1.3) (ALDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    edne
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TRANSIT 1 17 MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bateleustomi;
Anterkota; Memoriadae; Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Cloning and characterization of a new functional human aldehyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sherman D., Dave V., Hsu L.C., Peters T.J., Yoshida A.;
"Diverse polymorphism within a short coding region of the human
aldehyde dehydrogewase 5 (ALDH5) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :
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NAD (ADP PART) (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.5%; Score 1929; DB-1;
72.7%; Pred. No. 1.8e-140;
1.ive - 61; Mismatches - 73;
                                                                                                                                   15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * CIN ALDHA
ZFTIG VAR 002257
L > P CIT
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                            517 AA
                                                                                                         01-JUL-1993 (Rel. 26, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfan; PF00171; aldech; 1
PROSITE; PS00070; ALDEHYDE_DEHYDE_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDE_GLU; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biel, Chem. 266:12257-12265(1991).
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MEDLINE=94063858; PubMed-8244338;
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDEINE-91286241; PubMed 2061311;
                                                                               01-JUL-1993 (Rel. 26, Created)
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                                                                                                                                                                                                                  ALDHIBI OR ALDHS OR ALDHX.
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                            STANDARD;
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                                                                                                                                                                                                                                                                                                                            NCHI_TaxID=9606;
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                            DHA5_HUMAN
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                                                                                                                                    182 PALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGFTAGAAIASHEDVDK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 VAFTGSTEIGRVIQVAAGSSNLKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 VAFTGSTEVGHLIQKAAGDSNLKRVTLELGGKSFSIVLALALMEHAVEQCHEALFFNMGQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 CCCAGSRTFVQEDIYDEFVVPSVARAKSRVVGNPFDSKTEQGPQVDETQFKKILGYINTG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 KQEGAKLLCGGGIAADRGYFIQPTVFGDVQDGMTIAKEEIFGPVMQILKFKTIEEVVGRA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422 NNSTYGLAAAVFIKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGEY 481
                                                                                                                                                                                                                                                                        122 DESMYEKCERYYAGWAEKYHGKIIFIDGDFFSYIKHEFYGVGGQIIFWNFPILMQAWKIG 181
                                       1:11 | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.
SAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKIFPTVNPSTGEVICQVABGDKEDVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            undifferentiated chick retina.";
Exp. Eye Pes 54 297-305(1992)
--- FUNCTION: BINDS FREE PETINAL AND CELIMIAP RETINGL-BINDING PROTEIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
CATALYTIC ACTIVITY: An aldebyde + NAD(+) + H(2)∩ = an acid + NADH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Tast annotation update)
Aldehyde dehydrogenase 1Al (EC 1.2.1.3) (Aldehyde dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic.
SIMILAPITY: RELONGS TO THE ALDEHYDE DEHYDPOGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godbout R.; "High levels of aldehyde dehydrogenase transcripts in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY. Ethanol utilization, second step. SURUNIT: HOMOTETPAMEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOG AA
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MEDLINE=92217647; PubMed=1559558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482 GLQAYTEVKTVTVKVPQKN 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498 GLKAYTEVKTVTIKVPQKN 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992 (Pel 23, Treated)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
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P27463;
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entities requires a liberare agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 APEGPPGAPGLGSPWPPMDASHSGPLLNPLADLIERDRTYLAALETLDNGKPYVISYLVD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 LDMYLKGLKYYASWALKYHSKTIPILGDFFSYTKHEPVGVGGQIIPWNFPLLMQAWKLGP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 ALCCGNTVVVKPAEQTPLSALYMGSLIKEAGFPPGVVNIVPGFGPTAGAAISHHMDIUKV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.23 NSTYGLAAAVETKULEKANYUSQAUGAGTVWVNYYDVEGAQSPEGGYKMSGSRPELGEYG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AAAIQAVPAPNQQPEVECNQIFINNEWHDAVSRKIFPTVNPSIGEVICQVAEGDKEDVDK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 ALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 OTASSKTEVQELLYTHEVVESVARAKSEVVSNETISKTEVOTETQETQETQEKKTLOYTHTOK
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Pattus.
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16-021-2001 (Rel. 40, Last annotation update)
Aldehyde dehydrogenase 1A2 (EC 1.2.1.3) (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2).
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BY SIMILARITY.

77771181FA2F05DA9 CRC64;
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modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                              Eram, EFOUl71, aldedh, 1.
PMOSITE: ΡΕΘΌΦΑΤΘ: ALDEHYDE_DEHYDE_CYS; 1
PROSITE: PSOUGES? ALDEHYDE_DEHYDE_GLU: 1.
                                                                                                                                                                                                                                                                                                                           InterPro; IPR002086; Aldehyde_dehydr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               509 AA; 55809 MW;
                                                                                                                                                                                  EMBL; X58869; CAA41679.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 335; Conservative
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                                                                                                                                                                                                                                     S14629; S14629.
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                                                                                                                                                                                                                                                                             HSSP; P51977; 1BXS.
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                                                                                                                                                                                                                                 expression in Escherichia coli. Recognition of retinal as substrate.";
J. Riol Chem 271:16288-16293(1996).
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AND AGALLYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 = an acid + NADH.
PATHANY: RETINOIT ACID BLOGENESIS.
SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
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SIMILARITY: RELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                    Wang X., Penzes P., Napoli J.L.;
"Cloning of a cDNA encoding an aldehyde dehydrogenase and its
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E01EF471342267AA CRC64;
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Pred No 3 3e-130;
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                                                                                   MEDLINE=96279178; PubMed:8663198;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SMES institute of Bioinformatics and the EMBL outstation. The Detween Boolnformatics institute of Proper are no restrictions on its use by non-profit institutions as lond as its content is in no way modified and this statement is not tenoved. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch.) or send an email to licensee(isb.sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 VQAARLAFSIJGSVWRRMDASFRGRIJDKLADILVERDRATTATMESLN/GGRPFLQAFYTDL 121
422 SDFGLVAAVFTNDINKALMVSSAMQAGTVWINCYNALNAQSPFGGFKMSGNGREMCEFCH, 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4. AATQAVEARNIJOPEVEONGTETINIEMIRAAVSELTEPTVINESTOEVT QVAFOTERTIVOFA (6.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Modebular identification of a major retinate acid synthesizing enzyme, a retinaldebyde-specific debydrogenase.";

Eur. J. Blochem. 240:15-22(1996)

Fur. J. Blochem. 240:17-22(1996)

Fur. J. PRINDING PROTEIN BOHND RETINAL, DOES METABOLIZE OFTANAL, AND DECANAL, BUT DOES NOT METABOLIZE CITKAL, HENZALDEBYDE, ACID HOGHAL BEFILDEBYTY (BY SIMILARIY)

FUR. J. FUR. AND ALGEBRANAL BEFILDEBYTY (BY SIMILARIY)

FUR. J. FUR. AND ALGEBRANER (BY SIMILARIY).

FUR. SUBCELLULAR LACATION: Cytoplasmic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutberia; Rodentia; Sciuroquathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao D., McCaflery P., Ivins K.J., Neve R.L., Hoqan P., Chin W.M.
Draeger U.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         16-oct-2001 (Rei 40, East annotation update)
Aldebydd debyddogenase 1A2 (BC 1.2.3.3) (Retinaldebyde-specific
debydrogenase type 2) (RALDH(1!)) (RALDH 2).
ALDHTA2 GR ALDHTA7 OR RALDH2.
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                                                                                                                                                                                                                                                                                                         499 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
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Pfam: PF00171; aldcdh; 1.
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01-NOV-1997 (Rel. 35, Last sequ
                                                                 484 QAYTEVKTVTVKVPOKN 500
                                                                                                     FMRL; X99273; CAA67666.1; -
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267
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es 328; Conserv
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between the Swiss institute of Ricinformators and the EMRL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                LATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVA 243
                                                                                                                                                                  304 GAGSPTFVQEDIYDEFVVRSVARAKSPVVGN34 DSKIHQG9290F319FKKILGYINIGKQ 363
                                                                                                                                                                                                                                       124 DMVLKCLRYYAGWADKYHGKTIFIINGDERSYTRHFPVGVGGLIIPWNEFLLMQAWKLGPA 183
                     LCFGNTVVIKPAEQTPLSALYMGALIKEAGFPFGVVNILFGYGFFAGAAIASHIGIDKIA 241
                                                                                                                                             244 FIGSTEIGPVIQVAAGSSNEKPVILEEGGKSPN(IMSLANMEWAVEQAHPALFPNGGQCC 303
                                                                                                                                                                                                                                                                                         BGAKILFGGGTAADPGYFIQPTVFGTVQHGMTTAKEETFGPVMQILKFKTIEEVVGRANN 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RETINOL-BINDING PROTEIN-FOUND METINAL, DOES METABOLIZE OCTANAL AND BECANAL BUI DOES NOT METABOLIZE C'ITRAL, BENZALDEHYDE, ACETALDEHYDE AND PROPANAL BEFICIERTY (BY STRILLARITY).

CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ono Y., Fukuhara N., Yoshie O.;
"TALl and LIM-only proteins synergistically induce retinaldehyde dehydrogenase 2 expression in T-cell acute lymphoblastic leukemia by acting as cofactors for GATA3."
Mol Cell Biol 18-6939-6830(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniała, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldehyde jehydio-genase 182 (E7 1 2 1 3) (Fortinal dehydio-specific dehydrogenase type 2) (RaLDH(II)) (RALDH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic
SIMILARITY: RELONGS TO THE ALDEHYDE DEHYDPOCENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         484 QAYTEVKTVTVKVPQKN 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:15472; ALDH1A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
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64 PEGREGARGUDSEWREMDASHSGRUNPLADDLIERDFTYLAALESLONGKRYVISYLVEL 123
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                                                                                                                                                                                                                             4 AATQAVEAFNQQFEVECNQIFINNEWHDAVSEKTFFTVNFSTGEVICQVAEGDKEDVDKA
                                                                                                                                                                                                                                                              2 ASZHILEPSPTFNLEIKYTKIFINNEWQNSESGRVFFVYNPATGEQVCEVQEADKADIDKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chickon).
Erkaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutoleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
                                                                                                                                                                                                9. Teg
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16-orr-2001 (Rel. 40, Last annotation update)
Aldchyde dehydrogenase 1A2 (EC 1-21.3) (Retinaldehyde-specific dehydrogenase type 2) (RALDH(11)) (RALDH 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sockanathan 3., Jessell T.M., "Motor neuron derived retinoid signaling specifies the subtype identity of spinal motor neurons."; cell 94:803-514(1998).
                                                                                  NAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                               DB 1; Length 499;
                                                                                                                                                                                                16.4.18
                                                                                                                                499 AA; 54789 MW; FEGRS 4A475442448 CRC64;
                                                                                                                                                                               Pred. No. 8e-130;
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                                                                                                                                                              68.2%, Scure 1790,
66.0%; Pred. No. 8
                                                                                                POTENT I AL.
             Pfan, PF00171, aiddh; 1.
PROSITE: PS000703 ALCENYDE_BEHYDE_VS.
PROSITE: PR00687, ALDENYDE_DEHYDE_GLU,
Oxidoreductase; NAD.
                                                                                                                   POTENTIAL.
InterPro: :PR9U2U86; Aldehyde_dehydr.
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                                                                                                                                                                               Local Similarity 66.0%
es 428, Conservation
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301
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                                                                                              ACT_SITE
ACT_SITE
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                                                                                  NP_BIND
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 DMYLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEFVGVCGUIIPWNFPLLMQAWKLGPA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 REGPPGAFQLGSPWRRMDASHSGRLLNRLADLIERDRTYLAALETLDNGKPYVISYLVDL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 CAGSKTFVORDIYDEPVVPSVAPAKSPVVGNPFDSKTEQGPQVDFTQFKKILD3YINTGKQ 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 AATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVDKA 63
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FUNCTION: RECOGNIZES AS SUBSTRATES FREE RETINAL AND CELLULAR RETINOL-BINDING PROTEIN-ROUND RETINAL. DOES METAROLIZE OCTANAL AND DECANAL BUT DOES NOT METABOLIZE CITRAL, HENZALDEHYDE, ACETALDEHYDE
                                                          AND PROPANAL EFFICIENTLY (BY SIMILARITY).

AND CATALYTIC ACTIVITY: An aldebyde + NAD(+) + H(2)0 = an acid + NADH.

PATHWAY: PFFINALY ACID BLOGENESIS.

SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 VRAARLAFSLGSVWRRMDASBRQQLIDKTADI.VEPDPAVLATMESLNSGKPFLGAFYVDI.
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                                                                                                                                                          SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAD (ADF FART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.5%; Score 1771; DB 1;
65.8%; Pred No 2.30-128;
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                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                      SUBCELLULAR LOCATION: Cytoplasmic.
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                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002086; Aldehyde_dehydr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249
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Zheng C.F., Wang T.T., Weiner H.; "Cloning and expression of the full-length cDNAS encoding bullan liver class 1 and class 2 aldebyde debydrogenase.";
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Blochemistry 26:5679-5684(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hempel J., von Bahr-Lindstrom H., Joernvall H.;
"Aldehyde debydrogenase from human liver. Primary structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hormonal response, retinal exidation and implication in testicular
                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutberla, Primatos, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hsu L.C., Chang W.-C., Yoshida A.;
"Genomic structure of the human cytoselic aldehyde dohydrogenase
                                                                                                                         15-JUN-2002 (Ref. 41, Last annotation update)
Aldebyde dehydrogenase IAI (EC 1.2.3.3) (Aldebyde dehydrogenase,
eytosolici (ALDH class 1) (ALHDII) (ALDH-EI).
ALDHIAI OR ALDGII ALDGII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hsu L.C., Tari K., Fujiyeshi I., Kurachi K., Yoshida A., "Cloning of conas for human aldebyde debydrogenases 1 and 2.";
Proc. Natl. Acad. Sci. U.S.A. 82:3771-4775(1985).
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Yoshida A., Hsu L.C., Yanaqawa Y.;
"Biological role of human cytosolic aldohydo dchydroqenase 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agarwal D.P., Cohn P., Goedde H.W., Hempel J.; *Aldehyde dehydrogenase from baman erythro ytes, structural relationship to the liver cytosolic isozyme."; Enzyme 42:47-52(1989).
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MEDLINE:85252089; PubMed-4015823;
Yoshida A., Ikawa M., Hsu L.C., Tani K.:
"Molecular absormality and chNA cloning of human aldebyde
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500 AA.
                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alcohol, Clin, Exp. Res. 17:828-831(1993).
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PKT;
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MEDLINE-89377753; PubMcd 2776714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90077427; PubMcd-2591967;
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-9606;
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                       populs; 000768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dehydrogenases .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver
DHA1 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
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BOUND RETINAL. CAN CONVERTZOXIDIZE RETINALDEHYDE TO RETINOIC ACID

RESULT 13 DHA1\_HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 KAREGKPGAFQUSSPWKKMDASHSGPLLNPLADGIEFDFTYLAALEFLDNGKPYVISYLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEDMYLKELRYYAGWADKYHGKTIFIDGDFFSYTFHEFVGVCRQIIPWNFPLLMQAWKLG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 DLAGGIKTERYGAGWADKIQGRTIFIDGNPFTYTRHRPIGVGSQIIPWNPPLVMLIWKIG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 PALSCGNIVVVKPAEQTPLTALHVASLIKEAGFPPRVVNIVPRYRPTAGAAISSHMDIDK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 VAPTGSTEIGPVIQVAAGSSNLKRVTLEEGGKSPNLIMSDAEMEWAVEJAHFALFFNQGQ 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSGTPDLPVLLTDLKIQYIKIFINNEWHDSVSGKKFPVFNPATEEELGQVEEGDKEDVD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 PALATGNVVMKVAEQTPLFALYVANLIKEAGFPPGVVNIVPGFGPTAGAATASHEDVDK
              CATALYTIC ACTIVITY: An aldebyde + NAD(+) + H(2)D = an acid + NADH
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SIMILARITY: BELONGS TO THE ALFEHYDE DEHYDEWNENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACETYLATION.
NAD (ADP PART) (BY SIMILARITY).
POFENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.4%; Score 1769; DB 1; Length 500;
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> I (1N REF. 3 AND 4).
82646410564749677 @PM64;
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                            PATHWAY: Ethanol utilization; second step.
SUBUNIT: HOMOTETRAMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1
PROSITE; PS00687; ALDEHYDE_DHYDR_GIJT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002086, Aldehyde dekydr
                                                                                                                                                                                                                                                     AAA51692.1; JOINED.
AAA51692.1; JOINED.
AAA51692.1; JOINED.
AAA51692.1; JOINED.
AAA51692.1; JOINED.
                                                                                                                                                                                                             EMBL; M31994; AAA51692 1; -.
EMBL; M31982; AAA51692 1; JOINED
EMBL; M31983; AAA51692.1; JOINED.
                                                                                                                                                                                                                                                                                                                           AAA51692.1; JOINED.
AAA51692.1; JOINED
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AAA51692.1; JOINED.
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K03000; AAA51695.1; -.
M26761; AAA35518 1.
S61235; AAD13925 1;
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258
302
120
151
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268
302
120
161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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NP_BIND
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                    4.2. NNSTYGLAAAVETKELDKANYLSQALQAGTVWVN-YEVERTALSPEGGYKMSGSGPELGEY 481
(0.2. OPPAGSRIFFVQED1YDEFVVESVAPAKSPVVGNPFUSRIFFQGPQVDFTQFKKILGYINIG 361
                                                                          <u>36. KQEGAKIL.CGGGIAAPPRYFIQFIVPRINQKMTIAKEFIPSFVMQILKFKTIFEVNGKA 421</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- FTHN TONE BINDS PARE METINAL AND CELLULAR PETINAL-HINDING PROTEIN-
BOTHL FEINAL. CAN CONVERTY.XICIZE REINALCEHYDE TO RETINDIC ACID.
--- CATALYTIC ACIVILY: An aldehyde + NAD(+) + H(2)0 = an acid + NADH.
--- PATHWAY: Ethanol attilization, second step.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stayner C.K., Tweedie J.W.; "Cloning and characterisation of the cLMA for shoop liver \gamma^{rosolic}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cotaitiodactyla, Ruminantia, Pecora, Boroidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazba; Chordata; Craniata, Vertebrata, Bateleostumi,
                                                                                                                                                                                                                                                                                                                                                                                                                        01-ocr-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ald-hyde debydre-genase iA1 (F7 1.2 i.3) (Ald-hyde debydrogenase,
cytosolic) (ALDH class 1) (ALHDII) (ALDH-E1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moore S A., Baker H.M., Blythe T.J., Kitson K E., Kitson T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
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Ptam; PF00171; aldedh; 1.
PRGSITE: PS00070; ALMEHYDE_DEHYDE_CYS;
PPOSITE; PSWD6#7; ALMEHYDE_DEHYDF_CIG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-PAY CRYSTALLOGRAPHY (2.35 ANGSTROMS)
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                                                                                                                                                                                                                               482 GLQAYTEVKTVTVKVPOKN 500
                                                                                                                                                                                                                                                                     481 GFHEYTEVKTVTVKISQKN 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia, Eutheriu; Cutar
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aldehyde dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDB; 18XS; 27-APR-99.
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Ovis aries (Sheep).
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P51977;
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STRAIN=BALB/c, C57RL/6J, and 129/REJ; TISSUE Liver;

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241
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                                                                                                                                                                                                                                                62 KAREGRPGAFQLGSPWRRMDASHSGRLLNRLADLIERDRTYLAALETLDNGKPYVISYLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 NNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYLVVEGAQSPEGGYKMSGSGPELGEY 481
                                                                                                                                                                                       61
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                                                                                                                                                                                                                 1 SSSAMPDVPAPLTNLQFKYTKIFINNEWHSSVSGKKFPVFNPATEEKLCEVEEGDKEDVD 60
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                                                                                                                                                                                     2 SAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSKKTFPTVNPSTGEVICQVAEGDKEDVD
                                                                                                                                                                                                                                                                 122 DLDMYLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKLG
                                                                                                                                                                                                                                                                                                                                                                          182 PALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                      242 VAFTGSTEIGKVIQVAAGSSNI,KRVTI,EI,GGKSPNIIMSDADMDWAVEQAHFALFFNQGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia, Butheria, Rodentia, Sciurognathi, Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1992 (Rel. 21, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogcnasc 1A1 (EC 1.2.1.3) (Aldehyde dehydrogenase, cytosolic) (ALDH class 1) (ALHDII) (ALDH-EI).
ALDHIAI OR ALDHI OP AHD? OP AHD-2.
                                                                                                                                                          .;
             BY SIMILARITY.
ACETYLATION (BY SIMILARITY).
NAD (ADP PART) (BY SIMILARITY).
                                                                                                                            Length 500;
                                                                                                                                                        67; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rongnoparut P . Weaver S .;
Isolation and characterization of a cytosolic aldehyde
                                                                                          54693 MW; 68B8971968CEB8F8 CRC64;
                                                                                                                         Score 1758; DB 1;
Pred. No. 2.3e·127;
   Oxidoreductase; NAD; Acetylation; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dehydrogenase-encoding cDNA from mouse liver.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Rioinformatics and the EMHs outstain the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial central res regarres a license attendent (see http://www.isp.sub.ch.announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                  WELL AS THE ALDEHYDES GENERATED VIA LIFTD FEROXIDATION. HINDS FREE PERTINAL AND CELLOLIAR RETINOL, FUNDIO PROPERLY-HONDS RETINAL. CAN CONVERTZOXIDIZE FETINALDEHYDE TO PETINCIC ACID (BY SIMILARITY). CATALYTIC ACIIVITY: An aldehyde + NAD(+) + H(2)0 - an acid + NADH.
                                                                                                                                                                                                            SUBSTRATES, IS ALSO INVOLVED IN THE OXIDATION OF ALDERYDES DERIVED FROM BIOGENIC AMINES SUCH AS EPINEPHRINE AND NOREPINEPHRINE, AS
                                                   Bond S.L., Singh S.M.;
"DNA sequence analysis of the cytosolic acctaldehyde dehydroqenaso-
gene (Ahd-2) in mouse strains with variable ethanol preferences.";
Blochem. Med. Metab. Blot. 52:155-159(1994).
-i. FUNCTION: IN ADDITION TO THE ACTIVITY ON ACETALDEHYDE AND RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPARENTLY NOT EXPRESSED AT DETECTABLE LEVELS IN KIDNEY, STOMACH,
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PPGSITE: PS00687; ALDEHYDE_DEHYDE_GLU; 1.
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Title: US-09-830-751-4 Perfect score: 2625 Sequence: i MSAAAT@AVPAPNQ@PEVPC YGLQAYTEVKTVTVKVPQKN 500

Sequence: 1 MSAAAT@AVPAPN@@PEVP::
Scoring table: BLOSHM62

Searched: 671580 seqs, 206047115 residues

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## SUMMARIES

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## ALIGNMENTS

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Mammalia; Eutheria; Podentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-DEC-2001 (TrEMBLE). 19, Last sequence update)
01-MAR-2002 (TrEMBLE). 20, Last annotation update)
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Matches 420; Conservative
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                                                                                                                                             181 VDKVAFTGSTEVGHLIQVAAGSSNLKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFN 240
                                                                                                                                                                                            299 QGQCCCAGSRTFVQEDIYDEFVVRSVARAKSRVVGNPFDSKTEQGPQVDETQFKKILGYI 358
                                                                                                                                                                                                                        359 NTGKQEGAKLLGGGGIAADRGYFIQPTVFGDVQDGMTIAKFEIFGPVMQILKFKTIEEVV 418
                                                                                                                                                                                                                                                                                                                     419 GRANNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAGSPFGGYKMSGSGPEL, 478
                                                                                                                                                                                                                                                                                                                                                                                                                     179 KLGPALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHED 238
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBL_TaxID=7955;
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STRAIN-CSTBL/GS; TISSUE=EMBRYO;

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X MARAWA J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito, R., Saito, I., Golobori T., Hono H., Kasukawa I., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casuvant T., Saito R., Radota K., Matsuda H.A., Saito H.A., Standarili F., Harsh G., A. Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouarkenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Waqner L., Washio T., Sakai K., Okido T., Furuho M., Anno H., Raidarelli E., Harsh G., A. Blake J., Boftelli D., Bojunda N., Carnina i F., de Bonnido M.F., Gustincich S., Hill D., Hofmann M., Marzarelli J., Mombaert P., A., Suzuki R., Satoreh K. F., Sasaki H., Sato R., Schoenbach C., Schoenbach C., Schoenbach C., Schoenbach C., Schoenbach C., Muttanerica Y., Shibata Y., Storeh K. F., W. Weitz C., Muttanerica Y., Shibata Y., Storeh K. F., W. Weitz C., Muttanerica Y., Kohtsuki S., A., Weitz C., Muttanerica Y., Kawai H., Weitz C., Muttanerica Y., Kawai Y., Kawai H., Matsuki S., Kawai Y., Kawai Y
                                                 361 GRQEGARLLCGGGTAADRGYFTQFTVFGDVQDGMTTAREETFGFVMUTLRFYTTEEVVGR 420
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Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
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01-JUN-2001 (TrEMBLE). 17, Last sequence update)
01-JUN-2002 (TrEMBLE). 11, Last annotation update)
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PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; I.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU: 1.
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PROSITE; PSGOGTG; ALDEHVDE_DEHYDE_CYS;
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Oxidor-duotase.
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                                                                                                                                                         2 SAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGFV1~QVABGDKEDVD 61
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Mammalia, Eutheria; Primates, Catarrhini; Hominidae, Homo
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
8A113024.2 (aldehyde dehydrogenase 1 family, momber B1 (ALDHS
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                                        73, Indels
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EMBL, AL13785, CAD13246.1;
InterPro; IRR002086; Aldehyde_dehydr.
Pfam; PF00171; a136dh; 1.
PRGSITE; EXQUARY ALDEHYDE_DEHYDE_CYS; UNKN.WM.].
PROSITE; PS00687; ALDEHYDE_DEHYDE_GIJ, UNKN.WM.].
SEQUENTE: PS00687; ALDEHYDE_DEHYDE_GIJ, UNKN.WM.].
72.9%; Pred. No. 5.50 150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 GCCAGSPIFVQEDIYDEFVVPSVAPAKSRVVGNPFDSKTEQGPQVDETQFKKILGYINTG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 CCCAGSKTFVEESIYNEFLERTVEKAKORKVGNPFELDIQOGPQVDKEGFERVLGYIQLG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RÝZ KQEGAKLLGGGGIAADPGYFIQPTVPGDVQDGMTIAKEBIFGFVMQILKFKTIEEVVGRA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 KAPEGEPGAFQLGSPWPPMPASHSGPLJNPLADLIEPPTYLAALFTLDNGKPYVISYLV 121
                                                                      78 RAVKAAREAFRLISSPWPFMFASFRGRLLNRLAFILVERFRYYLASI FTLIFINGKPFQESYAL 137
                                                                                                                                                    122 DEDMVEKCERYYAGWADKYHGKIIPIEGDFFSYTPHEFVGVGGQIIPWNFPELMQAWKIG 181
                                                                                                                                                                                                                           138 DLDEVIKVYRYRAGWADKWHSKTIPMINGHPCFTRHEPVGVCGQIIPWNFPLVMQGWKLA 197
62 KAPPGPPGAFULGSPWPFMLASHSGFLLNFLADI IEFDETYLAALETLUNGKPYVISYLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVTCQVAEGDKEDVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 SSAA - ALPSTILNPITYNQLFINNEWQDAVSKKTFFTVNFTTGEVIGHVARGDRADVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 VAFTGSTELGEVIOVAAGSSNIKEVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQ
                                                                                                                                                                                                                                                                                                             182 FALATGNVVWKVARQTFLTALYVANLIFEANFHBOVNIVEGFGFTAGAATASHEDVEK
                                                                                                                                                                                                                                                                                                                                                                                        198 PALAIGNIVVMKVAEQTPLSALYLASLIKEAGFPPGVVNIITGYGPTAGAAIAQHVDVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryola: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia, Butheria, Pilmates, Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 8%, Score 1936, DB 4, Length 517;
72 9%; Pred. No. 1 9e-148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           517 AA; 57238 MW; A628E448D1E8689D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Croated)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAP-2002 (TrFMBLrel. 20, Last annotation update)
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RXGAN=BERELELY
RX Adams M.D. Celniker S.E. Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D. Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Admanaides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA GCOTGE R.A. Italia S.E., Sakhunner M. Henderson S.N.,
RA GCOTGE R.A. Flowis S.E., Flyhold S.P., Sahunner M. Henderson S.N.,
RA GCOTGE R.A., Barker E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F. Agbayani A. An H. J., Andrews Pfannkoch C., Baldwin D.,
RA Abril J.F. Agbayani A., An H. J., Andrews Pfannkoch C., Baldwin D.,
RA Berson K.Y., Hense P. V., Perman H. P., Bharktaroglu L., Beasiey E.M.,
RA Berson K.Y., Hense P. V., Perman H. P., Horkstein P., Brottler P.,
RA Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis S.,
RA Durbin K.J. Frangelista C., Perriara C., Ferriara S., Pleischmann W.,
RA Fosler C., Gabrielian A.E., Garq N.S., Berriara S., Pleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Herman T.J., Herman T.J., Herman C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Rennison J. A.,
RA Hostin D., Houston K.A., Howland T.J., Weil M., I., In X.,
RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Jiang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., J., J., Inang Y., Lin X.,
Mextulov G., Milshina N. W. Morbarry C., Mernison J. M., Melson D.L.,
RA Belazzolo M., Pithman G.S., Pallard J., Pori V., Revise M.S.,
RA Palazzolo M., Pithman G.S., Pan S., Pillard J., Pori V., Revise M.S.,
                                                                                                                                                                                                                                                                                                                                                                         378 OKEGAKLLGGGERFGERGFFIRPTVFGGVQNDMRIAKEEIFGPVQPLFKFKKIEEVVERA 437
                                                                                                                                                                                    422 NNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGEY 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 DLDEVIKVYRYFAGWADKWHGKTIPMDGQHFCFTRHEFVGVGGQIIPWNFPLVWQGWKLA 197
                                                                  182 PALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDK 241
                                                                                                                                                              242 VAFTGSTEICRVIQVAAGSSNLKRVTLELGGKSFNIIMSDADMDWAVEQAHFALFFNGGQ 361
                                                                                                                                                                                                                                                          302 CCCAGSRTFVQEDIYDEFVVRSVARAKSRVVGNPFDSKTEQGPQVDETQFKKILGYINTG 361
                                                                                                                                                                                                                                                                                                      318 CCCAGSKTEVEESIYNEFLERTVEKAKUKKVGNPFELL/PQQSPQVDKEQFEKVLGY1QLG 377
                                                                                              362 KQBGAKLLFGGGTAADPGYFIQPTVFGDVQDSMTIAKEEIFGPVMQILKFKTIEEVVGRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota, Melazea, Arthropoda, Tiacheata, Hexapoda, Insecta,
Pterygota: Neoptera, Endopterygota: Diptera, Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           520 AA.
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01-MAY-2000 (TrEMBLrel, 13, Last sequ
01-MAR-2002 (TrEMBLrel, 20, Last and
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91 TAVQAARNAFKLGSPWRRMIASEPGPLLYPLADLMEPDQVYLASLFTLDNGKPYSMSYNV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 KAREGREGAFÖLGSPWRKMDASHSGRUJNRIJABULLERURTFLAALELLUNGKPYVISYLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $20 COCAOSRIEVEDKIEDEEVERSAERAKKEIVGNPEDINLEGGEGVNEEGMEKTIGMEKTG (79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480 KKEGAKLVAGGSRPEGLE---GYPVOPTVFAPVGEDMTTAREETFOPVGOLIRFKKLDEV 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.18 VCMANNSTYCLAAAVETKUJIKANYI,SQALQAGTVWVNTYIVVEGAGSPEGTYKMSSSGRE 4.7.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SAAATQAVPAPNOOPEVECNOIFINNEWHDAVSRKTEPTVNPSTGEVICOVAEGDKEDVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AVANYSSEPOPOTTPDILYTGVFINNEWHKSKSGKIPETINPTTAEVIAEIUCADKEDID 80
                 Shure B.C., Siden-Kiamos L., Simpson M., Skupski M.P., Smith T., Spire B., Spradling A.C., Stapleton M., Strong R., Shu E., Svirskas R., Tector C., Tunner B., Wenter E., Wand A.H., Wand X., Mang Z.-Y., Wassarman D.A., Weinstrock G.M., Weissenbach J., Whilliams S.M., Wooder T., Weissenbach J., Weissenbach J., Zheng Z.-Y., Wassarman E.A., Zaveri J.S., Zhu M., Shu X., Zho G., Zheng L., Zheng X.H., Zhou F.N., Zhou M., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Weisser B.M., Webla G.M., Venter J.C.;
The genome sequence of thospophila metanodaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.2. PALATGNVVVMKVAEGTPELTALYVANLIKEAGPPPGVVNIVPGFOPTAGAATASHEDVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 VAPTGSTEIGRVIQVAAGSSNLKRVTLELBGKSPNITMSDADMDWAVEGAHFALFFNORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402 (COLASSRIPVQEDIYDE) VVPSVARAKSRVVGNPPDSKI EQCHQVDET QFKK LLGY I NTG
Reinert K., Remington K., Saunders R.D.C., Schoeler F., Shen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.1%; Score 1866; DB 5; Length 520;
69.8%; Pred. No. 9.3e-144;
ive 61; Mismatches 83; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                520 AA; 57019 MW; 82BF53FD573EC77B CR164;
                                                                                                                                                                                                                                                                                                                                                           PROSITE, PS00070; ALDEHYDE_DEHYDE_CYS: 1.
PROSITE; PS00687; ALDEHYDE_DEHYDE_GLU: 1.
                                                                                                                                                                                                                                                                                                                     InterPro: IPR002086; Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 LGEYGLQAYTEVKTVKVPQKN 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              497 NCEYALENYTEVKSVIVKVAUKN 519
                                                                                                                                                                                                                                                                                                 FlyBase; FBqn0032114; CG3752.
                                                                                                                                                                                                                                                     EMBL; AE003624; AAF52769.1;
HSSP; P05091; 10W3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.88;
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                                                                                                                                                                                                                                                                                                                                     Pfam; PF00171; aldedh; 1.
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  KKAA
KKAA
KKAAA
COCC
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<u> Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</u>

Xenopus laevis (African clawed frod).

RALDH2

AC DT DT DT DE COS

91-WAR-2001 (TrEMBLEel. 16, Created)
01-WAK-2001 (TrEMBLEel. 16, Last sequence update)
91-IUN-2002 (TrEMBLEel. 21, Last annotation update)

518 AA

PRT;

PRECIMINARY;

OGDEXS OGDEXS;

RESULT 7 09DEX5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 DMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVGGGIIPWNFPLLMQAWKLGPA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 LATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 FTGSTEIGRVIOVAAGSSNI:RRVTLEIJGGKSPNTIMSDADMEWAVEDAHFALFFNDGGGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGAKLECGOMIAADROYFIQPTVPOMQOMMTIAKERIFGPVMQIIKFKTIEEVVORANN 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     881 EGAKLEGGGKALGPRGFFIEFTVFSNVALJMRTAFEETFGPVQQTLFFKTVEEVTEFANN 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STYGLAAAVETKULDKANYLSQALQAGIVWVNCYDVEGAQSPEGGYKMSGSGRELAEYGL, 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 SDYGLVAAVFINDINKALTVSSAMQAGTVWINCYNALNAQSPFGGYKMSGNGKEMGEYGL 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 REGRPGAFQI/GSPWRRMDASHSGRI/INRI/ADLIERDRTYI/AAI/ETI/DNGKPYVISYLVDL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304. CAGSRIEVQEDIYDEEVVRSVARAKSRVVGNPEDSKTBQGPQVDETQEKKIIGYINTGKQ. 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 AATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVDKA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 ASLQLLPSPSANLEVKHSKIFINNEWQTSESGKAFPVYNPATGEQICEVĢEAEKSDVTKA 80
                                                                                                                                                                                                                    Then Y., Pollet N., Niebrs C., Pieler T.;
"Increased XPALDH2 activity has a posteriorizing effect on the central mervous system of Xenopus embryos.";
mervous system of Xenopus embryos.";
met. Dev 10.19-10.1(2001)
-!-SIMILARITY FELONGS TO THE ALDEHVNE DEHYDROGENASES FAMILY.
EMBL. AF310252, AAG32057.1;
--INSSP, P51977; 1835.
InterPro., IPR002056., Aldehyde-d-hydr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                   Glinka A., Delius H., Blumenstock C., Niehrs C.; "Combinatorial signalling by Xwnt-11 and Xnr3 in the organizer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 518;
Amphibia; Batrachia; Anura; Mesobatrachia, Eipoidea, Fipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1ndels
                                                                                                                                                                                                                                                                                                                                                                                                                                         518 AA; 56658 MW; DERER123D463BEE3 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 1805, DB 13,
; Pred. No. 8.2e-138;
64; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                         Interfector Annual Promise Property aldedh: 1. PROSITE; PS00171; ALDEHYDE_DEHYDR_CYS: 1. PROSITE; PS00170; ALDEHYDE_DEHYDR_GLU: 1.
                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSOOK87: ALDEHYDE_DEHYDP_GLU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9PWJ3;
01-MAY-2000 (TrEMBLrol 13, Created)
                                                                                                                                                                                                           MEDI.INE=21152889; PubMed-11231062;
                                                                                   MEDLINE=97177558; Pubmed=9025074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484 OAYTEVKTVTVKVPOKN 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.88;
68.08;
                                                                                                                                                       Mech. Dev 60-221-231(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 68.09
Matches 338; Conservative
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                  Xenopodinae; Xenopus
                                                                                                                                                                                        SEQUENCE FROM N A.
                                                                  SEQUENCE FROM N.A.
                             NORI_TAXID-8355;
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                                                                                                                                        epithelium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 VPAPNQQPEVFCNQTFINNEWHDAVSRKTFFPTVNPSTGEVIOQVAEGDKEDVDKAREGRP 68
                                                                                                                                                                                                                                                                                                                                                                           Yamauchi K., Nakajima J., Hayashi H., Horiuchi P., Tata J.P.;
"Kendeus cytustic thytoid hormone binding protein (POTRP) is aldehyde dehydrogenase catalyzing the formation of retinoic acid.";
J. Blod. Chem. 274.8460-8469(1999).
- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
EMBL. AB016718, BAA76412.1,
- HSSP: P51977; 18XS.
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                                                                                                                                         Eukaryota, Metazoa, Chordata, Craníáta, Vertebrata, Euteleostomi,
Amphibia, Ratrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 5%; Score 1798; DB 13; Length 502; 67,3%; Pred, No. 2,9e-137;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01 MAR 2002 (TrEMBLrel. 20, Last annotation update)
01 MAY-2600 (ILEMBLE). 13, Last sequence update)
MAK-2002 (TrEMBLE). 20, Last annotation update)
Aldehyde dehydrogenase class 1 (EC 1.2.1.3).
Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                  Xenopodinae; Xenopus.
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SEQUENCE FROM N.A.
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                                                      NCB1_Tax1D=7955;
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                                             Cyprinidae;
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                                                                                           Eukaryota; Metazoa; Chordata, Craniála; Vertebratu, Buteleustumi,
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 502;
                                                                                                                                                                                                                                                                                Indels
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01-DEC-2001 (TYEMBLrel, 19, Greated)
01-DEC-2001 (TYEMBLrel, 19, Last Sequence update)
                                                                                                                                                                                                                                                          68.3%; Score 1793; DB 13;
67.1%; Pred. No. 7.4e-137;
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                                                                                                                                                                                                                                                                               67; Mismatches
                                                                                                                                                                                         Pfam, PF00171; aldedh. 1
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                 InterPro; IPR002086; Aldehyde_dehydr.
                     Xenopus laevis (African clawed frog)
  Aldehyde dehydrogenase (EC 1.2.1.3).
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Retinaldehyde dehydrogenase type 2.
                                                                                                                                                                                                                                                                               Matches 330, Conservative
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                                                     Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                     Hest Local Similarity
                                                                                                                                                                        ; 1BXS.
                                                                                  SEQUENCE FROM N.A.
                                                               NCB1_TaxID=8355;
                                                                                                                                                                                                                           Oxidoreductase.
                                                                                                                                                                        HSSP; P51977
                                                                                                                                                                                                                                      SECUENCE
                                                                                                                                                                                                                                                           Query Match
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64 REGREGAFQLGSPWRRMDASHSCHLUNKLADLLERDRIYLAALELLUNGRPYVISYLVDL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 DMVLKCLRYYAGWADKYHGKTTP11GOPFSYTRHEPVGVCGQTTPWNFPLLAMQAWKLGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 - JAGSPTFVQEDTYDEFVVPSVAPAKSRVVGNPFDSRTFQGQQDPFTQFKFLLGYTNFGRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE-21543521; PubMed 11548558; Begemann G. Schilling T.E., Kauch G. J., Geisler K., Indham P.W.; Begemann G., Schilling T.E., Kauch G. J., Geisler K., Indham P.W.; "The zebasish neckless matation reveals a requirement for PALDH2 in mesodermal signals that pattern the hindbrain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sept.
Brachydanio rerio (Zebralish) (Zebra danio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, estariophysi, Cypriniformes,
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                                                                                                                                                                                                                                                                                                                                                                    *! SIMILARITY, BELONGS TO THE ALDERYDE DEHYDROGENASES FAMILY.
EMBL: AF339837; AALO0899.1; .
InterPro: IPR002086; Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.68; Score 1786; DR 13; Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 AA; 56515 MW; 2060451617E8E086 CR054;
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01-JON-2002 (TFEMBLACE, 21, Last aequence update)
01-JUN-2002 (TFEMBLACE, 21, Last annotation update)
Retinaldehyde dehydrogenase 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSTEE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_L.
PROSTEE: PS00687; ALDEHYDE_DEHYDR_CIU; UNKNOWN_2.
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66.
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                                                                                                                                                                                                                                                                                                                                             Development 128:3081-3094(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00171; aldedh;
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441 TEYGLAAAVFTRDISKAMTISAAVQAGTVWINCYNALSCQCPFGGFKMSGNGRELGEIGL 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 VQAAKSAFSLGSVWKKMDASEKGKLLFKLADLVEKDSAYLATLESLDSGKPFLPCFFVDL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 DMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHFPVGVGGQIIPWNFPLLMQAWKLGPA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 LATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTGSTEIGRVIQVAAGSSNLKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQCC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 FIGSTEVGKLIQEAAGKSNLKRVTLELGGKSPNIIFADADFELALEQAHQGVFFNNGQCC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 CAGSRTFVQEDIYDEFVVRSVARAKSRVVGNPFDSKTEQGPQVDETQFKKILGYINTGKQ 363
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                                                                                                                                                                                                                                                                                                                                                                              4 AATOAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAFGDKEDVDKA 63
                                                                                                                                                                                                                                                                                                                                                                                                                  21 ASLHLMPSPVPNPEIKYTKIFINNEWHDSVSGKVFHTYNPATGEKICDVQEADKADVDKA 80
                                                                                                                                                                                       pre-segmentation stages to pattern the anterior-posterior axis of the CNS and to induce a pectoral fin bud.";
                                                                                                                                                                     "Retinoic acid signalling in the zebrafish embryo is necessary during
                                                                                                  Grandel H., Lun K., Pauch G.-J., Phinn M., Piotrowski T., Houart C.,
Sordino P., Kuechler A.M., Schulte-Merker S., Geisler R., Holder N.,
Wilson S.W., Brand M.;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata: Euteleustomi;
Actinopterygii; Neopterygii: Teleostei; Ostariophysi; Cypriniformes;
Eukaryota, Metaassa, Chordata, Craniata, Vertebrata, Euteleostomi,
Artin-prepai, Ne-sterggii, Teleostel, Ostariophysi, Oprificioums,
Cyprinidae, Danio.
NCBL_FaxID=7955,
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                                                                                                                                                                                                                                                                                                 67.7%; Score 1777; DB 13; Length 518; 66.7%; Pred No. 1 50-135; tive 65, Mismatches 100, Indels 0
                                                                                                                                                                                                                                          EMBE. AF288764: AAR83071.2; -.
SEQUENCE 518 AA; 56537 MW; FU677A30P77974EA CRC64;
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20, Last annotation update)
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01-MAR-2002 (TremBirel, 20,
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                                                                                                                                                                                                                                                                                                                                         331, Conservative
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                                                                                            SEQUENCE FROM N.A. Grandel H , Lun K
                                                                                                                                                                                                                                                                                                                       Local Similarity
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Tanguay R.L., Pappa A., Vasilion V.;

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81 VQAARSAFSEGSVWHKMIASERGKELEKKLAULVEKUSAYLAILESEUSGKPFI.PGFFVUI, 140
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                                                                                                                                                                                                                                                                                                                                                                                                                              124 DMVLKELPYYAGWAFKYHGKTIFIFGEPSYTEHEPVRVERFIIPWNEFILMQAWKIGPA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 LATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVA 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 CAGSPTEVQEDIYDEEVVRSVARAKSRVVGNPFDSKTEQGDQVDFTQFKKILGYIN19KQ 363
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                                                                                                                                                                                                                                                                                                                21 ASCHEMPSEVENPETKYTKIFINNEWHUSVSGKVEHTYNEATGEKICEVÇESDKADVDKA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIGSTEIGRVIQVAAGSSNLKRVTLELGGKSFNIIMSDADMDWAVEQAHFALFFNQGQCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 TAGSPIFVEEPIYDEFVPASVERAQPHKVGNPFDPTTEHGPQVSFFQQPPVLELIQSGIT
                                                                                                                                                                                                                                           Gaps
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"characterization of the sobrafish aldehyde dehydrogenase 1A2.";
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             Submitted (PGT. 1600) to the EMBLYGenbank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
EMBL; AF315691; AAL26232.1; -.
                                                                                                                                                                                                      Length 518;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                               518 AA; 56579 MW; A4F08D06A8F19A2B CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01 MAR-2002 (TrEMRLrel. 20, Last sequence opdate)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                  h 67.5%; Score 1772; DB 13; Similarity 66.5%; Fred. No. 3.9e-135; 30, Conservative 65; Mismatches 101,
                                                                                      Pfam; PF00171; aldedh; 1.
PPOSITE; PS00070; ALDEHYDE_DEHYDP_CYS; UNKNOWN_1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU: UNKNOWN_2.
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                                                                    IPR002086; Aldehyde_dehydr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical 55.1 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               501 KEYLELKILTMKMSGK 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                 Oxidoreductase
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                                                                                                                                                                                                                                       330,
                                                                        InterPro;
                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                    Query Match
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73 LGSPWRRMDASHSGRILLNRLADLIERDRTYLAALETLDNGKPYVISYLVDLDMVLKCLRY 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 YAGWADKYHCKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKLGPALATGNVVVM 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 KVAEQTPLTALYVANI.IKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVAFTGSTEIGR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 VIQVAAGSSNIKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQCCCAGSRTFVQ 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 IVMKAAARSNVKKVTLELGGKSPNTTFADAPLNDSVHQANHGLFFNGGGCCCAGSRTFVE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 EDIYDEFVVRSVARAKSRVVGNPFDSKTEQGPQVDETQFKKII.GYINTGKQEGAKIL.CGG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 GKIYDDFVARSKELAEKAVIGDPFDLKTTQGPQVDGKQVETTLKYTAAGKKL63AQLV1GG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 GIAADRGYFIQPTVFGDVQDGMTIAKELFGPVMQILKFKTIEEVVGRANNSTYGLAAAV 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433 FTKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGEYGLQAYTEVKTV 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 AKHGDQGHFVKPT1FANVKDQMT1AQEE1FGPVMT11RFDTMEELVEKANNT1YGLAAGV 441
                                                                                                                                                                                                                                                                                                                                                                                                                         13 NQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVDKAREGRPGAFQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aldehyde dehydrogenase (omega-crystallin).
Placopecten magellanicus (Sea scallop).
Fukaryota: Metassa; Mcllusca, Bivalvia, Pteriomorphia, Fetlincida,
Pectinoidea; Pectinidae; Placopecten.
                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                       67.0%; Score 1760; DB 5; Length 510; 67.8%; Pred. No. 3 6e-134;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                 "The sequence of C elegans cosmid F54DB ";
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                    Submitted (NOV-2001) to the EMRL/GenBank/DDRI databases
                                                                                                                                                                                                                                                                                                                      510 AA; 55059 MW; 5995847747AU23B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 AA
                                                                                                                                                                                                                                                                                                                                                                                         70; Mismatches
                                                                                                                                                                                                                                                Pfam; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDE_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDE_GLU; 1.
                                                                                                                                                                                                                                      InterPro; IPR002086; Aldehyde_dehydr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                    EMBL; U12966; AAA20615.3;
                                                                                                                                                                                                                                                                                                                                                                                     Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                    "Direct Submission ";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              502 TIKVPOKN 509
                                                                                                                                                                                                                                                                                                    Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                               The sequence of C
                                                                                                                                                                                                                    P05041: 10W3
                                 STRAIN-BRISTOL N2;
                                                                                                                 SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
              SEQUENCE FROM N.A.
                                                                                                                                                    Waterston R.;
                                                   Bentley D.;
                                                                                                                                                                                                                                                                                                                         SECUENCE
                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 OLGSPWRRMDASHSGRIJUNLADI.LERDRITYLAALETLONGKPYVISYLVDI.DMVLKT.R 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 YYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGOLLPWNFPLLMOAWKLGPALATGNVVV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 MKVAEQTELTALYVANLIKEASSEPPGVVNIVESPSPTASAATASSEEVEKVAETSSTETG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>_</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 GEBLYPPEVVPSVAPAKSRVVGNPFDSKTEQGPQVDETGFKKILGYINTGKQEGAKLLCG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.2.2. GGTAADRGYFTOPTVEGDVOIXGMTTAKEETFGPVMOTLKFKTTEEVVGRANNSTYGLAAA 4.3.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : [1]:[] [ ::[][][]] ::[][][]] 424 [CTRD-TDKVMTYSSQVKACTVWVNSFNVFGQQPPGGPKMSGTGRELGESGLQQVSEVKT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432. VETKULDKANYUSQALQACI VWVNCYDVEGADAREGAYAMSGAGEGGETGEGAYTEVKT 491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 BIKNPEIRYKGLEINNEWVNAASGKTEPVINPATGKKIVFIQEGDKADVDKAVAAAKKAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 QIVMQAAARTNLKRVTLELGGKSPNVVESDADLDTAVEACHNGLEFNMGGCGCAASKTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12. PNGQPEVENN_TETNNEWHIAVSRETEPTVNPSTGEVT/QVAEGI/FEDVI/KAPEGRD/TAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 RVIQVAAGSSNIKRVTI.ELGGKSPNIIMSDADMDWAVEQAHFALFFNQGGCCCAGSRTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                    Kozmik P., Platigorsky J.;
"Identification and cloning of the major scallop eye erystallin.";
Submitted (MAY-1999) to the EMBL/GenBank/NIB3 databases.
                                                                                                                                                                                                                                                    J. Biol. Chem. 0:0-0(2000).
-i- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.5%; Score 1745; DB 5; Length 492; 67.0%; Pred. No. 5.6e-143; tive 62; Mismatches 99; Indels
                                                                                                                                                                                Piatigorsky J., Kozmik Z., Horwitz J., Dinq L., Carosa E.,
Poblson W.G., Steinbach P.J., Tamm E.R. and Corner of Mongra Crystallin of the Scallop Lens: A Dimeric Aldehyde
Pohydrogenase Class 1/2 Encyme Crystallin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  492 AA; 53669 MW; C612886FBAF2BBD0 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOL AA
                                                                                                                                                                                                                                                                                                                                           InterFro, IFRU-2086; Aldehyde_dehydr.
Pfam, PF00171; aldedh. 1.
PROSTE, PS00070; ALDEHYDE_DEHYDE_CYS;
PROSTE; PS00687; ALDEHYDE_DEHYDE_GIU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF148508; AAF74122.1;
EMBL; AF175578; AAG09204.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 67.0%
Matches 327; Conservative
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                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              HSSP; P05091; 1CW3
                                SEQUENCE FROM N.A.
NCBI_TaxID-6577;
                                                                                                                                                               FISSUE-FYE LENS;
                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase.
                                                      LISSUE-EYE;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 VDLDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LDVEISIKALQYFAGWADKIHGQTIPSPGNIFTYTPPRFIGVGGQIIPWNGPLIFTWKL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 ÖCCCAĞSRIFVÇEDIYDEFVVRSVARAKSRVVGNPFDSRIEĞGPQVDETQFKKILGYINT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 QICVAASRLEVEESIYDEFVRRSVERAKKYILGNPLNSGINQGPQIDKEQHNKILGLIES 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GKQEGAKLIZGGGTIAADHGYFTQPTVFGDVQDGMTIAKEEIFGPVMQILKFKTIEEVVGR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 ANNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELIGE 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSSPAQPAVPAPLANLKIQHTKIFINNEWHDSVSSKKFPVLNPATEEVICHVEEGDKADV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSAAATQAVPAPNÇQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDV 60
                                                                                                                    Mus musculus (Mouse).
Eukaryola; Metazoa; Chordata; Craniata, Vertebrata; Eutelenstomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                             Hsu L.C., Chang W.C., Yoshida A.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 66.4%; Score 1742; DB 11; Length 501; Local Similarity 65.4%; Pred. No. 1e-132; nes 327; Conservative 76; Mismatches 97, Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 AA; 54587 MW; 42DE97962799237E CHC64;
01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Aldehyde dehydrogenase Ahd-2-like. ALDH1A7 OR ALDH1A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE, PSO0070, ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PSO0687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1347050; Aldhla7.
InterPro; IPP^0020Rk; Aldehyde_dehydr.
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                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL; TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00171; aldedh; 1.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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Search completed: June 24, 2003, 10:17:09 Job time: 39.2679 secs

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Copyright (r) 1993 - 2003 Compugen 1.6d.
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OM protein - protein search, using sw model

June 24, 2003, 10-02:25 ; Search time 37.5254 Seconds (Without alignments) 1696 383 Million rell updates/sec Pun on:

US-09-830-751-6

1 MSVPVQHPMYIDGQFVTWRG..... ADGKHGLHGYLQTQVVYLQS 474 2446 Perfect score: Sednence:

BLOSUM62 Gapop 10 0 , Gapext 0 5 Scoring table:

908470 seqs, 133250620 residues Searched.

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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~	/SIDS2/grydata/geneseg/genesegp-emb1/AA1980.FAT:
	/SIDSE/gegdata/geneseg/genesegp-enh:/AAli81 [A]
3.	/SIDS2/gcgda+4/geneseg/genesegp-embl/AA1982 DAT
. 4	/SIDS2/gcgdata/geneseq/genesegp-embl/AA1983.DAT:
2:	/SIDS2/gcgdata/geneseg/genesegp-cmb1/AA1984.DAT:
. 9	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:
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16:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT
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20:	/SIDS2/gcgdata/geneseq/genesegp embl/AA1999.DAT
21.	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT
::	/SIDS2/gegdata/geneseg/geneseg.
53	/S1052/gegdata/geneseq/genesegp-emb1/AA2002.DAT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query				
No.	Score		Match Length DB	DB	ID	Description
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i Ca	2432	93.4	479	1 (1	AAU29333	2 22 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
3	1407			21	AAY81486	Pseudomonas putida
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S	931.5		479	(1) (7)	AAG82931	S. epidermidis ope
9	879 5	36.0		C1	AAIT33562	Pseudomonas acruati
7	873.5			C1	AAU34671	E. coli cellular p
8	858.5			C1 C1	AAU38454	Salmonella typhi c
σ.	827	33.8		2.1	AAG513F0	Arabidopsis thalia
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WP1, 2001-315988/33.

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AAG51348 AAG22558 AAR8729 AAR8729 AAG232550 AAG232550 AAG23148 AAG37064 AAG37064 AAG1709 AAG1709 AAG11709 AAG11700 AAG11700 AAG1700	AAU11705 AAU11707 AAU36239 AAV36413 ABP 401 ABP 401 AAU3609 AAU3609 AAU1364 AAU1364 AAU1364 AAU1364
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## ALIGNMENTS

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Aldehyde dehydrogenase, alycerol dehydratase, 3.8D, giycerol, foodstock, 3 hydroxyrreplonic and genetic engineering, glucose; besterial host, absorbable prosthering denice, surginal suture; beta-lactam; acrylic acid; trifluoromethylated alcohol; diol; polyhydroxyalkonate; copolymer; lactic acid.
                                                                       E. coli aldenyde dehydrogenase aldA protein sequence SEv ID No:6.
                                                                                                                                                                                                                                                                                                     (WISC ) WISCONSIN ALMMNI RES FOUND.
AAB74925 standard; Protein; 479 AA.
                                                                                                                                                                                                                                                                            990S-0151440.
                                                                                                                                                                                                                                                     30-AUG-2000; 2000W0-US23878.
                                                  26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                Suthers PF, Cameron DC,
                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                   WO200116346-A1.
                                                                                                                                                                                                                                                                            30 AUG-1999;
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                         AAB74925;
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                                                                                                                                                                                                                                                                                   1-typropriority and described an energy of the progress fermenting a recombinant microorganism in the presence of a source of glycerol (1) of glucose, where the microorganism: (i) expresses genes for non-native enzymes which catalyse the production of (3-HP) from (1), (ii) carries genetic constructions for the expression of a glycerol dehydratase (GDHT) and aldehyde dehydrogenase (ADH) capable of catalysing the production of (3-HP) from (1), or (iii) carries a genetic construct which expresses the dhaB gene from Klabsiella pneumoniae and a gene for an ADH capable of catalysing the production of (3-HP) from (1), 3-HP is a monomer, and is useful e.g. in the production of absorbable prosthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVNRLGEAMQAVOFGNPAERNDIAMGPLINAAALEPVEQKVAPAVEEGAPVAFGGKAVEG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    devices and surgical sutures or for incorporation into beta-lactams, production of acrylic acid or formation of trifluoromethylated alrehols
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Incorporation of genes encoding two enzymes makes the host organisms able to produce (3-HP) from (1). The biotechnological method of preparing (3-HP) is potentially cheaper than chemical synthesis. The present sequence represents the E. coli aldehyde debydrogenase aldA, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
3\text{-Hydroxypropionic acid preparation, for use e.g. as monomer, by fermenting recombinant microorganisms expressing genes for suitable enzymes in the presence of glycerol or glucose -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or diols, polyhydroxyalkonates and copolymers with lactic acid.
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                                                                                                                                                                                                                                                        The present invention describes a method for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 2446; DB 22; Length 479; 100.0%; Pred. No. 3.6e-217;
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                                                                                                                                                                    Claim 5; Page 39-41; 63pp; English.
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nes 479; Conserv
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ò qq ò q δ q òγ g ò q ò qq ò ò Db

q ò 2 à â ò d ć q 5 6 ć 361 KGYYYPPTLLLDVRQEMSIMHETFGPVLPVVAFDTLEDAISMANDSDYGLISSIYTONL 420 421 NVAMKAIKGLKFGETYINRENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQTQVVYLQS 479 AAU29333 standard; Protein; 479 AA. (first entry) 18-DEC-2001 AAU2933; RESULT 2 AAU29333

The invention relates to a method of identifying compounds that modulate a newly identified mar regulated (NIME) pelypetide activity. The method comprises contacting an NIME polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulate the activity or expression of the polypeptide, and selecting the of microbial infections, and in sereening for modulators of NIME expression and activity. These modulators can be used to reduce the infection, the microbe on a surface, and the virtulence of a microbe in a subject suffering from an infection. AAAD3429-AAAD3479 represent \ \ \ \ \ ÷ 007 97 361 KGYYYPPTILLDDVRQEMSIMHEETFGIVLPVVAFDTIJEGAISMANGSPYGLESSIYIGNI. 420 61 FALPATERASWERKISAGTPERASFISALIVEEGGRIQQLAEVEVAFTADYIDYMAEWAR 120 361 KGYYYPPTLLLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSSIYTONL 420 Ē 1 MSVPVQHPMYIDGQFVTWRGDAWIDVVNPATEAVISKIPDGQAEDARKAIDAAERAQPEW 121 RYEGELIQSDRPGENILLEKRALGVTTGILPWNFTFFLIARKMAPALLTGNTIVIKPSEF 121 BYEGELGSURPCENTILERRALOVITCHILITETTILETTILETTILITETTILETTI 1 MSVPVQHPMYIDGQFVTWRGDAWIDVVNPATEAVISHIPRGDAEDARKAIDAAERAQPEW 181 TTNNATAPAKTVDETGLPRGVFNLVLGRGETVGOELAGNPRVAMVSMTGSVSAGEKTMAT 241 AAKNITKVCLELGGKAPAIVMDDADLELAVKAIVDSRVINSGOV°N°AERVYVOKGIYDG §ÜL FYNKLISEAMQAVQEGNPAERNPTAMIPLINAANIERVEQKVAKAVEEGARVAFGGRAVEG 191 TPNNAIAFAKIVDEIGI PROVPNIJUGRGPTVÖQFIJAGNPKVAMVSMIGSVSAGPKIMAT Identifying compounds that modulate a newly identified man requiated polypeptide activity, useful as antimierobial compounds, involves contacting the polypeptide with a test compound. mar requiated polypeptide; NIMR; microlial infection; antibacterial 99.4%; Score 2432; B8 22; Length 479; 99.6%; Pred. No. 7.2e 216; Live 0; Mismatches 2; Indels 0 Disclosure; Page 160-161; 526pp; English. Novel mar requlated protein (NIMR) #5 Alekshun MN; 10-MAR-ZHOU; ZÖĞÖHS-188362P. 08-MAR 2001, 2001W0-US07478 Best Local Similarity 99.6 Matches 477; Conservative Levy SB, Barbosa TM, (TUFI ) TUFTS COLLEGE. WPI: 2001-602769/68. 479 AA; Escherichia coli. N-PSDB; AAS46235 W0200170776-A2 27-SFP-2001. Sedneuce Query Match

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70 SWLRKISAGIRERASEISALIVEFGSKIQQLAEVEVAFTAFYIFYMAEWARFYEGEIIQS 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 KIVPELGI PROVENLVI GROPTVOQELAGNEKVAMVSMTGSVSAGEKIMATAAKNI TKVÇ. 249
                                                                                                                                                                                                                                                                                             Aldehyde dehydrogenase, NAD+ dependent, oxidation, 2·oxoaldehyde;
hydroxypyruvaldehyde; qlyceraldehyde; methylglyoxal; hydroxypyruvic acid.
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ان
                  9 YIDNAFVPSEG--LIEVYNPANAQLLGRVPESPVEQVERAIAAAKKAQKGWAAKPAIEKA 66
421 NVAMKAIKGLKFGETYINKENFEAMQSFHAGWKKSGIGGADGKHGIRGYL@T@VVYRLGS 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New aldehyde dehydrogenase gene - for enzymatic synthesis of serine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 YIDGGEVTWRGDAWIDVVNEATHAVISKIEL®QAEDARKAIDAAEPAGPEWEALPAIHEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.5%; Score 1407; DB 21, Length 476; 58.9%; Pred. No. 3.9e-121; Live 77; Mismatches 112, indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthesis of serine or cysteine from glycerol.
                                                                                                                                                                                                                                                      Pseudomonas putida aldehyde dehydrogenase.
                                                                                                                                    AAY81486 standard; Protein; 476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 8-9; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0236691.
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                                                                                                                                                                                                                   (first cutry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-249678/22.
                                                                                                                                                                                                                                                                                                                                                       Pseudomonas putida.
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Hes 277; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 AA;
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                                                                                                                                                                                                                 03-JUL-2000
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                                                                                                                                                                         AAY81486;
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                                                                                               RESULT 3
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18.7 REVAETHEPAGVENVVQGRGASVGHGLSSHAGITH VSETGSVATGAREMAAAAFNTERN 246
                                   250 LELGGKAPALVMDDADLELAVKATVDSPVTNSGQVDVARREVYVQKGTYDQFVNFLGEAM 309
                                                                   247 LELGGRAPAIVLADADLDLATRAIVASPVINTGOVONOAEPVYVARKVADAFVDRVAQAM 306
                                                                                                                                                                           369 LLLDVRQEMSIMHEETFGPVLPVVAFUTLEDAISMANDSDYGLISSIYTÖNLNVAMKAIK 428
                                                                                                                                                                                                             367 VLA-CAADMEIMRKEIFGPVLPIQVVVDLDEAIALANDSEYGLISSLYTRDLNAALKAIR 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               frame (ORE) nucleic acid sequences which encode the amino acid sequences given in ABE-5124 to ABE-3790. The S. epidermidis sequences nave antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to seriem for compounds abic to interfere with the S. epidermidis life rycle or inhibit S. epidermidis infection.

N. The sequence data for this pricet did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
                                                                                                        31.0 DAVQEGNPAERNDIAMSPLINAAALEEVEQKVARAVEEGARVAFGGKAVE-GRGYYYPPT
                                                                                                                           Novel isolated nachers acid encoding a Starbyleococcus epidermidis
polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4388.
                                                                                                                                                                                                                                                                     429 GLKFGETYINRENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQTQVVYLQ 478
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<u>इ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID 4388; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                            ABP39543 standard; Protein; 493 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial, yene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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wes 181, Conserva
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69 ASWLRKISAGIRERASEISALIVEEGGKIQQLAEVEVAFTADYIDYMAEWARRYEGEIIQ 128
                                                                                                             84 AEHVKLLIPLLEKNRDETAQLYVKEQGKTLAQAYGETDKSISFIDYMTSLSMSDKGRVLQ 143
                                                                                                                                                   SDRPGENILLFKRALGVITGILPWNFPFFLIARKMAPALLIGNIIVIKPSEFIINNAIAF 188
                                                                                                                                                                       189 AKIVDEIGLPRGVFNLVLGRGETVGQELAGNPKVAMVSMTGSVSAGEKIMATAAKNITKV 248
                                                                                                                                                                                                                                                               204. AELFRASTIPAGLFQ1VPGTGETVGTGLASHKD1Q1.1St.TGSMFAGKSVYENAAQTVKKV-263
                                                                                                                                                                                                                                                                                                   249 CLELGGKAPAIVMDDADLELAVKAIVDSRVINSGQVCNCAERVYVQKGIYDQFVNKLGEA 308
                                                                                                                                                                                                                                                                                                                                                                               309 MQAVQFGNPAERNDTAMGPLINAAALEPVEQKVAPAVEEGAPVAFGGKAVEGKGYYYPPT 368
                                                                                                                                                                                                                                                                                                                                                                                                                 MKSLIVGDPFDEN-TDYGAIINQKQLDSIHEKVQDAIKNGAILMTGGHQLKRHGFFYAPF 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 LLLDVKQEMSIMHEETFGPVLPVVAFDTLEDA;SMANDSDYGLTSSIYTQNLNVAMKAIK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 VLDNVRKDYNVFKDF1FCPVLAITTYPPFEQVIEDANDTNAGLSSYIFSENLTEVMTATE 442
MYIDGOFVTWRGDAWIDVVNPATEAVISRIPFGQAEDAKKAIGAAEEAQPEWEALPAIER 68
                                 24 LFINNEPIESQSKETMDVINPATGEAFDTITLATEEEVNDALEKSQQAQLEWERVPQPTR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (1) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (1) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH52304 to AAH53970 represent nucleic acids (1) encoding polypeptides
                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. epidermidis open reading frame protein sequence SEQ ID NO:2956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     429 GLKEGPTYINPENFEAMOGFHAGWRKSGIGGADGKHGLHGYLQTQVVYLQ 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Page 773; 2188pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG82931 standard; Protein; 479 AA
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129 SERPGENTILLERRALGVITGTTPWNEPEFLLARRMAPALLTGNTTVIRESEFTTNNATAF TRB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 NSIANETIQIINKPIGVTAGIVPWNAPILVLMRKVIPAIVTGSSVVIAPSEETTLETLEL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSSIYTONLNVAMKAIK 42H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 VIDNVPKDDNVPKDELFGPVIALTTYRDLEQVIEDANDTNAGISSYLFSENIJEVMTATE 428
          priypertides. The priypertides (1) (angles on test and state the barterial priyettides. The priypertides (1) (angles on the barterial by peptides may also be used to raise antibodies against the barterial the polypeptides may also be used to assay for other inhibitors of their activity and therefore identity compounds that may be used for the treatment of S epidermidis infections, a g endersold for the polymerlectide sequences from the present invention. AAH55091 to AAH5509 represent objectide sequences and primers which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                               N.B. The present invention specifically cialins all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even the sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4474.
containing them which are used to produce hosts cells which express the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 MYIDGGFVTWKGDAWIDVVNPATEAVISRIPDGGAEDARKAIDAAERAQPEWEALPAIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LETINNEFTESOSKETMDVINPATGEAEDTTTLATEEEVNDATEKSOQAQLEWEKVPOPTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 CLELGGKAPAIVMDDADLELAVKAIVDSRVINSGOVCNCAERVYVOKGIYDQFVNRLGEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                  38.18, acore 931.5; Da 22; Length 479;
38.58; Pred. No. 3.5e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 109; Mismatches 179; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 479 AA;
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                                                                                                                                                                                                                                                                  The invention relates to antisense inhibitors of genes essential to genes, their use in the discovery of novel antibiotics, the essential genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The probatycles used are Escherichia coll, Staphylococcus areas. Salmonella typhi, Klebsiella promominar, Pseudomenas aeruginosa and Enterococcus faccalis. The promominary, Pseudomenas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids which are required for coll proliferation in a wide variety of organisms. The present sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 SWLPKISAGIPERASEISALIVEEGGKIQQLAFVEVAFTALYIDYMAEWARRYEGEILQS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKLRRWFDLMIENQDDLARLMTIEQGKPLAEAKGEIAYAASFLEWFGEEAKRIYGDTIPG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 KIVDEIGLPRGVFNLVLGRGFTVGGELAGNPKVAMVSMTGSVSAGEKIMATAAKNITKVC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 ELAERAGIPKGVFSVVIGSAGEVGGELTSNPIVRKLIFTGSTEIGRQLMAECAQDIKKVS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 LELGGNAPFIVFDDADLDAAVEGALISKYRNNGQTCVCANRLYVQLGVYDAFVDKLKAAV 31.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 AKLNIGNGLEAG-VTTGPLIDAKAVAKVEEHIADAVSKGAKVVSGGKPHALGGTFFEPT1 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 DRPGENILLFKRALGVTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNAIAFA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LELGGKAPATVMEDAFLELAVKATVDSEVINSGLVONGAREVYVQKGIYDQFVNELGEAM 3U9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 YVDGAWVDADNGQTIKVNNPATGEIIGSVPKMGAAETRPATEAADKALPAWPALTAKEPA 73
                                                                                                                                                                                                                                           Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 483;
                                                                                                                                                                                                                                                                                                                                                             New polynucleotides for the identification and development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                    antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           essential prokaryotic cellular proliferation protein.
Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.0%; Score 879.5; DB 22; 39.3%; Prod. No. 2.2e-72; ive 96, Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Seq ID No 5058; 511pp; English.
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200008-253625P.
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2001US-269308P.
OH [ROSH OM [DOZ
                                       Junior Philotapp
                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
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                                                                                                                                                                                                                                                          Xu HH;
                                                                                                                                                                                                                                                                                                WPI; 2001-611495,770
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                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS51421.
                                                                                                                                                                                                                                       Haselbeck R,
  21-MAR-2001;
                                                                                                                                                           16-FEB-2001;
                                                                                                                                                                                                                                                            Yamamoto RT,
                                                        23-MAY-2000;
26-MAY-2000;
                                          21 - MAP - 2000 c
                                                                                                  23-001-2400
                                                                                                                   27 - NOV - 2500,
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programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliteration in a wide variety of organisms. The present sequence represents an essential prokatyotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                    370 LLEVRQEMSIMHEETPGFVLFVVAFETLEBAISMANDSPYGUTSSIVTQALAVAMKAIKG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prokaryotic cellular productation, their use in identifying the genes, their use in the discovery of novel antibotics, the essential genes, themselves and the enough proteins. The prokaryotic staphylococcus amenas, salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Entercoccus faecalis. The invention is also usefui for the identification of potential new targets for antibictic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express those proteins, and to obtain antibodies capable of binding to the expressed proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynopleotides for the identification and development of
antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                    433 LFYGMVGINTGIJSNFVAPFGGIKASGIJGREGSKYGIEDYLEIKYLCL 480
                                                                                                                                        430 EKFRETYTNFFNFFAMOGFHAGWFKSGIGGAFGKHGLHGYLQTQVVYL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic collular proliforation protein;
antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                     AAU34671 standard; Protein; 482 AA.
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23-MAY-2000;
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71 WERKISAGIRERASEISALIVEEGGKIQQLAEVEVAFTANYIDYMAEWAPPYEGEI1QSD 130
                                                                                                                                                                  75 ILRNWFNLMMEHQDDLARLMTLEQGKPLAEAKGEISYAASFIEWFAEEGKRIYGDTIFGH 134
                                                                                                                                                                                                  131 RPGENILLFKRALGVTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNAIAFAK 190
                                                                                                                                                                                                                                                                  IVDEIGLPRGVPNLVLGRGETVGQELAGNPKVAMVSMTGSVSAGEKIMATAAKNITKVCL 250
                                                                                                                                                                                                                                                                                                 195 LAIRAGVPAGVFNVVTGSAGAVGNELTSNPLVRKLSFTGSTETGRULMEGCAKDIKKVSL 254
                                                                                                                                                                                                                                                                                                                                FLGGKAPAIVMDDADLELAVKAIVDSRVINSGQVCNCAERVYVQKGIYDQFVNRLGEAMQ 310
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                                                                                                                                                                                                                       11 IDGQEVIWRGDAWIDVVNPATEAVISKIPDGQAEDAKKAIDAAERAQPEWEALPAIERAS 70
                                                                                                  15 INGEWLDANNGEATOVTNPANGDKLGSVPKMGADETRAAIDAANRALPAWRALTAKERAT 74
                                     l, Gaps
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     Length 482;
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                                  91; Mismatches 187, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431 KFGETYINRENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQ 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense: prokaryotic cellular proliferation protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhi cellular proliferation protein #345
 35.7%; Score 873.5; DB 22; 39.5%; Pred. No. 8e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibiotic; antibacterial; drug design,
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2000US-257931P.
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                                  182; Conservative
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Query Match
Best Local Similarity
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                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 BQTDKRLLVIKQPIGVTAALTHWNFPSAMITEKAGPALAAGCTMVLKPASQTPESALALA 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 LLDVROEMSTMHEETFGPVL2VVAFULLEDA (SMANDSDYGG) SSTS (ONLNVAMKATK), 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 IADVEDNAKVARIDTEGETAFUTIGESDEABVIRQANGGGGAAYTYAEFLGBYFRYGGA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 NILKRWFNLMMEHQDDLARLMTLEQGKPLAEAKGETSYAASFTEWFAEEGKRTYGDTLFG 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli, Staphyloroccus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus tarcalis. The invention is also useful for the identification of potential new taracts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for antibiotic development. The antisense markete acids can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The proteins can be used to screen compounds in rational drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
                                                                                                                                                                                                                                                                       prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 YIDGQFVTWRGDAWIDVVNPATEAVISRIPDSQAEDARKAIDAAERAQPEWEALPAIERA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 GAVOFGNPAERNDIAMGPLINAAALERVEOKVARAVEEGARVAFGGKAVFGKGYYYPPTLL
                                                                                                                                                                                                                                             The invention relates to antisense inhibitors of genes essential to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a wide variety of organisms. The present sequence represents an essential problem profile profile. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
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                                                               New polynucleotides for the identification and development of
                                                                                                       antibiotics, comprise sequences of antisense muckeic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91; Mismatches 189; Indels
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                                                                                                                                                                          Example 3; Seq 1D No 14047; 511pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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N-PSDH; AAS56313.
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for homolog
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AAG51350 standard; Protein; 495 AA

AAG51350

18-00T-2000 (first entry)

AAG51350;

us-09-830-751-6.rag

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20-JUL-
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                 Arabidopsis thallada protein flagment SEQ ID NO: 65163.
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990S-0139462.
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990S-0139750.
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990S-0134941.
990S-0135353.
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990S-0137528.
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99US-0138847.
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990S-012548.
990S-0126264.
990S-0126785.
990S-0127462.
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990S-012744.
990S-0129445.
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                                                                                                                                                                        2000FP-0301439
                                                                          termination sequence.
                                                                                                  Arabidopsis thaliana.
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05-MAR-1999,
05-MAR-1999,
25-MAR-1999,
01-APR-1999,
01-APR-1999,
01-APR-1999,
16-APR-1999,
16-APR-1999,
16-APR-1999,
19-APR-1999,
19-APR-1999,
19-APR-1999,
10-MAY-1999,
14-MAY-1999,
16-JUN-1999,
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99US-0149992. 99US-0149930. 99US-0150566. 99US-0150884. 99US-0151065. 99US-0151065. 990S-0149175. 990S-0149426. 990S-0149722. 990S-0149723. 99US-0148341. 99US-0148565. 99US-0148684. 99US-0147038. 99US-0147204. 99US-0147302. 990S-0145276. 990S-0145913. 990S-0145918. 990S-0145919. 99US-0146386. 99US-0146388. 99US-0146389. 99US-0145192. 99US-0145145. 99US-0145218. 99US-0145224. 9905 - 014433 9905 - 014433 9905 - 0144334 9905 - 014435 9905 - 0144435 9905 - 0144814 9905 - 0144814 9905 - 0144814 99US-0148319 99US-0149368 99US-0147192 99US-0147260 99US-0147303. 99US-0147416. 99115-0147935 99US-0147493 99US-0148171 990S-0141842. 990S-0142055. 990S-0142055. 990S-0142390. 990S-0142302. 990S-0142320. 990S-014372. 990S-0143742. 990S-01444005. 99US-01440R6. 99US-0144325. 99US-0144331. 99US-0145088. 99US-0145087 99US-0139817. 99US-0139899. 99US-0140353. 99US-0140823 99US-0140991. 99US-0141287. 99US-0140354. 16-AUG-1999; 17-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 23-AUG-1999; 23-AUG-1999; 25-AUG-1999; 25-AUG-1999; 27-AUG-1999; 27-AUG-1999; 11: AUG-1999; 12-AUG-1999; 13-AUG-1999; 13-AUG-1999; 16-AUG-1999; 65-A0G-1999; 66-A0G-1999; 66-A0G-1999; 09-A0G-1999; 10-A0G-1999; 11: A0G-1999; 04 - AUG-1999; 04 - AUG-1999; 05 - AUG-1999; 05 - AUG-1999; 06 - AUG-1999; 06 - AUG-1999; 0.70L-1999; 1-70L-1999; 21 - JUN - 1999; 22 - JUN - 1999; 23 - JUN - 1999; 23 - JUN - 1999; 24 - JUN - 1999; 29 - JUN - 1999; 30 - JUL - 1999; 01 - JUL - 1999; 02 - JUL - 1999; 03 - JUL - 1999; 04 - JUL - 1999; 12 - JUL - 1999; 13 - JUL - 1999; 14 - JUL - 1999; 16 - JUL - 1999; 16 - JUL - 1999; 16 - JUL - 1999; 17 - JUL - 1999; 18 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 1999; 1999; 1999; 02-AUG-1 02-AUG-1 02-AUG-1 03-AUG-1 23-JUL-1 26-JUL-1 19-JUL-1 23-JUL-

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AAG51349 standard; Protein; 528 AA.
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99US-0134370.
99US-0134768.
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990S-0123180,
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99US - 0134219.
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99US-0142484
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                                                                                                                 468 GYLQTQVVYL 477
                                                                                                                                  480 EYLEIKYVCL 489
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28 APR-1999,
40 APR-1999,
30 APR-1999,
05 - MAY-1999,
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-AFR-1999;
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-MAR-1999;
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-MAY - 1999;
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18-MAY-1999;
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                                                                                                                                                                                                121 GASFIEFYAEEAKRVYGDIIPPNLSDRRLLVLKQPVGVVGAITPWNFPLAMITRKVGPAD, 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 KAIDAAFRAQPEWEALPATERASWLEKISAGIRERASEISALIVEEGGKIQQLAEVEVAF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OR TADYIDYMAEWARRYEGETIQSDRPGENILLFKRALGVTTGILPWNFPFFLIARKMAPAL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 TGSVSAGEKTMATAAKNITKVCEREGGKAPAJVMDDADEELAVKAJVDSKVINSGOVCNC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 MYIDGQEVIWR------GDAWID-----VVNPATEAVISRIPDGQAEDAR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSMDAQSVSEKTIKSSGLLAFTQGLIGGKWLDSYDNKTIKVNNPATGELIADVACMGTKETN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.8%; Score 827; DB 21; Length 495; 37 8%; Pred. No. 1.7e-67;
                                990S-0152363.
990S-0153070.
990S-0153758.
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hybridisation assay, genetic Mapping; done expression control; promoter;
termination sequence.
                                                                       90; Mismatches 193; Indels 22; Caps
                                  33.8%; Score 827; DB 21; Length 528; 37.8%; Pred. No. 1.8e-67;
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                                                     Similarity 37.8%;
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115-AuG-1999

115-AuG-199
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      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay, genetic mapping; gene expression control; promoter; termination sequence.
                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 26911.
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990S - 0123548
990S - 0126264
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                  17-OCT-2000 (first entry)
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301 ANEVLVÇERSIYERFARAFSEAVÇKLEVSERSEFERSTIĞGELINDAAVOKVETEVQDAVSK 359
                                                                  348 GAPVAPGGKAVEGKGYYYPPTLLLDVPQEMSIMHERTPGPVLPVVAFDTLEDAISMANDS 407
                                                                                                                            420 IAGLAAYIPINSVQRSWRVEPALEYGLVGVNEGLISTEVAPFGGVKQSGLGREGSKYGMD 479
        241 FGSTAVGKKLMAAAAPTVKKVSLELGGNAPSIVPDDADLUVAVKGTLAAKFENSGGTOVC 300
                            288 AERVYVÕKGIYINGFVNPLGFAMQAVGPGNPARPNDTAMGPLINAAALERVEQKVARAVEE 347
                                                                                                         408 DYGLISSIYIQNLNVAMKAIKGLEFGETYINPENFEAM GEHAGWEFSGIGGADGKHGLH 467
                                                                                                                                                                                                                                                                                            Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana protein fragment SEQ ID NO: 26912.
AAC23559 standard; Protein; 493 AA.
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37.6%; Pred. No. 2 1e 67;
Live 91; Mismatches 193; Indels 22; Gaps
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143 SPFRILVIK⊋FVGIVGAITFWNFFLAMITRKVGFALASGCTVVVKFSELIPLIALAAAEL 202
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                                                                                                                                                                                                                                                                                                                                                                                                                          203 ALGAGVPEGALNVVMGNAFEIGDALLISPQVRKIIFIGSTAVGKKEMAAAAPIVKKVSLE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 LGGKAPAIVMDDADLELAVKAIVDSRVINSGOVCNCAERVYVOKGIYPOFVNRIGEAMOA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 VQFGNPAERNDIAMGPLINAAALERVEQKVARAVEEGARVAFGGKAVEGKGYYYPPTLLL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 DVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSS1Y1QNLNVAMKAIKGLK 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 LRKISAGIPEPASEISALIVEEGGKIQQLAEVEVAFTADYIDYMAEWAPPYEGEIIQSDP 131
                                                                                                                                                                                                                                                                  83 ERRWYDLLIAHKEELGÖLIILEÚGKPLKEAIGEVAYGASPIEYYAEEAKKVYGDIIPPNL 142
                                                                                                                                                                                                                                                                                                          132 PGENILLFKRALGUTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNAIAFAKI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 LEVGD-GFRDGTTQGPLINDAAVQKVETFVQDAVSKGAKIIIGGKRHSLGMTFYEPTVIR 381
                                                                                                                                                    20 GDAWID------VVNFATEAVISKIPDGQAEDAKKAIDAAERAQFEWEALPAIERASW 71
                                                                                                                                                                                        23 GGKWLDSYDNKTIKVNNPATGEIIADVACMGTKETNDAIASSYEAFTSWSKLTAGERSKV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amend A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rusnick C, Fsihi H, Dehoux P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA, Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Carcia Del Portillo F, Comez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibacterial: gene therapy, earning: biosynthesis; biodegradation;
                                                                           DB 21, Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432 FCETYINRENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQTQVVYL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 YGLVGVNEGLISTEVAPFGGVKQSGLGPEGSKYGMDEYLEIKYVCL 487
                                                                         33.7%, Score 825.5; DB 21, Length
38 6%, Pred No 2 Re-67,
tive 88; Mismatches 189; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Couve E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listeria monocytogenes protein #511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB47807 standard; Protein; 488
                  99US-0161993.
99US-0142142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APP-20մո՞դ, Հմանոթթ-Ողոգե2Գ.
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Dussurget O, Chetowani F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-FEB-2002 (first entry)
                                                                                                               180; Conservative
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                                                                                           Similarity
28-001-1949;
28-001-1999;
29-001-1999;
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                                                                             Query Match
                                                                                               Best Local
                                                                                                                 Matches
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360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 AIERASWI,PKISAGIPEPASEISALI,VEPGGKIQQLAEVEVAFTANYINYMAEWAPRYFG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 LADRVKLLHKIADLMEEKADTLAKIMTLEQGKPLKESKGEVL/TGVENFRFAAFBARRL/YG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 DYDKGNFYKPTVLDNVTRKMDIFYEETFGPVIPLITFETEDEAIFMANDSEFGLASYFYT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      418 UNLNVAMKALKGLKFSETYINPENFEAMOSFHAGWPKSGLGGGALGKHGLRGYLQTQVVYL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 KPLARVEKVGAALEYGMVCANELAISNPFTPFGGVKHSGFGRENGHYGMEEYTQVKFTNL, 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VQHPMYIDGQFVTWRGDAWIDVVNPATEAVISRIPDGQAEDARKAIDAAERAQPEWEALP 64
                                                                                                                                                                                                                                                                          monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention, Floteins expressed from the genome sequence are useful for raising specific
                                                                                                    for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 TUNATAFAKTUDETGLPRGVENLVLGRGETVGOELAGNPKVAMVSMTGSVSAGEKIMATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 PLSALATPETFERAGLERGVANTVMGSSKEIGETTETTSTUVERTJETGSTRAGOTTPROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 VOTKLEINGKWINGDNKETKEIVNPANGEVIAKIAQAGESETKKAIKAAKDAEPEWAKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 ELLOSDPPGEN---ILLERPALGVTTGTLPWNFPFFLJAPKMAPALLTGNTIVIKPSEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 VNPLGEAMQAVGFGNPAERNDIAMGPLINAAALERVEÑKVARAVERGARVAFGGKAVFG -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.2. AKNITIKVOLEEGGKAFALVMDDADLELAVRALVDSRVINGGEVONGAERVYVQKGLYDQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 ADTLKKISLELGGHAPFIVFDDANLDAAVNDLVAAKFRNNGQVCVSPNRIFVAKFIKEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 175; Conservative 107; Mismatches 186; Indels 13; Gaps
                                                                                                                                                                                                                                                       The present invention relates to the genome sequence of Listeria
                                                                                               Genomic sequence for Listeria monocytogènès, useful e.g. for treadud prevention of Listeria and related bacterial infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 2%; Scripe 811 5; DB 23; Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                      Claim 6; SEQ ID No 512; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monocytogenes and related organisms.
                                                                                                                                                     related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                WIT, LUCE-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  488 AA;
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RESULT 15

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Cyclododecanone; degradation; lauryl lactone esterase; cddA; cddB; cddX; dodecanonic diacid; cyclododecanone monooxygenase; cyclic Ketone; cddY; l2-hydroxylauric acid dehydrogenase; l2-oxo lauric acid dehydrogenase; macrolactone; microbiological; cddC; cddD.
                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids encoding dodecanoic diacid synthesizing enzyme,
                                                                                                                                                                                                                                                                                                                                                                   eyclododecanone monooxygenase for bioproduction of dodecanoic diacid from cyclododecanone -
                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to genes from Rhodococcus tuber involved in
                                                                                                                                                                                                                                                                                                 Chen MW, Cheng Q, Gibson KJ, Kostichka KN, Thomas SM;
                                                                               R. ruber 12-oxo lauric acid dehydrogenase.
                                                                                                                                                                                                                                                                           (DUPO ) DU PONT DE NEMOURS & CO E 1.
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 61-62; 78pp; English.
            AAB85329 standard; Protein; 474 AA
                                                                                                                                                                                                                               08-DEC-2000; 2000WO-HS33426
                                                                                                                                                                                                                                                    9905-0170214
                                                        17-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                      2001-451630/48.
                                                                                                                                                             Rhodococcus ruber.
                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAH22876.
                                                                                                                                                                                 WO200142436-A2.
                                                                                                                                                                                                                                                    10-DEC-1999;
                                                                                                                                                                                                         14-JUN-2001.
                                    AAB85329;
AAB85329
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cyclododecanone degradation pathway and occurs tuber involved in the cyclododecanone degradation pathway and occurs tuber in the cyclododecanone degradation pathway and comprises genes (designated cdaA, cddB, cddX, cddY, cddC and cddD) enroding enrymes such as dodecanote discid synthesizing enryme, cyclododecanone monocygenase, laryl lactone caterase. Host cells comprising the nucleic acid are used for the production of dodecanedioic acid when contacted with cyclododecanone, l2-hydroxy lauric acid when contacted with 12-hydroxy lauric acid when contacted with 22-oxo lauric acid when contacted with 12-hydroxy lauric acid and dodecanedioic acid when contacted with 12-oxo lauric acid when contacted with 12-oxo lauric acid with cycloic acid when contacted with 12-oxo lauric acid with cycloic ketones with 6 to cight carbon atoms like C6, C10, C11, C12, C13 and C15 cyclic ketones with 6 to cight carbon atoms like C6, C10, C11, C12, C13 and C15 cyclic ketones, cycloidexanone, and cyclodecanone. The host cells are also used for the production of macrolactones with a tycloic ketone when contacted with a cyclic ketone when contacted with a cyclic ketone when contacted with a cyclic ketone for the bioproduction of macrolactones with a tyclic contacted with a cyclic ketone when contacted with a cyclic ketone contacted with a cyclic ketone for the bioproduction of macrolactones with a tyclic contacted with a cyclic ketone contacted with a cyclic ketone contacted with a cyclic ketone contacted with a cyclic ketone when contacted with a cyclic ketone when contacted with a cyclic ketone with a cyclic contacted mannotation of sequence of ORFG (cddb qene) encoding a 12-oxo lauric acid dehydrogenase enzyme isolated from a 10kb nucleic acid flaqment from K ruber SC1.

474 AA; Sednence

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69 ASWLRKISAGIPERASFISAIIVEEGGKIQQLAE-VEVAFTADYIDYMAEWAPPYEGEII 127
                                                                                               9 MYIDGQFVTWRCDAWIDVVNPATEAVISRIPDGQAEDAAEKAIDAAERAQPEWFALPAIER 68
                                                                                                                                              9 LYINGSWVASTSKTVIEVLNPATEEVIGTVPDGTAADVDAAVAARAAFDGWASTPVDKR 68
                                                 Mismatches 189; Indels 11; Gaps
32.8%; Score 801.5; DB 22; Length 474; 38.5%; Pred. No. 3.5e-65;
                                                 87;
                                                 Conservative
                    Best Local Similarity
Matches 180; Conserva
Query Match
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244 VALELOGKSANIVLIDDADIDELMPNAVQWAMINSGQTGSALTRILVPRATITEAETAAKT 403 128 OSDRPGENTILFRRALGUTTGILPWNFPFFLIARKMAPALLIGNTIVIRPSEFTINNAIA 187 -RTEGSSVIVREPTGVVGATTPWNYPLHQTAAKVAYALAAGNTTVVKPSEVAPLNAWM-183 188 FAKTVDETGLPROVENLVLGROETVGOELAGNPKVAMVSMEGSVSAGEKTMATAAKNTTR 247 248 VCLEEGGKAPATVMDIALELAVKATVDSFVTNSGUVCNCAFRVYVGKGTY102FVNRGE 307 11.4 365 YPPTLLLDVRQEMSIMHEETFGPVLPVVAF17TLEDAISMANDSDYGLISSIY1GNIAVAM 424 463 VKPTTESEVTPDMTTHREETFGPVLSTAPYDTEEDAVKTANDSEYGLRGGVWSKDVDRAK 422 3.08 AMQAVQFGNPAERNDIAMOPLINAAALERVEQKVARAVEEGARVAFGG KAVEG KGYY 425 KATKGEKEGETYINPENERAMOGEHAGWPKSGLGGADGKHGLHGYLQ 471 q ŝ ą g S qq ŝ 9 ò

Search completed: June 24, 2003, 10:13:45 Job time : 40.6254 secs

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OM protein - protein search, using sw model

June 24, 2003, 10 13 Fs., Scarch time 13,2854 Seconds (without alignments) 1062 435 Million cell updates/sec Run on:

US-09-830-751-6 2446 Perfect source

ADISKHGTHGYTQPQVVYTQS 479 1 MSVPVQHPMYIDGQFVTWKG. Sequence:

BLOSUM62 Gapop 10 0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Issued\_Patents\_AA:\* Database :

1. /cgr2\_6/ptodata/1/laa/5A\_COMB.pep.\*
2. /cgr2\_6/ptodata/1/laa/5B\_COMB.pep:\*
3: /cgr2\_6/ptodata/1/laa/6A\_COMB.pep:\*
4: /cgr2\_6/ptodata/1/laa/6B\_COMB.pep.\*
5: /cgr2\_6/ptodata/1/laa/PCTUS\_COMB.pep:\*
6: /cgr2\_6/ptodata/1/laa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	932.5	38.1	493	4	US-09-134-001C-4388	Sequence 4388, Ap
2	767.5	31.4	506	4	-09-134-001C-438	4383,
m	~		488	*	134-001C-424	
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7	683.5	27.9	497	₹	-60-	Sequence 2, Appli
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11	625.5		518	4	US:09-134-001C 4451	Sequence 4451, Ap
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15	448		487	4	US-09-351-224E-5	'n
16	53.	14.5	464	4	US 08-134-001C-4701	470
17	221.5	9.1	133	-	US-08-446-611-2	cì
18	221	<u>_</u>	133	۲.	C-+6+-+64-80-SH	Sequence 2, Appli
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23	118	4.	72	4	US-09-655-270A-33	33
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	100	4.1	564	-	US-08-427 097-2	cì
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27	100	4.1	564	2	US-08-878-957-2	2, 1

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	3.66	4.7	732	54	US-08-843-530B 28	Sequence 28, App
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	ta		5.64	-	115-08-427-083-28	28
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	95.5	3.9	743	C	US-08-590-451-2	Sequence 2, Appli

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TITLE OF INVENTION: NUCLEIC ACTO AND AMINO ACTO SEQUENCES RELATING TO STAPHYLOCOCO
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSPICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 IQSDRPGENJILFKRALGVTTGILPWNFPFFLJARKMAPALLIGNTIVIKPSEFTTNNAL 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 KUCLELGGKAPAIVMDDADLELAVKAIVDSRVINSGGVCNMAERVYVGKGIYDGEVNRLG 306
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STREET: 1755 Jefferson Davis Highway, Suite 400
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                30.2%; Score 737.5; DB 4; Length 488; 35.8%; Pred. No. 1.2e-67;
                                                                                                CURRENT AFFLICATION NUMBER: 05/09/134,0010* CURRENT FILLING DATE: 1998-08-14 PRIOR APPLICATION NUMBER: 05-60/064,964
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Staphylococcus epidermidis
       APPLICANT: Lynn Doucette Stamm et al
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Patent No. 5753481
                                                                                                                                                                               PRIOR FILING DATE: 1997-11-08
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APPLICANT: Ishii, Yoshimori
APPLICANT: Yoshida, Masaru
APPLICANT: Suzuki, Hiromi
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APPLICANT: Saito, Yoshi
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CORRESPONDENCE ADDRESS:
                                                                            FILE REFERENCE: CTC-007
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LENGTH: 488
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AMING ACID SEQUENCES KELATING TO STAPHYLOCOCOUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER- 05/04/144,001C
369 LLLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSSIYTQNLNVAMKAIK 428
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                                                                                                   429 GLKFGETYINFENFEAMQGFHAGWRKSGIGGAEGKHGLHGYLQIQVVYLQ 478
                                                                                                                             31.4%: Score 767.5; DB 4; Length 505; 36.6%; Pred. No. 1e-70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
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                                                                                                                                                                                                                                                                             Sequence 4383, Application US/09134001C
Patent No. 6380370
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Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1998-08-13
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NUMBER OF SEQ ID NOS: 5674
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429 DIDKALAVTRPVRAGPFWVNTIMSGGPETPLGGFKQSGWGPFAGLYGVEEYTQIKSVHIE 488
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APPLICANT: Saito, Yoshimasa
APPLICANT: Ishii, Yoshinori
APPLICANT: Yoshida, Masaru
APPLICANT: Hayashi, Hiromi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (703) 413-3000
(703) 413-2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 497 amino acids
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INFORMATION FOR SPO ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Niwa, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virginia
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                                    614 8 614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 RYEGETTGSDRPGENTLIFKRALGVITGILPWNFPFFLIARKMAPALLFGNTTVIKESEP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 GEVNELGERAMOAVGEGRERERINTAMORI, TRAAAT ERVEGEVARAVEEGAEVARGERAVE, 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 NLNVAMKAIKGLKFGETYINRENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQTQVVYLQ 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 TSATTLLLAEILADAGLPKGVFNVVIGTGRTVGQAMTEHQDIDMLSFTGSTGVGKSCIHA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 TAAKNITKVCLELGGKAPAIVMDDADLELAVKAIVDSPVINSGQV″NGAPPVYVQKGIYD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 AADSNLKKLGLELGGKNPIVVFADSNLEDAADAVAFGISFNTGQCCVSSSRLIVERSVAE 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Motch 27.9%, Shure 68% 5, PB 1: Length 497; Local Similarity 33.1%; Pred. No. 56-62; es 159; Conservative 107; Mismatches 206; Indels 9.
          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 50 inch, 1 44 Mb storage COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..497
DENTIFICATION METHOD: experimentally (IS-08-513-841-2
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 241851/1993
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 JMBER: US/08/513,841
01-NOV-1995
                                                                                                                                                                                                                      UMBER: UK 9304700.9
08-MAR-1993
                                                                       OPERATING SYSTEM: PG-LOS/MS-LOS
SOFTWARE: MS-DOS Editor
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TELEFAX: 703-413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 amino acids
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                                                                                                                CURRENT APPLICATION DATA
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                                                                                                                                                                                                                   APPLICATION NUMBER: C
FILING DATE: 08-MAR-1
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                           FILING DATE:
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61 EALPAIERASWLRKISAGIPERASEISALIVEEGGKIQQLAEVEVAFTADYIDYMAEWAR 120
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                                                                                                                                                                                                                                                                                TITUE OF INVENTION: Method for Producing 2-Keto-L-Gulonic Acid
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 27.9%; Score 683.5; DB 2; Length 497; Most Local Similarity 33.1\%, itself Nr. Serb2; Matches 159; Conservative 107, Mishatches 206; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                Oblon, Spivak, Medlelland, Maier & Neustadt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette - 2.50 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                            1755 Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD: experimentally
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FILING DATE: 25-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US/08/696,834
24-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Gluconobacter oxydans
US-08-696-834-2
; Sequence 2, Application US/U8696834
; Patent No. 5834263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
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APPLICANT: Yoshida, Masaru
APPLICANT: Suzuki, Hiromi
TITLE OF INVENTION No. 5R61292el Lesurkoso Fedystrogenaso and No. 5R61132el
TITLE OF INVENTION: Lesorbosone Debydrogenase Obtained from Gluconobacter
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                          181 TINNAJAFAKIVDEIGLPRGVFNLVI,GRGETVGQELAGNPKVAMVSMTGSVSAGEK-IMA 239
                                                                                                                             190 TSATTLLLAEILADAGLPKGVFNVVTGTGRTVGQAMTEHQDIDMLSFTGSTGVGKSCIHA 249
                                                                                                                                                                               240 TAAKNITKVCLELGGKAPAIVMDDADLELAVKAIVDSRVINSGOVGNGAERVYVQKGIYD 299
                                                                                                                                                                                                                        250 AADSNLKKIGLELGGKNPIVVFADSNLEDAADAVAFGISFNTGOCCVSSSRLIVERSVAE 309
                                                                                                                                                                                                                                                                     300 QEVNRLGEAMQAVQFGNPAERNDIAMGPLINAAALERVEQKVARAVEFGARVAFGGKAVE 359
                                                                                                                                                                                                                                                                                                                310 KFERLVVPKMEKIRVGDPFD-PETQIGAITTFAQNKTILDYIAKGKAEGAKLLGGGGTVD 368
                                                                                                                                                                                                                                                                                                                                                             360 -GKGYYYPPTLLLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSSIYTQ 418
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FILING DATE: 28-SEP-1993
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01-NOV-1995
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Patent No. 5861292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
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Ishii, Yoshinori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-1993
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ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NORMAN F. OBLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Niwa, Mineo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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STRAIN: T-100
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Patent No. 6197562
                                                           TELEFAX: 703 414-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
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Suzuki, Hiromi
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703-413-2220
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LOCATION: 1..497
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Best Local Similarity
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NUMBER OF SEQUENCES:

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Matches 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 AGLAAADRAAVILKAAGLLRERRDDIAYWEVLENGKPISQAKGEIDHCIACFEMAAGAAR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TTNNAIAFAKIVDEIGLPRGVFNLVLGRGETVGQELAGNPKVAMVSMTGSVSAGEK-IMA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 TAAKNITKVCLELGGKAPAIVMPDADLELAVKAIVPSPVINSGQVCNCAERVYVQKGIYD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 PREFGFFIDGE---WRAGKDFFDRSSPAHDVPVTFIPFCTPEDLDEAVAAARFAFENGSW 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PVQHPMYIDGQPVTWR-GDAWIDVVNPATEAVISEIPDGQAEDARKAIDAAERA--QPEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Gaps
              .: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
1755 Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 98, Schref83 C, 58 4) Length 497;
33.18, Pred. No. 5e-62,
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                                                                                                                                      Diskette, 3.50 inch, 1 44 Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-909-0 PCT
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FILING DATE: 28 SEF-1993
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
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                                                                                                                                                                                                                                                                                                                               17K 9304700 9
                                                                                                                                                                   OFFRATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: MS-DOS Editor
CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: IK 93
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PRIOR APPLICATION DATA:
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TELEPHONE: 703-413-2220
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                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COPPESPONDENCE ADDRESS:
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                                                                                                                                                                                                                        APPLICATION NUMBER.
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                                                                  Virginia
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                ADDRESSEE:
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                                  STREET
                                                 CITY:
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83 ASELSALIVEE---GGKIQQLAEV-EVAPTADYIDYIDYMAEWARFYEGE--1IQSDRPGENI 136
310 REBELVVFEMEKIRVGDFFD-FETGIGATITEAGNKTILLEYTAKGKAEGAKLLGGGGIVD 358
                                                         Pyg - GKGYYYPPFTTJL DVEQEMSIMHEETPGFVI PVVARTH LELAISMANESIYSETTSSIYTQ-418
                                                                                                                                                                     419 NLNVAMKAIKGLKFGETYINFENFEAMQGFHAGWFKSGIGGADGKHGLHGYLQTQVVYLQ 478
                                                                                                                                                                                                                           429-DIDKALAVTERVEAGEFWONTIMSGSPETFLAGFRQSGWGPFAGLYGVEEYTQIKSVHIE 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alessandro Massimo Gianni
VENTION: A Patroviral Vastor Capable of Transducing the
VENTION: Aldehyde Dehydrogenase-1 Gene and Uses of Said
VENTION: Vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Riccardo Dalla-Favera and
APPLICANT: Alessandro Massimo Gianni
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-PERATING SYSIEM: PC-LOUS/MS-DOS
SOFFWARE: PATENTIN Release #1.24
SUSPERNT APPLICATION DATA:
AFFLICATION NUMBER: US/09/221,294
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
FELETAX. 212-351-6535
INFORMATION FOR SE, 11 NO. 2:
SEQUENCE CHARACTERISTICS:
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NAME: White, John P.
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
TITLE OF INVENTION:
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; Patent No. 6380370
; GENERAL INFORMATION:
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232 AGPPPGVVNIVPGYGPTAGAAISSHMDIDKVAFTGSTEVGKLIKEAAGKSNLKRVTLFLG 291
                                                                  254 GKAPAIVMDDADLELAVKALVDSRVINSGQVCNCAERVYVQKGIYDQFVNRLGEAMQAVQ 313
                                                                                                                                                            314 FGNPAERNDIAMGPLINAAALERVEOKVARAVEEGARVAFGGKAVEGKGYYYPPTLLLDV 373
                                                                                                                                                                                                     352 LGNPLTPG-VTQGPQTDKEQYPKILDLIFSGKKEGAKLEGGGPWGNKGYPVQPTVFSNV 410
                                                                                                                                                                                                                                                    374 RQEMSTIMHEETFGPVLPVVALDFLEDATSMANDSDYGL/TSSTYTQNL/NVAMKATKGL/KFG 433
                                                                                                                                                                                                                                                                                               411 TDEMRIAKEEIFGPVQQIMKFKSLDDVIKPANNTFYGLSAGVFTKDIDKAITISSALQAG 470
                                                                                                               292 GKSPCIVLADADI.DNAVEFAHHGVFYHQGQCCIAASRIFVEESIYDEFVRRSVERAKKYI 351
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33.1%: Pred. No. 1.7e-57;
Live 88, Mismatches 216; indels 17
                                                                                                                                                                                                                                                                                                                                            434 ETYINKENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQTQVV 475
                                                                                                                                                                                                                                                                                                                                                                                    471 TVWVNCYGVVSAQCPFGGFKMSGNGRELGEYGFHEYTEVKTV 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 20747/100
CURRENT APPLICATION NUMBER: US/09/155,183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: GR96/06187
EARLIER FILING DATE: 1996-03-23
NUMBER OF SEQ ID NOS- 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09155183
Patent No. 6323011
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APPLICANT: Narbad, Arjan
APPLICANT: Rhodes, Michael J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 1999-05-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOGOGY TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                      417 RALALAQRVESGICHINOPTVHDEAOMPF-GOVKSSOYGSFOOKASTEHFTOLAWYLLON 475
                                                                   357 GSILQPTLLDGVDASMRLYREESFGPVAVVLAGEGEEALLGLANDSEFGLSAATESKOTG 416
34.2. GYYYPPTLLLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLISSIYTQNIN. 4.2.1
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nes 146; Conservative 100; Mismatches 222; Indels
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30.6%; Pred. No. 8e-57;
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CURRENT APPLICATION NUMBER: US/O9/134,0010
CURRENT FILLING DATE: 1998-08-13
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08 14
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// Patent No. 6480370
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                                                                                                                                                                                                                                                                                                                                                            US-09-134-001C-4541
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION, NGCLEIC ACID AND AMINO ACID SEQUENCES KELALING TO STAPHYLOCOCOUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 FRASWLRKISAGIRERASEISALIVEEGGKIQQLAEVEVAFTADYIDY----MAEWARRY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 DPAELLI-PVAATIPPPKEELSATMVYEAGKPWDEAVGDAAEGIDFIEYYAPSMMELA--- 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417 TONLANAMKAIKGLKEGETYINRENFEAMÇGFH--AGWEKSGLGGALGKHGLHGYL 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 25.6%; Score 625.5; DB 4; Irrngth 518; Best Local Similarity 32.6%; Pred. No. 5.5e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98; Mismatches 198; Indels
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FILE REFERENCE: BC1022 US NA
CURRENT APPLICATION NUMBER: US/09/651,941
                                                                          FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,0010
                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
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PRIOR APPLICATION NUMBER: 60/152,545
PPPIOR FILING DATE: 1991-10-03
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Staphylococcus epidermidis
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                                                                                                                                   1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 155; Conservative
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                                                                                                                                   CURPFNT FILING DATE:
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                                                                                                                                                                                                                                                                                                                      LENGTH: 518
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186 IAFAKIVDEIGLPPGVFNLVLGPGETVGQFLAGNPKVAMVSMTGSVSAGEKIMATAAKNI 245
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                                                                                                                                                                                                                                                                                               68 KASWLKKISAGIPERASEISALIVERSGK-IQQLAFVEVAFTARVIDYMAHWAFREGEI 126
                                                                                                                                                                                                                                                                                                                                                69 PTPLMFFYAALTEEHKTELAQLQSPDMGKPIRESLGIDLPIMIETLEYFAGLVTKIEGR- 127
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                                                                                                                                                                                           8 PMYIDGGFVTWRGDAWIDVVNPATEAVISKIPDGGAEDARKAIDAAERAQPEWEALPAIE 67
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                                                                                   DB 4; Length 485;
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PULICANT: RAINER, RUSS
TITLE OF INVENTION: Genes Encoding Pictic Acid Degradation
FILE REFERENCE: BC1022 US NA
                                                                             Query Match 25.5%; Score 623.5; DB 4;
Bost Loral Similarity 29.4%; Pred. No. 8e-56;
Matches 142, Conservative 99, Mismatches 225,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.9%; Score 6.23.5; DB 4; 29.9%; Pred. No. 8e-56, ative 99; Mismatches 225;
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ORGANISM: Phydogoggus grythropolis HL PM-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 9, Application US/09955597
; Patent No. 6461856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-09-17
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NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ROUVIER, PIERRE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURPENT APPLICATION NUMBER: CHEPENT FILLING DATE: Zool-9
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Matches 142; Conservative
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าด	128 -TIPAPGRFLNYILKEPIGVVGAITPWNFPAVQAVWKIAFALAMGNAIVLKPAQLAPLVP 186	OY 362 GYYYPPTLLLOVRQEMSIMHEETFGPVLFVVAFD
Oy	LGRGETVGQELAGNPKVAMVSMTGSVSA	
qu	187 VALGELALEAGLUPPGLVNVLPGPGSVAANALVQHPSVKVLFTGSTFVGGGTGPMAARPEL 24.6	422 VAMPATPER FERFIX INDENDED MANAGER HAVOREN
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g qa	QARVEAARVGDPLD-PDTEIGPLISAEQRESVHSYVVSGTEEGATLISGGDQSPTGAPEQ	. 55 93 51 2246 5 58 93 51 2246 5 September 5 Application US/09351224E 5 Patent No. 6388171
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qa	366 GFYYRPTLFSGVTADMRIAREFIFGDVLSVLPFEGEERAITLANDTVFGLAAGVFTRDVG 425	APPLICANT: Maddox, Joyce APPLICANT: Gilliam, Jacob
oy 4	422 VAMKAIKGETYINPENFEAMOOFHATWEKSAIGGALGKHGLHGYLOTOVY 476	APPLICANT: FOLKETIS: OTTO: APPLICANT: Crasta, Oswald K. TITLE OF INVENTION: Compositions and Mothess t
g G	426 KALKFAQTLUAGNVWINSWGVLNFASPYRGFGQSGYGSDLGQAAIESFTREKSIW 480	FITTHE OF INVENTION: Detoxitication FILE REFERENCE: 5718-111 Automotive Additional Automotive Research
RESULT 14 US-09-655	RESULT 14 US-09-655-270A-9	CORKENT APPLICATION NUMBER: US/09/701, ZZ4E; CORKENT FILING DATE: 1999-07-12; NUMBER OF SEO ID NOS: 11
; Seque	Sequence 9, Application US/09655270A	SECTION S. SECTION WINDOWS Version 4.0
	GENERAL INFORMATION: APPLICANT: Rounions District F	, SIGT NO 3
TITE	50	) OKGANISM: Exophiala spinitera 
	CURRENT FILING DATE: 2000-09-05 PRIOR PELLING NUMBER: 60/120,702 PRIOR FITING DATE: 1000-505-03-03-03	
	FRIOR FIZING DATE: 1333 FEBILIALY 13 PRIOR APPLICATION NUMBER: 60/155,542 BDTADE FITING DATE: 1000.000000000000000000000000000000000	Matches 135
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TYPE	STATE OF THE PROPERTY OF THE PARTY OF THE PA	
) OKO 08-09-6	CHOMANISM: MIGGOCOCCUS ELYUNTOPOIIS HL PM-1 US-09-655-270A-9	72
Ouery M Best Lo Matches	Ouery Match 25.5%; Score 623.5; DB 4; Length 508, Best Local Similarity 29.9%; Pred. No. 8.6e-56; Matches 142: Couservative 99; Mismatches 225; Indels 9; Gaps 5;	
ζò	ATEAVISEIPLIGQAEDARKAIDAAERAUPEWEA	185
QC!	32 PLVIGDQLTPSSTGATFDSINPADGSHLASVAEATAADVARAVEAARAARTWQRMRPAQ 91	06.1 (
Oy	68 RASWLRKISAGIRERASEISALIVEEGGK 100LAEVEVAFTADYIDYMAEWARRYEGEI 126	
qa	92 RTRLMFRYAALIEBHKTELAQLQSRDMGKPIRESLGIDLPIMIETLETYFAGLVTKIEGR- 150	7 6 7 6
Qy	127 IOSDRPGENI-LLEKRALGVITGILPWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNA 185	303
υp	151 -TTPAPGRELNYTLREPIGVVGAITPWNFPAVQAVWKIAPALAMGNAIVLKPAULAPLVP 209	) (1)
δλ	186 IAFAKIVDEIGLPRGVENLVLGRGETVGQELAGNPKVAMVSMTGSVSAGEKIMATAAKNI 245	252
QQ	210 VALGELALEAGLIVPGLIVIVILPGRGSVAGNALVQHPSVGKVTFTGSTEVGQQIGEMAADEL 269	785
Qy	246 TKVCLELGGRAPAIVMDDADLELAVKAIVDSKVINSGUVCNCAEKVYVUKGIYLUJEVNKI, 305	07
Ωp	270 ITASLELGCKSALVAFGDSSPKAVAAVVFQAMYSNQGETCTAPSRLLVERPIYDEVVELV 329	
ογ	306 GRAMQAVQFGNPAERNDIAMGPLINAAALERVEQKVARAVEEGARVAFGGKAVEGK 361	7

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242; Indels 42; Gaps 14;
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                                               PEGEERATTANDTVFGLAAGVETRIVG 448
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Perfect, score: 2446 Sequence: 1 MSVPVQHPMYIDSQFVIWRG .....ALASKHGLHAYLQTVVYDJS 479

Scoring table: RIASIM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%

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Database : Published\_Applications\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	879.5	36.0	483	100	118-09-818-242-5058	A MAGE GOODENAA
C1	873	35. 7	482	10	MS-09-815-242 10264	Section 16.64 A
3	858.5	35 1	482	-	US-09-815 242-14047	Sequence 14047. A
4	830	33 9	492	c	TIS-10-268-518-4	Sequence 4. April
5	819.5	33.5	493	σ	ns-10-175-696-21	Segrence 21 April
7.	819 5	۳.	493	10	75 09-823-901-9	Sequence 9, Appli
7	771 5	31.5		10	US-00-815-242-5644	Segmence 5644, Ap
œ	771 5			10	US-09-815-242-12657	Sequence 12657, A
6	768.5	31.4		10	US-09-815-242-13829	Sequence 13829, A
10	762	31.2		10	US-09-815-242-10550	
11	756.5	30.9		10	US-09-815-242-12375	Sequence 12375, A
12	748.5	¥.	501	7	US-09-344-882-22	Sequence 22, Appl
13	748.5	30 Y	501	c	US-10-293-865-22	Sequence 22, Appl
14	729	39 B	490	c	11S-09 738 626.1558	in N
15	729	29.8	490	10	US 09-815-242-12102	Sequence 12167, A
16	719 5	\$ 6C	512	c	118-89-961-403 12	Sequence 12. Appl
17	719.5	29.4	512	œ	US:10 268:518:2	Sequence 2, Appli
18	719.5	29.4	512	ۍ.	US 10 205-823-14	Sequence 14, Appl
19	712	29.1	490	្ដ	US-09-815 242-10057	Sequence 10057, A

Score 879.5, DB 10, Length 483, Fred No. 2 3c 68;

36.03, 39.33

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Sequence 5241, Ap Sequence 143, App Sequence 24, Appl	45.00	17,	Sequence 59, Appl Sequence 4, Appli Sequence 12, Appl	Sequence 11, Appl Sequence 3, Appli	Sequence 4, Appli Sequence 6572, Ap	Sequence 5430, Ap Sequence 4037, Ap	Sequence 13:16, A Sequence 13:16, A	Sequence 6482, Ap Sequence 1348, Ap	Sequence 736, App Sequence 5, Appli	Sequence 406, App
1 US-08-781-986A-5241 0 US-09-919-039-143 4 US-04-444-882 24	9 US-10-203-865-24 9 US-09-344-882-20 0 US-10-04-866-00	9 US-10-135-805-20 9 US-10-175-696-17 10 US-09-823-901-5	9 0S-09-84/-208-59 9 0S-10-166-087-4 9 0S-10-272-419 12	9 US-09-847-208-11 10 US-09-997-564-3	10 - 115-119-733-383-4 9 - 115-09-738-626-6572	9 US-09-738-625-6430 4 US-04-738-626-4037 1 MS-04-038-06-04	1 05 04 815-242-1331e 10 05-04 815-242-1331e 9 05-04-738-626-4108	9 US-U9-738-525 6482 10 US-09-925-300-1348	10 HS-00-025-302-736 9 US-09-882-694-5	19 98-94-741-554-495
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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PRIOR PULL AND LATE 2000-03-21

PRIOR APPLICATION NUMBER: 60/205,848

PRIOR PULL AND LATE 2000-05-33

PRIOR FILMS LATE 2000-05-35

PRIOR FILMS AND EXCESSOR 50.5

PRIOR FILMS AND EXCESSOR 50.5

PRIOR FILMS AND LATE 2000-10-23

PRIOR FILMS LATE 2000-10-23

PRIOR FILMS LATE 2000-11-27

FRIER AFFLICATION NUMBER: 60/257,931

PRIOR FILMS LATE 2000-11-27

PRIOR FILMS LATE 2000-12-22

PRIOR FILMS AND LATE 2001-12-12

PRIOR FILMS AND LATE 2001-12-12

PRIOR FILMS LATE 2001-13-14
                        Sequence 5658, Application 08/09815242
Fatent No. US20020061569Al
GENERAL INFORMATION:
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                                                                                                                                                                                          APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
                                                                                                                                    Ohlsen, Kari L.
Syskind, Judith W.
                                                                                                            APPLICANT Haselbeck, Robert
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08-09-815-242-5058
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US:09:815-242-10264

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70 SWLRKISAGIRERASEISALIVEEGGKIQQLAEVEVAFTADYIDYMAEWARRYEGEILGS 129
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                                               10 YIDGQFVTWRGDAWIDVVNPATEAVISRIPDGQAEDARKAIDAAERAQPEWEALPAIERA 69
                                                                                     14 YVDGAWYDADNGQTIKVNNPATGEIIGSVPKMGAAETRRAIEAAFKALPAWRALTAKERA 73
    1; Gaps
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  96; Mismatches 187; indels
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020061569A1
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PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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PRIOR APPLICATION NUMBER: 60/269, 308
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Zyskind, Judith W.
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APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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ORGANISM: Escherichia coli
Matches 184; Conservative
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71 WERKISAGIRERASEISALIVEEGGKIQQIAEVAFTADYIDYMAEWAKRYRGEIIOSD 140
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                                                                                                                                                                                                                                                                       75 ILRNWFNLMMEHQDDGARLMTLEQGKPLAEAKGEISYAASFIEWFAEEGKRIYGDTIPHH 144
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                                                                                                             11 IDGQEVTWEGDAWIDVVNPATEAVISKIPDGQAEDARKAIDAAERAQPEWEALPATERAS 70
                                                                                                                                                            15 INCENTUANNOEATIVENFANCIELOSSVERMOAPETEAATIVAANKALPAWRALLAKERAT
35.7%; Score 873.5; DB 10; Length 482; 49.5%; Pred. No. 7.5e 68;
                                                     Mismatches 187; Indels
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Probaryotes
FILE REFERENCE: ELITEA.011A
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Patent No. US20020061569A1
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PRIOR APPLICATION NUMBER: 40,2342,578
PRIOR PELLING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 62,254,625
PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 64,252,931
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PRIOR FILING DATE: 2000 05 23
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Zyskind, Judith W.
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Trawick, John D.
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                                                        Matches 182; Conservative
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                         Hest Local Similarity
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                                                                                                                                                                                    Gaps
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                                                                                                                                 35.1%; Score 858.5; DB 10; Length 482; 39.2%; Pred. No. 1.5e-66; Live 91; Mismatches 189; Indels 1;
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IIILE OF INVENIION: 9136, A HUMAN ALGERYGE GERYGEWSENASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUPPENT APPLICATION NUMBER: US/10/264,518
CUPPENT FILLNG DATE: 2002-10-10
PRIOF APPLICATION NUMBER: h0/424, M44
PROP FILLNG DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PASTSEQ for Windows Version 4 0
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                                                                                                                                                                               181; Conservative
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Matches 203; Conservative
                                           TYPE: PRT
ORGANISM: Salmonella typhi
                                                                                                                                                            Best Local Similarity
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                                                                                        US-09-815-242-14047
SEQ ID NO 14047
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                                                                                                                                      Query Match
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Best Local S
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APPLICANT: BUGGES, Rechel
APPLICANT: Budolph-Owen, Laura A,
TITLE OF INVENTION: NOVELHUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
TITLE OF INVENTION: NOVELHUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
TITLE OF THE REFERENCE: 10448-193001
CURRENT APPLICATION NUMBER: 1070-06-20
PPLOR APPLICATION NUMBER: 1070-06-204
PPLOR FILING DATE: 2001-06-20
PPLOR APPLICATION NUMBER: 60/266,140
PPLOR APPLICATION NUMBER: 60/266,140
PPLOR PILING DATE: 2001-06-30
PROR R PILING DATE: 2001-06-31
NUMBER OF SED ID NOS: 31
NUMBER OF SED ID NOS: 31
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71 WLPKISAGIPEPASEISALIVEEGGK--1<u>0</u>01AEVEVAPTADYIDYMAEWAPPYEGE--1 126
                                                                          62 TERELABETERREDELAALETEDIGKPLABAKGDTEVGRAIDETRYYAGWARKLMGFRRV 121
                                                                                                                                                                 127 IQS-DRPGENILLFKR--ALGVTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEFTTN 183
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Publication No. US20030092658A1
GENERAL INFORMATION:
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78; Mismatches 175; Indels 35; Gaps 15;
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                                                                                                                                   33.5%; Score 819.5; DB 9; Length 493; 41.3%; Pred. No. 4e-63;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                OTHER INFORMATION: consensus sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                          Matches 203; Conservative
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                                                                                                                                      Query Match
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                            FEATURE:
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71 WLKKISAGIRERASEISALIVEEGGK - 100LAEVEVAFTADY IDYMAEWARRYEGE | 1 126
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OPEWEALPATERAS 70
                                              Z. WVDSASCKITECVNPANKCHV LTPVPEATAETVDAAVKAAKFAFF STHWAKVPASEKAR (6.)
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Progaryotes
  23 WID------VVNPATEA-VISKIPIKQAEDARKAIDAAERA
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CURRENT APPLICATION NUMBER: US/09/915,242
CURRENT FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PLILING TATE: 2000-10-24
PRIOR PLILING TATE: 2000-10-24
PRIOR PLILING DATE: 2000-11-27
PRIOR PPLING DATE: 2000-11-27
PRIOR PLILING TATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,941
PRIOR PLILING TATE: 2000-12-22
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| Sequence 5644, Aprilianing/09815242
| Patent No. US20020061569A1
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PRIOR FILING DATE: 2000-03-21
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Zyskind, Andith W.
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NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wall, Daniel
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                                                                                                                                                               7, Gaps
                                                                                                  / Match 31.5%; Score 771.5; DB 10, Length 496, Local Similarity 36.4%; Fred. No. 6.28 59, nes 170; Conservative 90, Mismatches 200; indels 7,
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKARYOUES
FILE PREFENCE: ELTIPA.0118.
CUPRENT APPLICATION NUMBER: US/09/R15,242
CUPRENT FILING DATE: 2001-03-21
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Patent No. US20uzuu61569Al
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELLIO EATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PPIOR FILING LATE: 2000-05-26
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PRIOR APPLICATION NUMBER: 60/204, 308
PRIOR FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/253,625
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                    ; ORGANISM: Staphylococous aureus
US-09-815-242-5644
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Trawick, John D.
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TYPE: PRT
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                                                                                                                                                                                                                                             7; Gaps
                                                                                                                                                                                               DB 10; Length 496;
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                          31.5%; Score 771.5; PH 10; 36.4%; Pred. No. 6.2e-59; Five 90, Mismatches 200;
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4 0
SEQ ID NO 12657
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; Patent No. 0S20020061569A1
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PRIOR APPLICATION NUMBER: 60/206,848
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PPIOR PILLING DATE: 2000-95 26
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PRIOP APPLICATION NUMBER: 802254,525
PRIOP FILING DATE: 2006-11-27
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US-09-815-242-12657
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Xu, H. Howard
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Zyskind, Judith W.
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Carr, Grant J.
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Rest Local Similarity
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                                                                           LENGTH: 496
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03 21
PRIOR APPLICATION NUMBER: 60/191,078
                                                  PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ 1D NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                     LOCATION: (1)...(481)
OTHER INFORMATION. Xad = Any Amino Acid
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Patent No. US20020061569A1
PRIOR APPLICATION NUMBER: 60/257,931
                                   APPLICATION NUMBER: 60,7269,308
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                                                                                                                                                         TYPE: PRT
ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                           Conservative
              PRIOR FILING DATE: 2000 12
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es 179; Conserv
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                                                                                                                                                                                                                       NAME/KEY: VARIANT
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                                                                                                                   SEQ 1D NO 13829
                                                                                                                                      LENGTH: 481
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TITLE OF INVENTION. Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/257,941
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,408
PRIOR FILING DATE: 2001-02 16
NUMBER OF SEQ ID NOS: 14110
SOFTWAKE: FASTSEQ FOR WINDOWS Version 4.0
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; Sequence 12375, Application US/09815242
; Patent No. US20020061569Al
                    PRIOR FILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                   PRIOR APPLICATION NUMBER: (0/242,578 PRIOR FILLING DATE: 2000-10-24
                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/254,625
PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: (0/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Enterococcus faecalis
US-09-815-242-10550
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Zyskind, Judith W.
                                                                            2000-05 26
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Trawick, John D.
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Best Local Similarity
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                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 10550
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 496
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                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ 1D NOS: 14110
SOFTWAPE: FastSEQ for Windows Version 4.0
CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                  PRIOR FILLING JABEL 2000 05.29 PRIOR PELLING TATE. 2000 05.23 PRIOR PAPLICATION NUMBER: 60/207,727 PRIOR PELLING TATE. 2000 05.26 PRIOR PILLING TATE. 2000 05.26 PRIOR PILLING TATE. 2000 05.26 PRIOR PILLING TATE. 2000-10-23 PRIOR PILLING DATE. 2000-11-27 PRIOR PILLING DATE. 2000-11-27 PRIOR PILLING DATE. 2000-11-27 PRIOR PILLING DATE. 2001-12-22 PRIOR PILLING DATE. 2001-12-22 PRIOR PILLING DATE. 2001-02-22 PRIOR PILLING DATE. 2001-02-21
                  CURPENT FILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER- 60/141, 078
PRIOR FILLING DATE: 2000-03-21
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patest No. 0520020162137A1
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Oliver, David J
Behal, Robert
Schnable, Patrick S
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US-09-815-242-12375
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Iohnson, Ter
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 12375
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APPLICANT: Fatland, Beth APPLICANT: Fatland, Beth APPLICANT: Lutager, Isabelle APPLICANT: Lutager, Isabelle TAPPLICANT: Wen, Tsui-June Tarials and Methods for the Alteration of Enzyme and IIILE OF INVENTION Materials and Methods for the Alteration of Enzyme and IIILE OF INVENTION MATERIALS APPLICANT OF STAIL THE PREPREPRICE TO STAIL SON OF STAIL THE DATE: 1999 OF 25 OFFICE THIS DATE: 1999 OF 25 OFFICE THIS DATE: 1998 OF 25 OFFICE THING DATE: 1998 OF 25 OFFICE THING DATE: 1998 OF 25
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APPLICANT: Wen, Tsui-Jung
TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
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US-09-344-882-22
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Johnson, Jerry L
Allred, Carolyn C
Fatland, Beth
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Allred, Carolyn C
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Rehal, Pobert
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APPLICANT: Wurtele, Eve S
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TITLE OF INVENTION: Acetyl CoA Levels in Plants
                TITLE OF INVENTION: NOVEL POLYNICLEOTIDES
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CURRENT APPLICATION NUMBER: US/09/738.626
CURRENT FILING DATE: 2000-12-18
                                                                                PRIOR APPLICATION NUMBER: US 09/344,882
PRIOR FILING DATE: 1999-06-25
                                                                                                                           PRIOR APPLICATION NUMBER: US 60/090,717 PRIOR FILING DATE: 1998-06-26 NUMBER OF SEQ ID NOS: 38
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ORGANISM: Arabidopsis Thaliana
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SEQ ID NO 22
LENGTH: 501
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TATEISHI, NAOKO
SENOH, AKIHIRO
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GENERAL INFORMATION
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APPLICANT: TATEISI
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34.48; Pred. No. 4.1e-55;
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                       PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR AFFLICATION NUMBER: JF 00/280988
PRIOR FILING DATE: 2000-08-03
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Patent No. US20020061569Al
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PRIOR FILLING DATE: 2000 05 23
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Yamamoto, Robert T.
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PRIOR FILING DATE: 1999-12-16
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                                                                                                                                  NUMBER OF SEQ 1D NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ 1D NO 3558
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Zyskind, Judi
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ORGANISM:
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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PRIOR FILLING DATE: 2001-02-16
RUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12102
LENGTH: 490
TYPE: PRI
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Best Local Similarity 34.2%; Pred. No. 3.1e-55;
Matches 164, Conservative 101, Mismatches 206; Indels
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                                                                                                                 424 LARAHRAIHRLEAGICWINTWGESPAEMPVGGYKQSGVGRENGLTTLAHYTRIKSVQVE 482
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SUMMARIES

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7		10000 03787	mre 127,	10	27.15	65163,	13, App	uence 13,	4, Appl	lence 10932,	Sequence 11863, A	17169,		12633,	14047,	e 14047,	14047,	e 7938,	2 13957,	23511,	10264	10264,	$^{\circ}$	10264,	27749,	4476	3454,	2636, A	, 850s	e sij58,		98728,	nce 13571	. 18139,	n 2956,	ro 4782,	ce 20873,	CC 3024,

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						EOF	TITLE OF INVENTION: METHODS OF USE THEREOF	HODS OF	: MET	VENTION	OF IN	TITLE
D FAM	LES AN	FAMILI	TEIN	PRO	HO SHAL	RUCTU	TITLE OF INVENTION. THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY M	E DIMEN	. THPE	VENTION	OF IN	TITLE
								фh	Danzer, Joseph	Danzer	ANT:	APPLICANT:
									Derek	Debe, Derek	ANT:	APPLICANT:
								•	x, Inc	APPLICANT: Rionomix, Inc.	ANT · I	VI'IAdV
									-	RMATION	INFO	GENERAL INFORMATION
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ORGANISM: Escherichia coli
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901 FYNRIAGAMQAVQEGNPAERNDIAMGPLINAAALERVEQKVARAVEEGARVAFGGKAVEG 360
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
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cal Similarity 99.6%;
477; Conservation
421 NVAMKAIKGLKFGETYINFENFEAM@GEHAGWEKSGIGGALSKHGLHEVLQTQVVYLQS 479
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US-09-489-039A-13820 ; Sequence 13820, Application US/09489039A

GENERAL INFORMATION

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                                               US-09-791-537-40455
                                                                                    CUPRENT APPLICATION NUMBEP 115/09/791.537
CUPPENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 40455
LENGTH-480
TYPE: PRT
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SEQ ID NO 13820
LENGTH: 514
    Query Match
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Best Local Similarity
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBITITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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                                                                  ORGANISM: Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 NVAMKAIKSIKFISETYINPENFEAM@IFHAGWEKSOIGGAFRIKHISLHGYLQTQVVYLQS 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361
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                                                                  meningitidis MC58
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    Score 1557;
  DB 21;
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US-09-791-537-115281
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US-09-791-537-115281
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 115281
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/791,537
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                                                                     123 IIQSDRPRENILLFKRPLGVIAGILPWNFPFFLIARKMGPALVTGNTIVVKPSSVTPINC 182
                                                                                                                                          126 TIQSDRPGENITLEKRALGVTTGTIPWNEPEELTARKMAPALLTGNTIVIKPSEETTNNA 185
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TAFAKTVDETGLF5GVFNLV50SK3E1V0@ELAGNFKVAMVSMT0SVSAGEK1MATAAKNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%; Score 1552; UB 21; 63.0%; Pred No 5 5e-145;
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: Sequence 5824, Application 08/092526910
: GENERAL INFORMATION:
: APPLICANT: Keith G. Meinstock et al.
: TITLE OF INVENTION: NUCLEIC ACTO AND AMINO ACTO SEQUENCES RELATING TO ENTERORACTER
: TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
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: GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
: TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.135
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LENGTH: 319
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CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
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                                                                                                                                                                                                                                                                                                                                                                                                                                         341 VARAVEEGARVAFGGKAVEGKGYYYPPTLILIDVRQEMSIMHEETFGPVLPVVAFDTLEDA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TGGVCNCAERVYVGKGIYDRFVNRLGEAMKAVGFGNPAERTDIAMGPLINAAALERVEGK 180
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                                                                                                                                                                                                                 DGKHGLNEYLQTQVVYLQS 319
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LENGTH: 393
                                                                                                                                                                                                            Query Match
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LENGTH: 319
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                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                       151 PWNEPFELIARKMAPALLTGNTIVIKPSEFTTNNAIAFAKIVPEIGLPRGVENLVLGRGE 210
  Conservative
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; ORGANISM: Enterobacter cloacae
US-09-252-5910-5824
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                                                                                                                          461 DGKHGLHGYLQTQVVYLQS 479
                                                                                                                                                                                                                                                         181 VARAVQEGAKVVLGGKAAEGKGYFYPPTLLLDVRQDMAIMHEETFGPVLPVVAFDTLEEA 240
                                                                                                                                                                                                                                                                                                                   341 VARAVEEGARVAFGGKAVEGKGYYYPPTLLLDVRQEMSIMHEETFGPVL/PVVAFDTLEDA 400
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301 DGKHGLNEYLQTQVVYLQS 319
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; ORGANISM: Campylobacter jejuni US-09-791-537-20873
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THERBOP
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER 08/04/741,537
CURRENT FILING DATE: 2001 2 22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                     y Match 52.3%; Score 1279.5; DB 21; Length 393; Local Similarity 63.1%; Pred. No. 6.2e-118;
                                                                     91 VEESSKIQQLAEVEVAFIALYILYMAEWARKYEGEILQSURPGENILLEKRALGVTTGIL 150
1 MQEQGKTRVLASIEINFTADYMDYTAEWARRYEGEIIQSDRANEHIYLYKSAIGVIGGIL 60
                                                                                                                                               52; Mismatches 90; Indels
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61 PWNFPFFLIARKMAPALLTGNTIVIKPSSETPNNAFEFAKLVSQSSLPKGVENLVACKCS 120

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CURRENT APPLICATION NUMBER: US/09/450,969
CURPENT FILING DATE: 1999-11-29
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   429 GLKEGETYINEENEEAMOGEHAGWKKSGIGGALGKHGLHGYLQTQVVYLQ 478
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                                                                       383 VIDNVRKDYNVEKDEIFGPVLAITTYKDFEQVLEUANLTNAGLSSYIFSENLTEVMTATE 442
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                                                                                                                                               369 LLLDVRQEMSIMHEETFGEVLEVVAFUTLEDAISMANDSDYGLTSSIYTQNLNVAMKAIK 428
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                                                                                                                                                                                                                      MKSLTVGDPPDFN-TDYGATTNQKQLDSTHEKVQDATKNGATLMTGGHQLKRHGFFYAPT
                                                                                                                                                                                                                                                                                          MÓAVÓFGNPAERNDTAMGPLTNAAALERVEÓKVARAVEEGARVAFGGKAVEGKGYYYPPT 368
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US-60-360-039-18199
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                                                                                                                                                                                                                                                 Sequence 18199, Application 85/60360039
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NUMBEE OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
APPLICANT: Goldman, Rarry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
FITLE OF INVENTION: EXPRESSION OF MICHORIAL PROTEINS IN PLANTS FOR PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/164,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHERENT APPLICATION NUMBER HS/09/710,279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: PU3480US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOGOGOUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
                                                                                                                                       APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence OTHER INFORMATION: amino acid sequence
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38.5%;
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Pred No 4.6e-83;
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; ORGANISM: S.epidermidis US-09-450-969-4782

Matches Query Match

181;

Local Similarity

NUMBER OF SEQ ID NOS: 7544 SEQ ID NO 4782

ENGTH:

493

FILE REFERENCE: PATH99-09A

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US-09-450-969-4782; Sequence 4782; Appli; GENERAL INFORMATION:

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APPLICANT: Cao, Your APPLICANT: Chen, Xi. APPLICANT: Chen, Xi. APPLICANT: Goldman, APPLICANT: Hinkle, APPLICANT: Slater, APPLICANT: Slater, TITHE OF INVENTION:
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                                                                                                                ; ORGANISM: Thermoplasma volcanium US-60 460 039·13571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 13571, Application US/60360039
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                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13571
                          Query Match 46.8%; Score 900; DB 27; Length 473; Best Local Similarity 48.5%; Pred. No. 6.2c-80;
  Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                        APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROHIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
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                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/60/360,039 CURRENT FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cao, Yongwei APPLICANT: Chen, Xianteng
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                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                       LENGTH: 473
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95; Mismatches 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 88728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURKENT FILING DATE: 2001-02-22 NUMBER OF SEQ ID NOS: 153055 SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE LIMENSTONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/791,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptomyces coelicolor A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 492
198 RECREAGYPTGLESVYCGEGKDTGRALYTHPGYGMYTMTGSTRGGREILAQVADQI1PVS 257
                                                                                                                                              130 DRPGENILLFKRALGYTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNAIAFA 189
                                                     190 KIVDEIGLPRGVENLVLGRGETVGGELAGNPKVAMVSMTGSVSAGFKIMATAAKNITKVC 249
                                                                                                             139 E-PGRSLGVREEPIGVVAAILPWNFPVAIFARKVAPALMAGNAVVLKPSELTPLSALALA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 EAAERIPFGELYINMPGPEASQGYHTGFRITGQAGEGSRYGILFYLKIKNIYV 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 LELGGKAPEMVWKDADINNALKTILLWAKYWNAGQSGIAAERLYVHEDIYDTFINKEVELS
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                                                                                                                                                                                                                           79 AVLEAVRDATAVHADELARTVSVEQGKPLSDARGETEGACAFFDFATSQKYRAVGSMMAS 138
                                                                                                                                                                                                                                                                                                                                                                                                  10 YIDGQFVTWRGDAWIDVVNPAFEAVISRIPDGQAEDAKKAIDAAERAQPEWEALPAIERA 69
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                                                                                                                                                                                                                                                                              SWLPKISAGIPEPASEISALIVEEGGKIQQLAEVFVAFTADYIDYMAEWARRYEGEIIQS 129
                                                                                                                                                                                                                                                                                                                                         FVAGEYELDSSHGTLPVINPANGQLVAEVPSSSSSTVDRAVTAAVAAQREWGRRSHVARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.5%; Score 894; DB 21; 38.9%; Pred. No. 2.6e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       92; Mismatches 191;
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PCT-US02-03987-5058
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CUPRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5058, Application PC/TUS0203987 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: ELITRA.028VPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Elitra Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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433 LEYGMVGINTGLISNEVAPFGGIKASGLGREGSKYGIEDYLEIKYLCL 480
                                                      430 LKFGETYINRENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQTQVVYL 477
                                                                                                                                                                                                                      314 AKLNIGNGLEAG-VTTGPLIDAKAVAKVEEHIADAVSKGAKVVSGGKPHALGGTFFEPTI 372
                                                                                                                                                                                                                                                                                                                             254 LELAGNAPFIVFODADIDAAVEGALISKYRNNSQTCVCANFLYVQDGVYDAFVDKLKAAV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                       194 ELAERAGIPKGVESVVTGSAGEVGGELTSNPIVEKLTFTGSTEIGEQLMAECAQDIKKVS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 HQPDKRIIVIKQPIGVTAAITEWNEPSAMITKKAGPALAAGCTMVLKPASQTPYSALALA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 DRPGENILLFKRALGVTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNAIAFA 189
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                                                                                                            373 LVDVPKNALVSKDETFGPLAPVFRFKDEAEVIAMSNDTEFGLASYFYARDLARVFRVAEQ 432
                                                                                                                                                             370 LLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSSIYTQNLNVAMKAIKG 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96;
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Search completed: June 24, 2003, 10:30:41 Job time: 176.414 secs

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Database
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Maximum DB seq length: 2000000000
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-10-242-122A-654340
US-10-242-124A-76474
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Sequence 1819, Apsequence 1819, Apsequence 1819, Apsequence 70076, Apsequence 77077, Asequence 2774, Asequence 2774, Asequence 2774, Asequence 2774, Asequence 2774, Asequence 2351, Asequence 2351, Asequence 2351, Asequence 2351, Asequence 2551, Asequence 2554, Asequence 7938, Apsequence 7938, Apsequence 7938, Apsequence 7938, Apsequence 55544, Asequence 5554, Asequence 5554, Asequence 5554, Asequence 5554, Asequence 1243, Asequence 1716, Aseq
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Sequence 823, App
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Sequence 16681, A	Sequence Sub58, A	Sequence 12251, A	Sequence 8449, Ap	Sequence 125211,	Sequence 162810,	Sequence 21219, A	Sequence 49742, A	Sequence 4763, Ap	Sequence 7523, Ap	Sequence 17031, A	Seguence 501, App	Sequence 28, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 10932, A	Sequence 11863, A	Sequence 67328, A	Sequence 51224, A

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US-09-830-751-6
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CHERKNI APPLICATION NUMBER: 08/09/840,751
CHERKNI APPLICATION NUMBER: 09/0-04-30
FRIOR APPLICATION NUMBER: 60/151,440
FRIOR FILLNA DAIE. 1999-08-30
PRIOR FILING DATE: 2000-08-30
PRIOR FILING DATE: 2000-08-30
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TITLE OF INVENTION: Production of 3 Hydroxypropionic Acid in Recombinant TILLE OF INVENTION. Organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suthers, Patrick F APPLICANT: Cameron, Douglas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 2446; DB 5; Length 479; Local Similarity 100.0%; Prod. No. 1.9e 205; ncs 479; Conservative 0; Mismatches ?
                                                                                                                   241 AAKNITKYCLELGGKAFAIYMDDAELELAVKATVDSRVINSGQVCNCAEFVYVQKGIYDQ 300
                                                                                                                                                                181 TINNATAFAKTVDETGLDFGVFNLVLGFGETVGQELAGNDKVAMVSMTGSVSAGEKIMAT
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                                                                                                                                                                                                                                                             121 RYEGEITQSDRFGENILLFKRALGVTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEF 180
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                           301 FVNELGEAMQAVQEGNPAEFNDTAMOPLTNAAALEFVEQKVAPAVEEGAFVAFGGKAVEG
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US-10-369-493-823
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Rest Local Similarity 99.6%;
Matches 477; Conservative
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52652)8
CURRENT APPLICATION NUMBER: US/10/364,443
CURRENT FILING DATE: 2003-02-28
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Pred. No. 3.2e-204;
0; Mismatches 2; Indels (
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LENGTH: 514
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CURRENT FILING DATE: 2003-05-27
PRIOR APPLICATION NUMBER: US/09/489,039
PRIOR FILING DATE: 2000-01-27
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TITLE OF INVENTION: NUCLEIC ACLU AND AMINO ACLU SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29
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456 NVAMKAIKGLKFGETYINRENFEAMQGFHAGWKKSG1GGALGRHGLNEYLQTQVVYLQA 514
                         421 NVAMKAIKGLKFGETYINRENFEAMOGFHAGWRKSGLGGADGKHGLHGYLQTQVVYLQS 479
                                                                                                      396 KGYFYPPTLLLDVRQEMDIIHEETFGPVLPVVAFSTLDEALAMANDSDYGLTSSIYTRDL 455
                                                                                                                                                      361 KGYYYPPTLLLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSSIYTQNL 420
                                                                                                                                                                                                            336 FVNPLGEAMKAVQEGDPATPDDTAMGPLTNAAARTQVAGKVAKAVAQGARVALGGQPLEG
                                                                                                                                                                                                                                                               301 FVNRLGEAMQAVQFGNPAERNDTAMGPLINAAALERVEQKVARAVEBGARVAFGGKAVEG
                                                                                                                                                                                                                                                                                                                  276 AAKNITKVCLELGGKAPAIVMDDADLELAVKAVVDSKVINSGOVCNCVERVYVQQGIYDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TTNNATAFAKTVDETGLPRGVFNLVLGRGETVGQELAGNPKVAMVSMTGSVSAGEKIMAT 240
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Similarity 85.8%;
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Pred. No. 4.6e-180;
D3; Mismatches 25; Indels
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US-10-282-122A-65716
: Sequence 65716, Application US/10282122A
; GENERAL INFORMATION:
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                                                                                                 APPLICANT:
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 TITLE OF
               APPLICANT:
                             APPLICANT:
                                                APPLICANT:
                                                                APPLICANT:
                                                                                  APPLICANT:
INVENTION: Identification of Essential Genes in Microorganisms
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Malone, Chery)
                                                              Carr, Grant
                                                                                                Wall, Daniel
                             Forsyth, R.
                                                Yamamoto, Robert
                                                                              Trawick, John
                                                                                                               Zyskind, Judith
                                                                                                                                 Ohlsen, Kari
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Best Local :
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PRIDE FILINS DAIE: 2000-05-26
PPIOP APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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OR FILING DATE: 2000-11-27
OP APPLICATION NUMBER: 50/257,931
OR FILING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/267,636
OP FILING DATE: 2001-02-05
OP APPLICATION NUMBER: 60/266,308
OP APPLICATION NUMBER: 60/266,308
OP FILING DATE: 2001-02-16
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423 FYVTPRIQESETYINKENFEAMQOPHAGWKKSGIGGAGAKHGLEEYLGTQVVYLET 478
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                                                                                                                                                                                                                                                                                                        TKVSLELGGKAPAIVLKDADLDLAVKSILASRVGNTGQICNCAERVYVHSSLKDAFIEKM 302
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                                                MKAIKGLKEGETYINEENEEAMQGEHAGWEKSGIGGAGGKHGLHGYLQTQVVYLQS 479
                                                                                                FFEPTLLIDIENSMOIMKEETFGPVLPVSAFOILE-QVIALAND-CEFGLISSVYTINLNEA
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Sequence 5824, Application US/10417886 GENERAL INFOPMATION:

US-10-417-886-5824

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HS-10-282 122A-54340
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SEQ ID NO 5824
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PRIOR FILING DATE: 1998 07:24
PRIOR APPLICATION NUMBER: US 60/074,787
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES PELATING TO ENTEPOBACTER
TITLE OF INVENTION: CLOAGRE FOR DIAGNOSTICS AND THEPAPEUTICS
FILE REFERENCE: 107196.135
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                          TITLE SE INVENTION. Identification of Essential Genes in Microorganisms FILE REFERENCE: ELTERA 034A CHERENN APPLICATION NUMBER: HS/10/282,122A CHERENT FILING DATE: 2003-02-20
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Local Similarity 41.5%; Prod No. 9.46-123;
hos 292, Conservative 17, Mismatches 10, Indels
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Xu, H.
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Wall, Daniel
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Malone, Cheryl
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                                                                                                                                                                                                                                                                                                                          Trawick, John
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Sequence 488, Application US/10092411A
GENERAL INFORMATION:
APPLICANT: LIVEN DESCRIPTION:
TITLE OF INVENTION: NUCLEIC ACID AND AMIN
TITLE OF INVENTION: EPIDERMIDIS FOR DIAG
FILE REFERENCE: 082796-101
CURRENT APPLICATION NUMBER: US/10/09/2 411
CURRENT FILING DATE: 2002-03-07
FRIGE REPLICATION NUMBER: US/09/144,001
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US-10 282 122A-54340
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Hest Local Similarity 63.1%, Prod. No. 2.3e-103;
Matches 245; Conservative 52; Mismatches 90; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 245;
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                                                                                                                                                                                                                                                        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-101
                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/092 411A
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR EFILING DATE: 1997-08-14
                                                                                                                               PRIOR APPLICATION NUMBER: US 09/134,001 PRIOR FILING DATE: 1998-08-13
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 EAIKASRICHNOQVONCAERAYVHTSVYDEFVDKFVKAMSKVSVGNTL-KGDFDMGPLVN 239
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                                                                                                                                                                                                                                                               SEQ ID NC 18199
                                                                                                        Query Match
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                                                     Matches 182;
                                                                                Best Local Similarity
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SEQ ID NO 4388
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                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE PEFERENCE: 38-10(52952)B
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APPLICANT:
                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/360,039
FRICE FILING DATE: 2002 02 21
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                                                                                                                                                                                                               TYPE: PRT
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9 MYIDGQEVTWRGDAWIDVVNPATEAVISPIPDGQAEDARKAIDAAFRAQPEWEALPAIER 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinkle, Gregory J.
Slater, Steven C.
Goldman, Harry S.
Chen, xianfeng
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                                                   Conservative 100; Mismatches 184; Indels
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                                                                           36.9%; Score 903; DB 6; Length 493; 38.4%; Pred. No. 3.3e-70;
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38.5*;
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                                            PRIOR ETLING DATE 2001 02-16
                                                                                            FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/242,578 FILLING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
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                                                                                                                                                                                     FILING DATE: 2000-11-27
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  Prior Application data removed - See File Wrapper or PALM SEQ ID NOS: 78614
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Fursyth, P.
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LENGTH: 480
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                                                                                                               PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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PRIOR EILING DATE: 2000-00 PRIOR APPLICATION NUMBER:
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PRIOR FILING DATE: 2000 05-26
FRAME APPLICATION NUMBER: 60/240,435
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Malone, Cheryl
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60/230,347
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-28
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
APPLICANT: Cao, Yongwei
APPLICANT: Stater, Steven C.
APPLICANT: Stater, Steven C.
APPLICANT: Chen, Xianteng
APPLICANT: Chen, Xianteng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 48-10(52052)B
CHERENT ENLING DATE: 4003-02-8
CHERENT ENLING DATE: 2003-02-8
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                         CURRENT APPLICATION NUMBER: US/10/28,122A CUPRENT FILING DATE: 2003-92-29 PPIOP APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR PPILICATION NUMBER: 66/206,848 PRIOR FILING DATE: 2000-65-23 PRIOR FILING DATE: 2000-65-23 PRIOR APPLICATION NUMBER: 66/207,727 PRIOR APPLICATION NUMBER: 66/207,727
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
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          PRIOR APPLICATION NUMBER: 60/230, 347
                                                              PRIOR APPLICATION NUMBER.
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                                     PRIOR FILING DATE:
                                                                                         PRIOR FILING DATE:
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Malone, Cheryl
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418 EAAERIREGELYINMPGPEASOGYHTGERLTGOAGEGSRYGILEYLKIKNIYV 470
                                                                                     425 KAIKGLKEGETYINRENEEAMQGEHAGWPKSGIGGADGKHGIHGYLQTQVVYL 477
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                                                                                                                                                                                                 358 FLPTIIDNVDQKSKIFQEEIFAPVIGARKVSDVEEMYSLANDSKYGLASYLFTKDPNL1F 417
                                                                                                                                                                                                                                                                                            365 YPPTLLLDVROEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSSIYTONLNVAM 424
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APPLICANT:
                         CURRENT APPLICATION NUMBER: US/10/366,683 CURRENT FILLING DATE: 2003-02-13 PRIOK APPLICATION NUMBER 09/25/391 PRIOK FILING DATE: 1999-02-18
                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPPULICS FILE REFERENCE: PATH03-04
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOK APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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NUMBER OF SEQ ID NOS: 33142
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Local Similarity 39.3%; Pred. No. 3.7e-68;
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                                                                                                                                                                                                                                      Deloughery, Craig
Bush, David
                                                                                                                                                                                                                                                                                                      Nolling, Jork
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                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas deruginosa \overline{u}s-10-419-128-27749
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LENGTH: 594
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                                                                                                               Matches
                                                                                                                                                            Duery Match
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                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/419,128
CURRENT FILING DATE: 2003-04-21
FPTOF AFFLICATION NUMBER: US/09/252,391
PPTOP FILING DATE: 1949-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc J. Rubenfield et al.
FITLE OF INVENTION: NUCLEIC ACID AND AMING ACID SEQUENCES FELATING TO PSEHFOMONAS
TITLE OF INVENTION: AERUGINGSA FOR DIAGNOSTICS AND THEPAPEUTICS
FILE FEFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: HS 60/094,190 PRIOR FILING DATE: 1998-07-27
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125 YVDGAWVDADNGGTIKVNNEATGELIGSVEKMGAAEIFFAJFAADKALPAWFALTAKERA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   544 LEYGMVGINTGLISNEVAFFGGIKASGLGREGSKYGIEDYLEIKYLCL 591
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                                                                                                         184; Conservative 95; Mismatches 187;
                                                      10 YIDGQEVTWRGDAWIDVVNPATEAVISKIPDGQAEDARKAIDAAERAQPEWEALPAIERA 55
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                                                                                                                                       Similarity
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                                                                                                                                    39.3%; Pred. No. 5.2e-68;
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                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
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APPLICANT:
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PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 70/191,078
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SOFTWARE:
                         Remaining Prior Application data removed. See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 78614
                                                                                       PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                       PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/267,636
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Patentin version 4.1
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Carr, Grant
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Malone, Cheryl
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UMGANISM: Escherichia coli
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434 FYGIVGINTGIISNEVAPFGGIKASGLGREGSKYGIEDYLE 474
                                                          431 KFGETYINRENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQ 471
                                                                                                                374 VDVPANAKVSKEETFGPLAPLFRFKDEADVIAQANDTEFGLAAYFYARDLSRVFRVGEAL 433
                                                                                                                                                                          371 LDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSSIYTQNLNVAMKAIKGL 430
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Search completed: June 24, 2003, 10:35:22 Job time: 52.8555 secs

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probable aldehyde	S50576		520	31.5	769.5	41
probable aldehyde	AG0669	ω	481	31.5	769.5	40
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succinate-semialde	P8107/	^	47/	31.9	780.5	36
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probable aldehyde	C85733	to	474	32.0	782.5	نى دى
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aid⊬hyd⊏ dehydroge	A/23078	ب	484	32.1	784.5	ند د ـ د
succinate-semialde	F98208	ŧ٥	184	32.1	784.5	30

A;Note: acts also on other aldehydes c,Superfamily: aldehyde dehydrogenase homology C,Keywords: NAD; oxidoreductase A.C.LUSS REFERENCES. GB.AE000239; GB.900096; NID-31787682, PIDN AAC74497.1; PID:g17876 A.Experimental source. strain K-12, substrain MG1655 C.:Genetics: Science 277, 1453-1462, 1997
A:Titie: The complete genome sequence of Escherichia coli K-12.
A:Peference number A64720, MUTD 97426617, PMID 9278803
A:Accession: B64893 A Class references GR:MG4541, NID.g145221, PIDH.AAA23427.1, PID.g145222 R:Blattner, F.B.: Plunkett TII, G.: Bloch, C A.: Perna, N.T.: Burland, V.: Riley, M.: A : Rose, D J : Man, B : Shao, Y: Ϋ́ 7 G ďζ E,45-305/homain. aldehyde dehydrogenase bomology. ALUON E,178-257/Domain. NAD binding #status predicted -:NADNE,251,285/Active site. Glu. Cys #status predicted ý A, Gene: aldA C, Function: A;Residues: 1-479 <HID> A;Ctoss references GR:N A, Reference number A, Accession: A38165 A;Title: Molecular cloning and DNA sequencing of the Escherichia coli K 12 ald gene e A;Reference number: A38165; MUTD 92011371, PMID 1917845 A; Description: catalyzes oxidation of lactaldehyde to lactate using NAD A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A;Status: preliminary Best Local Similarity 99.4%, Matches 477; Conservative Bacteriol. 173, 6118-6123, 1991 121 RYEGEIIQSDRPGENILLFKRALGVTTGILPWNFPFFLTARKMAPALLTGNTIVIKPSFF 180 121 FYEGETIONORPGENILLEKKALGVITGILPWNEPEFLIARKMAPALLIGNTIVIKPSEF 180 61 EALFATERASWILKTISACTEERASETSALTVEEDGKIDOLAEVEVARTADYTDYMARWAR 120 0; Mismatches Score 2432, DB 2, Pred, No. 5,4e lb2; ALIGNMENTS Length 479. Indels 0. Gaps

20	361 KGYYYPPILLLIDYRQEMSIMHEETEGPYLDYVAFDTLEDAISMANDSDYGLTSSIYTQNL 4	ζ,
360 	301 FUNKLGEAMQAVQFGNPAEKNDTAMGPLINAAALERVEGKVARAVEEGARVAFGGKAVEG 3 	оy
300	241 AAKNITKVCLEIGGKAPAIVMDDADLELAVKAIVDSRVINSGOVCNCAERVYVOKGIYDO 3 	96 49
240 240	THI TENNATAFAKTYDETGLPRGYFNLYLGKGETYGGELAGNPKVAMYSMTGSVSAGEKIMAT 2 	del VO
180	121 RYEGELIQSDREGENILLEKRALGVTTGILEMNEPFFLIARKMAPALLTGNTIVIKPSEF 1 	Oy Db
120 120	61 FALPATEKASWIJKKISAGIKEKASEISALIVEEGGKIQQLAEVEVAFTADVIDYMAEWAR I 	Db VY
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0;	ch 99.2%; Score 2426; DB 2; Length 479; il Similarity 99.4%; Pred. No. 1.7e-161; 476; Conservative 0; Mismatches 3; Indels 0; Gaps	Query Match Best Local: Matches 47
7 54	A:Status: preliminary A:Molecule type: DNA A:Molecule type: DNA A:Residues: 1-479 <hay 0509952="" a:cross-references:="" a:experimental="" a:gene:="" c:genetics:="" e:s2021="" e:s2021<="" gb:ha000007;="" gspdb:gn00154="" ol57:h7,="" pid:q1336]487;="" pidn:hab35444.1;="" rimd="" source:="" strain="" substrain="" td=""><td>A: Status: A: Molecule A: Residues A: Cross-re A: Cross-re A: Experime C: Genetics A: Gene: Ec</td></hay>	A: Status: A: Molecule A: Residues A: Cross-re A: Cross-re A: Experime C: Genetics A: Gene: Ec
Han, C.G.	_change 03-Aug-2001 _change 03-Aug-2001 hii, K.; Yokoyama, K ri, M.; Shinagawa, H	C:Species C:pate: 18 C:pate: 18 C:paccessic R:Hayashi, qasawara, DNA Res. 8 A:Title: 0 A:Referenc
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	421 NVAMKATKOLKEGETYTINENEEAMOGEHASWRKSGTODAFOKHGLHGYLGTOVVELQS 479 	da Yo
420 420	361 KGYYYPPILLLDYMQEMSIMHEETFGPYLPVVAFDTLEDAISMANDSDYGLTSSIYTONL 4 	dd
360	901 FYNKLGEAMQAVQEGNEAEKNDTAMGPLINAAALERVEGKVARAVEEGARVAEGGKAVEG 3 	Db GA
300	241 AAKNITKVCLELGGKAPAIVMDDADLELAVKAIVDSRVINSGQVCNCAERVVQKGIYDQ 3 	ag dy
240	181 TINNATAFAKTUDETGLPRGVFNLVLGRGETVGOELAGNPKVAMVSMTGSVSAGEKIMAT 2 	dd VV

C;Accession: A81023 R;Tettolin, H.; Saunders, N.J.; Heidelberg, J.; Jeftries, A.G.; Nelson, K.E.; Eisen, Hickey, F K ; Haft, D H ; Salzberg, S.L.; White, O.; Fleischmann, B.D.; Hougherty, B

aldehyde dekydrogenase A NMB1968 [imported] - Neisseria meninqitidis (strain MC58 ser C;Species: Neisseria meninqitidis C;Datro: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001

A81023 RESULT 4

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RESULT 3
D85737
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A; Accession: D85737
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A;Experimental source: strain 0157:H7, substrain ED1933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lactaldehyde dehydrogenuse (EC l 2 l 22) A RMA0480 [imported] - Neisseria meningitidis C:Species: Neisseria meningitidis C:Date: 05-May-2000 #sequence_rovision 05-May-2000 #text_thange 02-Feb-2001 C:Accession: F81965
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C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
C;Keywords: oxidoreductase
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Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, G.M.; Moxon, E.P.; Rapppoli, P.; Ve
A.Title: Complete geometasapusoce of Neisseria meningitidis serogroup B strain MC58.
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A;Feference number = A8:77°; MORE IO2225°°, EMEC 1078143°
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C;Superfamily: aldehy
C;K-ywords: oxidoredu
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Hest Local Similarity 63.0%, Pred. No. 1 50-100;
Matches 300; Conservative 64; Mismatches 110; Indols
        211 TVGQELAGNPKVAMVSMTGSVSAGEKTMATAAKNTTKVCLELGGKAPAIVMDDADLELAV 270
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424 MKATKSI KESETYI NENEFEAMWITEHAISWEKSSI ISSAIISKHSI HTVI QTTQVVYLQS 479
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423 FYVTPPLQPGETYINPENERAM@GEHAGWEKSGIGGALGKHGLBEYLQIQVVYLEI 478
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probable lactaldshyds dehydrogenase (EC 1.2.1.22) truncated homolog Cj0490 [similarit C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #text\_change 03-Jun-2002

R;Parkhill, J.; Wren, F.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, I.C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000 ; Basham, D.;

A;Cross-references GR.AH.139075, GR-AH.111168; NID-95967817; PIDN-CAB75128 1, FID 9696 A:Experimental source: serotype 01, strain NCTC 11168

Superfamily: aldehyde dehydrogenise (NAD+); aldehyde dehydrogenise

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PWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNAIAFAKIVDFIGLPRGVFNLVLGRGE

Db

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Craccession: DB3613
RSTOVET, C.K.; Pham, X.G.: Erwin, A.L.; Mizoguchi, S.D.; Warreber, P.; Hickey, M.J., Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A: Experimental source: strain PAol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-483 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: A82950; MOID:20437337; PMID:10984043
A:Accession: D83613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Cross-references: GB:AE004464; GB:AE004091; NID-q9946099; PIDN AAG03654-1; GSPER:GNOO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 36.0%; Score 879.5; DB 2; Length 483; Best Local Similarity 39.3%; Pred. No. 1.2e-53;
373 LVDVPKNALVSKDETEGPLAPVEREKDEAEVIAMSNDTEFGLASYFYARDLARVFRVAEQ 432
                                                                                                                                            *14 AKLNIGNGLEAG-VTTGPLIDAKAVAKVEEHIADAVSKGAKVVSGGKPHALGGTEFEPTI
                                                                                                                                                                                                                                                                                      254 LELGGNAPFTVFDDADLDAAVEGALISKYRNNGQTCVCANRLYVODGVYDAFVDKLKAAV
                                                                                                                                                                                                                                                                                                                                                              250 LELGGKAPATYMDDADLELAVKATYDSRYTNSGQYCNCAERYYYQKGTYDQFYNRLGEAM
                                                                                                                                                                                                                                                                                                                                                                                                                                      194 ELABRAGIPKGVESVVTGSAGEVGGELTSNPIVPKLTFTGSTETGRQLMAECAQDIKKVS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 KIVDETGLPRGVFNLVLGRGETVGQELAGNPKVAMVSMTGSVSAGEKIMATAAKNITKVC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 HQPDKRIIVIKQPIGVTAAITPWNFPSAMITKKAGPALAAGCTMVLKPASQTPYSALALA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 DRPGENILLEKRALGVTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNAIAFA 189
                                                                370 LILDVROEMSIMHEETIFGPVLFVVAFDILEDAISMANDSDYGLTSSIYTONLNVAMKAIKG 429
                                                                                                                                                                                                                 410 QAVQFGNPAERNDIAMGPLINAAALERVEQKVARAVEEGARVAFGGKAVEGKGYYYPPTL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 GWRKSGIDGADGKHGLHGYLQTQVVYLQ 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 GFRKSGIGGADGKHGLEEYLATHVVYLQ 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 OAGVENALAMLORATAKGAIVEGGGKITDTSGYYFPASVLTNVKHEDEIMOKEIFAPILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 AAALERVEQKVARAVEEGAKVAFGGKAVEGKGYYYPPTLLLDVRQEMSIMHEETFGPVLP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 EAIKASRICHNGQVCHCAERAYVHTSVYDEFVDKFVKAMSKVSVGNTL-KGDFDMGPLVN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 NKLRRWFDLMIENQUDLARLMTIEQGKPLAEAKGEIAYAASFLEWFGEEAKRIYGDTIPG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 YVDGAWVDADNGQTIKVNNPATGELIGSVPKMGAAETRRALEAADKALPAWRALTAKERA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 SWILKTISACTREMASETSALTVEFEGGETQQLAEVEVAFTADYTDYMAEWARRYEGETTQS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 YIDGOFVIWKIDAWIDVVNPATEAVISKIPDGOAEDARKAIDAAERAOPEWEALPAIERA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAKFUTLDEVIUMANUXEYGLTSSTYTQNLDTAMRASRETKFGETYINRENFEAMQGFHA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVAFOTLEDAISMANDSDYGLTSSIYTQNLNVAMKAIKGLKFGETYINRENFEAMQGFHA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KATVDSRVINSGQVCNCAERVYVQKGIYDQFVNRLGEAMQAVQFGNPAERNDIAMGPLIN 330
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R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A,Title. The complete genume sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accression: F65045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: gabD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GR:AE000851; GH:000046; NID:g17840]]; PIDN:AAC75708 ]; PID:g17890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-482 <BLAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 succinate-semialdehyde dehydrogenase [NAD(P)] (EC 1.2.1.16) - Escherichia coli (strai
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434 EYGIVGINTGIISNEVAPFGGIKASGLGEEGSKYGIEDYLE 474
                                                                  431 KFGETYINRENFEAMQGFHAGWPKSGIGGADGKHGLHGYLQ 471
                                                                                                                                                                                                        371 LDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSSIYTQNLNVAMKAIKGL 430
                                                                                                                                                                                                                                                                                   315 KLHIGDGLD-NGVTIGPLIDEKAVAKVEEHIADALEKGARVVCGGKAHERGGNEFQPTIL
                                                                                                                                                                                                                                                                                                                                                                                                                         255 ELGGNAPFIVFDDADLDKAVEGALASKFRNAGQTGVCANKLYVQDGVYDRFAEKLQQAVS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 RPGENILLFKRALGVTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNAIAFAK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 LATRAGYPAGYFNYYTGSAGAYGNELTSNPLYRKLSFTGSTETGROLMEQCAKDIKKYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 ILRNWENLMMEHQUULAKLMILLEQGKFLABAKGELSYAASFIEWFAEEGKRIYGDTIPGH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 WIRKISAGIRERASEISALIVEEGGKIQQLAEVEVAFTALYIDYMAEWARRYEGEIIQSU 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 INGEWLDANNGEAIDVTNPANGDKLGSVPKMGADETRAAIDAANRALPAWRALTAKERAT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 IDGQFVTWRGDAWIDVVNPATEAVISRIPDGQAEDARKAIDAAERAQPEWEALPAIERAS
                                                                                                                                                                                                                                                                                                                                                      AVQFGNPAERNDLAMGPLLNAAALERVEQKVARAVEEGARVAFGGKAVEGKGYYYPPTLL 370
                                                                                                                                         VDVPANAKVSKEETFGPLAPLFRFKDEADVIAQANDTEFGLAAYFYARDLSRVFRVGEAL 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELOGKAPATYMDDADLELAVKATYDSRYTNSGQYCNCAERYYVQKGTYDQFVNELGEAMQ H10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QADKRLIVIKQPIGVTAAITPWNFPAAMITRKAGPALAAGCTMVLKPASQTPFSALAIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVHEIGLERGVENLVLGRGETVGGELAGNEKVAMVSMTGSVSAGEKIMATAAKNITKVCL 250
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C:Species: Escherichia coli C:Date: 18 Jul 2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001

succinate semialdehyde dehydrogenase [imported] - Escherichia coli (strain 0157:H7,

R.Hayashi, T.: Makino, K.: Ohnishi, M.: Kurokawa, K.: Ishii, K.: Yokoyama, K.: Han, gasawara, N.: Yasunaga, T.: Kuhara, S.: Shiba, T.: Hattori, M.: Shinaqawa, H.

C;Accession: B91069 R,Hayashi, T., Makin

в91069

RESULT 9

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A;Gene:
C;Superf
                                                                                                                  A:Molecule type: DNA
A:Residues: 1 482 kSTO:
A:Cross-teferences: GB-AE005174: NTD:g12517094. FIDE-AA357768.1; GSPDB:GN00145; UWGP-2k9
A:Experimental source: strain 0157:H7, substrain EDL933
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                   succinate-semialdebydo debydrogenase [imported] - Escherichia celi (strain 0157:H7, subs
C:Spacies: Escherichia celi
C:Space: 16:Feb-2001 **sequence_revision 16 Feb-2001 *text_change 27.Nov 2001
C:Accession: D85913
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A.Cross-references- GR:RA0000007: FIDN-RARX6445 1: FID:91846.9493: GSPDB GN00154
A:Experimental source: strain 0157:H7, substrain RIMO 0509952
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A:Title: Complete genome sequence of enterchemorrhagic Escherichia coli 0157:H7 and gend
A.Reference number A99629, MOTD:21156231; FMTD:11258736
                                                      A;Gone: gabD
C:Superfamily. aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
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                                                                                                                                                                                                                                                                    A.Accession. D85913
                                                                                                                                                                                                                                                                                         A;Title. Genome sequence of enterchemorrhagic Escherichia coli 0157:H7
A;Peference number: A85480; MUID:21074935; FMID:11206551
                                                                                                                                                                                                                                                                                                                                             iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
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A, Residues: 1:482 - H
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Best Local Similarity
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39.3%; Pred. No. 4.9
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Pred No 4 9e-53;
                  Score 870 5:
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                  D# 2:
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anta, E.; Potamousis, K.; Apodaca
                    Length 482
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2:Superfamily: aldebyde debydregenase (NAD+), aldebyde debydrogenase homelegy
C:Keywords: oxidoreductase
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A; Residues: 1-482 - PAR-
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.P.; Pickard, D.; Wain, J.;
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sucrinate-semialdehyde dehydrogenase [NAP(P)] (FC i 2 l lb) - Salmonella enterica sub E/Species. Salmonella enterica subsp. enterica serovar Typhi A:Note: this species has also been called Salmonella typhi C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 03-Jun-2002
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Nature 413, 848-852, 2001 A:Authors: Parry, C.: Quail, M.: Patherford, K.: Simmonds, M.: A; Status: preliminary A; Accession: AE0839 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A;Reference number: AB0502; PMID:11677608

Connerton, P ; Cronin, A ; Davis, P ; Davies, R M ; Dowd, L ; White, N ; Farr

Skelton, J.: Stevens,

Church

STY2911

SK ALSTRIBZ, PION CAGOSHOO 1; PID:gleSorR74, GSEGE GNEO176

Query Match Local Similarity 130 DEPGENILLEKFALGVTTGILFWNFPFFLIAFKMAPALLTGNTIVIKPSEFTTNNAIAFA 189 74 NILKEWENLMMEH@GDLAFLMTLE@GKELAEAKGEISYAASFIEWFAEEGKRIYGDTIPG 133 14 FILIGUWKDANGGIVLEVSNEANGKELGNVPKMGAEETRDATNAANRALEAWRALTAKERA 10 YTHSQEVTWESDAWTDVVNPATEAVTSRTPLEQAEDARKATDAAERAQPEWEATPATERA 69 SWLRKISAGIRERASEISALIVEEGGKIQQLAEVEVAFTADYIDYMAEWARRYEGEIIQS Conservative 35.1%; Score 858.5; DB 2; 91; Mismatches 189; Length 482; Indeis

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OY 466 PPTLILLDVROEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDVGLTSSIYTONLNVAMK 425	OY 807 EAMOAVOFONPAERNDIAMOPLINAAALERVEOKVARAVEEGARVAFGGKAVEGK-GYYY 365 105 GKVVOLKVONGLEEG-VHIGPLIEKKGYEKVKAHVDDAVAKGARVVIGGKGOEGNDSYFY 361	OY 247 KVCLEIGGKAPATYMDDADLELAVKATYDSRYTNSGOVCNCAERYYVOKGTYDGFVNRLG 306 : TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	QY 187 AFAKIVDEIGEPRGVFNLVIGRGETVGQELAGNPKVAMVSMTGSVSAGEKIMATAAKNIT 246 EE EL TELLITET ET EL TELLITET	QY 127 IQSDRPGENILLEKRALGVTTGILPWNEPEELIARKMAPALLTGNTIVIKPSEETTNNAI 186 : : :   :   :	QY 67 ERASMIRKISAGIRERASHISALIVEEGGKIQQLAEVEVAFTADYIDYMAEWAPRYEGEI 126 	ARKAIDAAERAQPEWH 	44.6%; Score 845.5; DB 2; Length 475; imilarity 39.1%; Prod. No. 2.7e-51; Conservative 84; Mismatches 195; Indels 7;		A;Status: preliminary A;Status: preliminary A;Molecule type: DNA A;Rosidues: 1475 (STO) A;Cross references: db:AP001518; GB:BA000004; NID:q10175792; PIDN:BAB07035.1; GSPDB:GN00 A;Cross references: db:AP001518; GB:BA000004; NID:q10175792; PIDN:BAB07035.1; GSPDB:GN00	R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, E.; Hira R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, E.; Hira Nucleic Acids Res. 28, 4417-4341, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A84650; MUID:20512582; PMID:11058132	D84064  Survinate-semialdehyde dehydrogenase gabD [imported] - Bacillus halodurans (strain C-125 C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-bec-2000 *sequence_revision 01-bec-2000 *text_change 15-Jun-2001	RESULT 12	4 10 LKEGETYINKENFEAMOGEHAGWPKSGIGGALIGKHGLHGYLQ	173 LADVPDNAKVAKEETFGPLAPLERESDEADVIRQANDTEFGIAAVFYAPDLSRVFPVGEA	370 LLIJVROEMSTMHEETEGPVLFVVAFDTLEDATSMANDSDYGLTSSTYTONLAVAMKATKG	OY RIO QAVQEGNPAEKNDIAMGPLINAAALEKVEUKVAKAVEEGARVAPGGKAVEGKGYYYPPTL 369  :  :	OY 250 LELGGKAPATYMDDADLELAVKATYDSRYTNSGQVYNCAERYYYOKGTYDGFYNRLGEAM 309		
455	Db 395 TEGPLAPTEFETAEQVVAEANDTIYGLAAYFYAENLKRVWHVAFALEYGMVGINTGKMS 454  OV 444 AMOGEHAGWEKSGIGGADXKKHGLHGYLA 471	324 AMGPLINAAALERVEGKVARAVEEGARVAFGKAVEGKGYVPPTILLIDVROEMSIMHEE	QY 264 ADLIBLAVKATVESHVINSGUVCNI AEFVYVQKGIYLQFVNRLGEAMQAVQFGNPAERNDI 323		OY 145 VTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNAIAFAKIVDEIGLPRGVFNL 204	Qy 85 EISALIVEEGGKIQQLAEVEVAFTADVIDYMAEWARKYEGEIIQSDRPGENILLFKRALG 144	QY 25 DVVNPATEAVISRIPDGQAEDARKAIDAAERAQPEWEALPAIFPASWI.RKISAGIRERAS 84	Ouery Match 34.2%; Score 836; DB 2; Length 491; Best Local Similarity 39.3%; Pred. No. 1.3e-50; Matches 176; Conservative 85; Mismatches 185; Indels 2; Gaps 2;	A;Gene: qabb2; SMb21185 A;Genome: plasmid C;Superfamily: aldehyde dehydrogenase (NAD*); aldehyde dehydrogenase homology C;Keywords: oxidoreductase		pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R. L.; Hyman, R.W.; Jones, T. Science 293, 688-672, 2001 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau	A:Residues: 1-491 <kur> A:Cross:references. GB.AL591985, PIDN CAC49251 1; PID:q15140747; GSPDB-GN00167 A;Experimental source: strain 1021, megaplasmid pSymB R:Galibert, F.: Finan, T.M.: Lond, S.R.: Publer, A.: Abola, P.: Ambe, F.: Barlov-Hubl</kur>	A H .	A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing e A:Poference number: A98842; MUID:21306508; PMID:11481431	R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her Proc Natl Acad Sci H.S.A. 98 9889-9894, 2001	probable socihale semia melijoti C;Species: Sinorhizobium melijoti C;bate: 24 Aug 2001 *sequence_revision 24 Aug 2001 *text_change 03 Jun 2002 C:Accession: C95948		OY 420 AINJUNESCELLINGUE FRANCIS FROM KASO (GEADIA KROLDE) LO TOVY 4/5  1	<b>.</b> ω

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succinate-semialdehyde dehydrogenase BH0995 [imported] - Bacillus halodurans (strain C-1 C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: C83774
R:Takami, H.: Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, P.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MTD:20512582, FMTD 11058132
A;Accession: C83774
A;Status: preliminary
A;Molecule type: DNA
A,Residues: 1468 'STO-.
A;Cross-references: GB:AF001510; GB:BAUSHURL, NID g101/440; PIDN-BAR04714.1; GSPIB-SQNOC
A;Experimental source: strain C-125
C;Gene: BH0945
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
                 Succinate semialdehyde dehydrogenase [imported] - Caulobacter crescentus C.Species: Caulobacter crescentus C.Species: Caulobacter crescentus C.Date 20-Apr-2001 #scquence_revision 20-Apr-2001 #text_change 10-May-2001 C.Accession: B87638

R Niarman, W C Feldblyum, T V.; Paulsen, I T; Nelson, K.E.; Eisen, J.; Heidelberg, J. B: Laub, M T. DeBey, R T; Dedson, F.I; Purkin, A S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, J.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad Sci. N S.A. 98, 4135-4141, 2001

A, Title. Complete Genome Sequence of Caulobacter crescentus.

A, Reference number: A87249; MCID:21173698; pMID:11259647

A, Accession: B87638
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A; Status: preliminary
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Pred. No. 1.4e-50;
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A:Molecule type: DNA
A:Residues: 1-82 <STO>
A:Cross:references. GB.AE005673, NID:gl3424806, FIDN.AAK25102.1, GSFDB.GN00148
C:Genetics:
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C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase
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                                                MKATKGLKEGETYTNPENFEAMQGEHAGWRKSGTGGADGKHGLHGYLQTQ 473
                                                                                                FYQPTVLVGATPEMRIFQEEIFGPVAPIVKFETEAEAVELANATPFGLAAYFYSRDVGRC 423
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Search completed: June 24, 2003,  $10\cdot18\cdot31$  Job time : 19.3303 secs

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DHAR_BACSH
                                                                                                                                                                                                                                                                                                                                                                                                                                   SSDH_HUMAN
DHA5_YEAST
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p51647 rattus norv
027640 enchytraeus
P81178 mesocriectu
P47738 mus musculu
P11884 rattus norv
P42236 bacillus su
P15437 equus cabal
                                                                                                             p38067 saccharomyc
p17445 escherichia
p41751 aspergillus
p49189 homo sapien
p56533 gadus calla
p56533 gadus calla
p75891 homo sapien
p42757 atriplex ho
p59808 schizesacch
p51647 rattus norv
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Result No.

DHAM\_MESAU DHAM\_MOUSE DHAM\_RAT DHA1\_BACSU DHA1\_HORSE

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"A 570 kb DNA sequence of the Escherichia corresponding to the 28 0-40.1 mln region of paa Res. 3:363 377(1996).  [4] SEQUENCE OF 1-11. STRAIN K12 / EMG2, MEDILINE-9744.975; PubMed-9298646; MEDILINE-9744.975; PubMed-9298646; Link A 7, Pobison K, Church G M; "Comparing the prodicted and observed progion the growleted and observed progion the growleted and observed progion the growleted and statuted programme of Escherichia coli K-12."; Electrophoresis 18:1159-1313(1997)!- FUNCTION: ACTS ON LACTALDEHYDE AS WELL-1: CATALYTIC ACTIVITY. (S)-lactaldehydo-lactate + NADH.	RP SEQUENCE FROM N.A.  RDININE-97426617, PubMeds-9278503;  RX MEDLINE-97426617, PubMeds-9278503;  RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Bur RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Bur RA Gregor T., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose RA Mau B., Shao Y.;  "The complete yenome sequence of Escherichia culi K 12.";  RT "The complete yenome sequence of Escherichia culi K 12.";  RT Science 277:1453-1474(1997).  RI Science 277:1453-1474(1997).  RI Science 277:1453-1474(1997).  RR SEQUENCE FROM N.A.  RC STRAIN-K12;  RR MEDLINE-97251357, PubMed-9097033,  RA MEDLINE-97251357, PubMed-9097033,  RA MEDLINE-97251357, PubMed-9097034,  RA MICHAEL Baba I., Fujita K., Hayashi K., Inada T., Isono K.  RA ALLa H., Baba I., Fujita K., Hayashi K., Irada T., Isono K.  RA ALLa H., Baba I., Fujita K., Michael K., Kirakawa M.,  RA McLomura K., Makade S., Nakamura Y., Nashimeta H., Mishio Y.  RA Oshima T., Saite N., Sampei G., Seki Y., Sivasundaram S.,  RA Yamamoto Y., Horiuchi T.;  RT "A 570-kb DNA Sephence of the Escherichia culi K 12 genome  "A 570-kb DNA Sephence of The Escherichia culi K 12 genome	sequence annotati En 1 2 1 En	DHALL DHALL DHALL DHALL DHALL DHAN DHAN LHAM DHAM DHARE DHARE FEARE FEARE FEARE
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SWISS 2DPAGE; P25553; COLL.
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478 AA;
                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-K12 / JM103;
MEDLINE-94137927; PubMed=8297211;
Niegemann E., Schulz A., Bartsch K.;
Niegemann E., Schulz A., Bartsch K.;
"Molecular organization of the Eschorichia coli gab cluster:
nucleotide sequence of the structural genes gabb and expression of the GARA permease gene.";
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01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Succinate-semialdehyde dehydrogenase (NADP+) (EC 1.2.1.16) (SSDH).
GABD OR B2661.
                                                                                                                              Pfam; PF00171;
                                                                                                                                                               EcoGene; EG11329; qabD
                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (see http://www.isb-sib.ch/announce/
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-!- CATALYTIC ACTIVITY: Succinate semialdehyde + NAD(F)(+) + H(2)0 succinate + NAD(P)H.
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                                                                                                                                                                                                                                            EMRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: 4-aminobutyrate (GABA) degradation.-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analysis of its sequence features.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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199890; BAA16522 1: ALT_FRAME

D90890; BAA16523 1: ALT_FRAME

D90890; BAA16524.1; ALT_FRAME
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                            "Molecular basis of symbiosis between Rhizobium and legumes."; Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Khizobiaceae group;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)
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ACT_SITE
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                                           STRALN-168 / JH642;
MEDLINE-96359364; PubMed=8752328;
Boch J. Kempf B., Schmid R., Bremer E.;
"Synthesis of the osmoprotectant glycine betaine
subtilis: characterization of the gbsAB genes.":
                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last annotation update)
Betaine aldehyde dehydrogenase (EC 1.2.1.8) (BADH).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
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                                                                                                                                               SEQUENCE FROM N A , AND SEQUENCE OF 1-25
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297
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STRAIN=168

SEQUENCE FROM N.A.

MEDLINE=98044033; PubMed=9384377

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Best Local Similarity
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the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commen
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FILE THIS IS A SOLUBLE NAD-DEPENDENT BETAINE ALDEHYDE SPECIFIC DEHYDROGENASE, ESSENITAL FOR THE UTILIZATION OF CHOLINE AS A PRECURSOR.
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Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
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Azevedo V., Bertero M.G., Bossieres P., Bololin A., Borchert S.,
Borriss R., Houssier L., Brans A., Braum M., Brimmell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Caphano V., Carter N.M.,
Choi S.K., Codani J.J., Connecton I.F., Cummings N.J., Isuiel R.A.,
Connector C., Caldwell B., Caphano C., Carter N.M.,
Caphano C., Caldwell B., Caphano C., Carter N.M.,
Connector C., Caldwell B., Caphano C., Carter N.M.,
Caphano C., Caldwell B., Caphano C., Carter N.M.,
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EMBL; Z99119; CAB15084.1;
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                                                67 ERASWIRKISAGIRERASEISALIVEEGGKIQQLAEVEVAFTADYIDYMAEWARRYEGEI 126
                                                                                                                                                                          5 LFTIDGEWISAEKEQIRSIINPENQEEIATVSEGGREDAIKAIAAARRAEDKGEWSSLSGL 64
                                                                                                                                                                                                                                                                                 MYTIMIQFVTWRGDAWIDVVNPATEAVISRIPDGQAEDARKAIDAAERA--QPEWEALPAI 66
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283
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17.18;
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Pred. No. 9.6e-47;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                        Itoh T., Kasai H., Kashimoto K., Kimbura S., Kitakawa M., Kitagawa M., Makito K., Miki T., Mikobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Cshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blattner F R., Plunkett G. III, Bloch C A , Perna N T , Burland V , Filey M., Collado-Vides J., Glasner J.D., Kode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                    Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                          -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                   CATALYTIC ACTIVITY: Betaine aldehyde + NAD(+) + H(2)O = betaine
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01-NOV-1995 (FF) 32; Cteated)
01-NOV-1997 (Rel 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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InterPro: IPR002086; Aldehyde_dehydr
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                                                    NCBI_TaxID=4932;
                                                                 Saccharomycetales;
                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes
                                                                                                    Saccharomyees cerevisiae (Baker's yeast)
                                                                                                                    Potassium-activated aldehyde dehydrogenase, mitochondrial precursor
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MEDLINE-9113163, PubMed-1989592;

Chalmers F M, Keen J N, Fewson C.A.;

Chalmers F M, Keen J N, Fewson C.A.;

"Comparison of body advanced behydrogenases and behydre dehydrogenases from the benzyl alcohol and mandelate pathways in Active beauter calcoacetious and from the "Ob. plasmid-encoded toluene pathway in Pseudomonas putida N-terminal amino acid sequences, amino acid compositions and immunological cross-reactions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bisinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Larsson T , Norbeck J , Karlsson H., Karlsson K -A , Blomberg A.; "Identification of two-dimensional gel electrophoresis resolved yeast proteins by matrix-assisted laser desorption ionization mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUL-1996) to the EMRL/SenBank/DDBJ databases. [2]
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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-i- CATALYTIC ACTIVITY: An aldehydd + NAD(+) + H(2)O = an acid +
-i- Suggelluilae Lucation. Mitochondrial matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acetaldehyde dehydrogenase of Saccharomyces cerevisiae.", FFMS Microbiol Lett 164\cdot29-34(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE, AND CHARACTERIZATION. MEDLINE=98340498; PubMed=9675847;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tessier W.D., Meaden P.G., Dickinson F.M., Midgley M.; "Identification and disruption of the gene encoding the K(+)-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Electrophoresis 18:418-423(1997).
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                                                                                                                                                                                                                                                                                Local
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169 TGNTIVIKPSEFTTNNAIAFAKIVDEIGLPRGVFNLVLGRGETVGQELAGNPKVAMVSMT
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                                                                                                                                                51 DAAEPA--QPEWEALPATEPASWLPKTSAGTPEPASETSALTVEEGGKTQQLAEVEVAFT
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                                   INYEKSSAGFADKIDGEMIDTGETHESYTE-EQFLGVCGQIIPWNFFLLMWAWKIAPALV
                                                                     ADYTOYMAEWARRYEGETTQSDRFGENTLLFKRALGVTTGTLPWNFPFFLTARKMAPALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 oCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Aldehyde dehydrogenase (EC 1.2.1.3) (ALDDH).
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-1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)U = an acid + NADH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schaap P.J., Muller Y., Visser J.;
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2 SVPVQHPMYTGGQFVTWKGDAWTDVVNPATEAVTSKTPDGQAEDARKATDAAERA-QPEW 60
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PS00687; ALDEHYDE_DEHYDR_GLU; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 270:461-467(1995). 
 -i- \text{CAMALYTIC} APTIVITY: Succinate semialdehyde + \text{NAP}(+) + \text{H}(2)O =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Succinate semialdehyde dehydrogenase (EC 1.2.1.24) (NAD(+)-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                evolutionary homology, and tissue expression."
J. Biol. Chem. 270:461-467(1995).
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                                            the European Bioinformatics Institute. There are no restrictions on
                                                                                             between
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                     -1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and short form; may be produced by alternative splicing. short form; may be produced by alternative splicing.
1- TISSUE SPECIFICITY: MAKIN, PANCREAS, HEART, LIVER, SKELETAL, MUSCLE, KIUNEY, LUWER IN SPLEEN, LUNG, KIDNEY AND TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: 4-aminobutyrate (GABA) degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 semialdehyde dehydrogenase from rat and human. cDNA isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley; TISSUE=Brain; MEDLINE=95113870; PubMed=7814412;
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Mammalia; Eutheria; kodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         succinic semialdehyde dehydrogenase).
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                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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                                                                                    the Swiss Institute of Bioinformatics and the
non-profit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERHGNEGYFIQPTIFTDTTPDMKIVKEEIFGPVGAVIKFKDGKEVIKQANDSNYGLAAAV 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTYDQFVNRLGEAMQAVQFGNPAERNDTAMGPLTNAAATERVEQKVARAVEEGARVAEGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLNCSGSKRGDMLYKLAQLMEKNIDDLSAIEALDNGKTFLWAKSVDLSLSISTIKHYAGW 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EA-LPAIEKASWLKKISAGIKEKASEISALIVEEGGKIQQLAE-VEVAFTADYIDYMAEW 118
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        institutions as long
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        as its content is
                                                                                             EMBL outstation
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and for commercial
               (See http://www.isb-sib-ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 LGEAM-QAVQFGNPAERNDIAMGPLINAAALERVEQKVARAVEEGARVAFGGKAVEGKGY 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                   13 RGDSFVGGRWLPTPATFPVYDPASGAKLGTVAL«GVPEARAVFAAVFAAYIAFSSWKEJSVKE 72
                                                                                                                                                                                                                                                                                                                                                                                                 19 PGDAWI-------PVVNPATEAVISRIPDGGAEDARKALDAAERAQPEWEALPAIE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chambliss K.L., Hinson D D, Trettel F , Malaspina P, Novelletto A.,
                                                                                                                                                                                                                                                                                                                                                           16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24) (NAD(+)-dependent surcinio semialdehyde dehydrogenase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 MKAIKGLKFGETYINRENFEAMQCFHAGWRKSGIGGADGKHGLHGYLQTQVV 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Frimates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0cT-1996 (Rel. 34, Greated)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UIN-2002 (Pel 41, Last annutation update)
Succinate semialdehyde dehydrogenase, mitochondrial precursor
                                                                                                                                                                                Oxidoreductase; NAD; Alternative splicing.
NP_BIND 237 242 NADF (ADF FART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                       Length 488;
                                                                                                                                                                                                                                                                                                                                                           Matches 168; Conservative 110; Mismatches 178; Indels
 Usage by
                                                                                                                                                                                                                                                              MISSING (IN SHORT ISOFOPM)
                                                                                                                                                                                                                                                                                  52188 MW; AR002A91E7E60E26 CRC64;
                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.1e-44;
                                                                                                                                                                                                                                                                                                                     Score 767; PR 1;
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modified and this statement is not removed.
                                                                                                                                                                                                                          BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                 PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1. PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                 entities requires a license agreement (S
or send an email to licensealsh-sib eh)
                                                                                                               InterPro: IPR002086; Aldehyde_dehydr.
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                                                                                                                                                                                                                                                                                                                     3] 48;
                                                                                                                                                                                                                                                                                                                                       35.68;
                                                                         EMBL; L34821; AAA67058 1; -
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                                                                                                                                                                                                                                              293
                                                                                                                                 Pfam; PF00171; aldedh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                               1BXS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISSUE=Lymphocytes;
                                                                                                                                                                                                                                                                                488 AA;
                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                          259
                                                                                             HSSP; P51977;
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                                                                                                                                                                                                                            SITE
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                              ACT_SITE
                                                                                                                                                                                                                                                                                    SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 GGEMEPAAATEPVULPASGAALGMVALCOVEEARAAVRAAYEAECEMREVSAKERSSLLR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 GDAWI-----DVVNPATEAVISRIPDGQAEDARKAIDAAFRAQPEWEALPAIERASWLR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DISEASE: DEFECTS IN ALDHSAI ARE THE CAUSE OF 4-
HYDFOXYROTYFICACIDUDIA, A RARE INBORN ERROR IN THE METAROLISM OF
4-AMINOBUTYFIC ACID (GABA). THE DISEASE IS CHARACTERIZED BY SEVERE
ATAXIA AND BY MILDLY RETARRED PSYCHOMOTOR PEVELOPMENT.
-!- SIMILAPITY: RFLONGS TO THE ALDEHYDE DEHYDEGGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 11; Gaps
          Two exon-skipping mutations as the molecular basis of succinic semialdehyde dehydrogenase deficiency (4-hydroxybutyric aciduria)."; Am. J. Hum. Genet. 64-49-408(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                          Slaughter C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUCCINAIE SEMIÁLDEHYDE DEHYDROGENASE.
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                        Trettel F., Malaspina P., Jodice C., Novelletto A., Slaughter C.A., and in L. Hinson P.D., Chambliss K.L., Gibson K.M.; "Human succinic semialdehyde dehydrogenase. Molecular cloning and chromosomal localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Exp. Med. Biol 414-254-260(1997)
CATALYTIC ACTIVITY: Succinate semialdehyde + NAD(+) + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- TISSUE SPECIFICITY: BRAIN, PANCREAS, HEART, LIVER, SKELETAL
                                                                                                                                                                                                                      Chambliss K.L., Caudle D.L., Hinson D.D., Moomaw C.R., Slaughter C.A., Jakobs C., Gibson K.M.; "Molecular cloning of the mature NAD(+)-dependent succinic semialdehyde dehydrogense from rat and human crwA isolation, Julicultionary homology, and tissue expression."; J. Biol. chem. 270.461-467(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.1%, Score 759.5, DB 1, Length 535; 35.8%; Pred No. 1.1e-43;
                                                                                                                                Submitted (DEC-1998) to the EMBL/Genbank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MILOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C63A9431D3FA16C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSTTE; PSOUGART; ALDEHYDE_DEHYDE_GLU; 1.
Oxidoreductase; NAD; Transit peptide; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Similarity 35.88; Pred No. 1.1e-43; 167; Conservative 102; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: 4-aminobutyrate (GABA) degradation.
-!- SUBUNIT: HUML/ELFKAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
BY SIMILARITY
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PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUSCLE, KIDNEY. LOWER IN PLACENTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR002086; Aldehyde_dehydr
                                                                                                                                                                                       TISSUE=Liver;
MEDLINE-95113870; PubMed-7814412;
                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
MEDLINE=97212810; PubMed=9059628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL031230; CAA20248.1; -.
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                                                                                                                                                                     SECUENCE OF 213-535 FROM N.A.
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HSSP, P51977; 1BXS.
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Takobs C , Gibson K.M.;
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535 AA;
                                                                                         SEQUENCE FROM N.A
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186 RRALVLKQPIGVAAVITPWNFPSAMITRKVGAALAAGCTVVVKPAEDTPFSALALAELAS 245
                                                                                                                                                                                                                                                                                                                                           194 EIGLPRGVFNLV---LGKGETVGQELAGNPKVAMVSMTGSVSAGEKIMATAAKNITKVCL 250
                                                                                                                                                                                                                                                                                                                                                                                                                            246 QAGIPSGVYNVIPCSRKNAKEVGEALCIDPLVSKISFTGSTITGKILLHHAANSVKRVSM 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 ELGGKAPALVMDDADLELAVKAIVDSRVINSGQVCNCAERVYVQKGIYDQFVNRLGHAMQ 310
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74 KISAGIRERASFISALIVERGGKIQQLAEVEVAFTADYIDYMAEWARRYEGETIQSDRPG 133
                                                                                     126 KWYNEMIONKDDIARIITAESGKPEKEAHGEIL/YSAFFLEWFSEEARFVYGDIIHTPAKD 185
                                                                                                                                                                          134 ENILLFKRALGVTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNAIAFAKIVD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 KNLRVGNGFEFG-TTTGGPLINEKAVEKVEKQVNDAVSKGATVVTGGKRHQLGKNFFEPTL 424
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Wang X., Mann C.J., Bai Y., Ni L., Weiner H.;
"Molecular cloning, characterization, and potential roles of cytosolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 = an acid + NADH. PATHWAY: Ethanol utilization; second step.
SURCELLULAR LOCATION: Mitochondrial matrix (Potential).
SIMILARITY: HELONGS TO THE ALLEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang X., Bal Y., Nl L., Weiner H., ^{\circ} "Saccharomyces cerevisiae aldehyde dehydrogenases. Identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dietrich F.S. Mulligan I.T., Hennessey K.M., Alles F., Arauje P., Akviles E., Berno A., Breonan T., Carpenter J., Chen E., Cherry J.M., Chung E., Puncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Nicgren P., Geffner P., Gherler P., Wei Y., Yelton M., Boristein D., Pavis R.W.; Sulth V., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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1-01-CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase, mitochondrial precursor (EC 1.2.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 LKFGETYINRENFEAMQGFHAGWRKSGIGGANGKHGLHGYLQTQVV 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 LEVGMVGVNEGLISSVECPFGGVKQSGLGREGSKYGIDEYLELKYV 530
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between the Swiss Institute at Wicintormalies and the EMML outstation the Puropean Ricintormalies institute. There are no restrictions on its use by non-profit institutions as lond as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license adjustment (wee bith //www.isb.sib.ch/communic)
this SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 SAHPIVKKIAPTGSTATGRHIMKVAADTVKKVTLELGGKSPNIVFAGAGGRAVKNIAFG 412
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NAD (ADP PART) (HY SIMILARITY).

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TRANSIT 1 23 MITOCHONDRION (POTENTIAL).
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PROSITE; PS00687; ALDEHYDE_DEHYDR_GUU; 1.
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EMPL; U18814; AAB44612.1;
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316 VSRLRKNAEARKVG-PGNDTGNNMGPLVSKKQHEPVLGYTFDGVKAGATVVTGGKKIGUK 374

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 GTV--PPRSGNFLGTVKR@PIGVFGQIIPWNFPLLMAAFKLSPALAMSNLVVLKPAEQTP 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 IQEKLLINGKEVPAVSGKTFEVVNPADEKVIANVAEAEKADVDLAVKAARHAFESFRMTD 77
                                                                                                                                                                                                                                                                                                                                                                         Leishmania tarentolae (Sauroleishmania Larentolae).
Eukaryotu: Euglenosoa, Kinetoplastida. Trypunosomatidae, Leishmania.
01-NOV-1997 (Rel. 35, Created)
U-NOV-1997 (Rel. 35, Last sequence update)
15-UNV-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase, mitorbondrial procursor (RC 1 2 1 3) (ALDH
                                                                                                                                                                                                                                                                                                                                                          11 - PHNCTION: COULD HAVE A RNA-BINDING ACTIVITY IN ADDITION OF ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interro; Armonia adddh; 1.
Pfam; PF0200; aldddh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDE_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDE_GLU; 1.
Oxidoreductase; NAD; Mitochondrion; Transit peptide; RNA-binding.
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                                                                                                                                                                                                                                                           Bringaud F., Peris M., Zen K.H., Simpson L.; "Characterization of two nuclear-encoded protein components of
                                                                                                                                                                                                                                                                                                                                                                                                                --- PATHWAY: Ethanol utilization; second ster.
--- SUBCELLULAR LOCATION: Mitochondial.
--- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
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NAD (ADP FART) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                               mitochondrial ribonucleoprotein complexes from Leishmania
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                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 10-31.
                                                                                                                                                                                                                                                                                                                                      Biochem, Parasitol, 71-65-79(1995)
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                                                                                                                                                                                                                                       MEDLINE=95356798; PubMed=7630384;
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265
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Matches 168: Consery
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                                                                                                                                                        NCBI_TaxID=5689;
                                                                            class 2) (P51).
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Mol. Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MI POLLINKLADIMERDIFFIAATESI,FINGKAPTMAKVI (JANSTROTERYAGWAFKTHOOFF 140)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 DIN---FETLITTERHEPVGVCGQIIPWNFPLLMWSWKIGPAVAAGNTVVLKTAQQTPLSA 197
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422 VAMKAIKGLEFGETYINM-ENFEAMÇGFHAGWEKSGIGGADGKBGTBGYLQIQVVYLQS 479
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                                                                   435 TALRYSTYLNAGTVWVNTWNNFCPSMPF-GGFKQSGIGRELGKEVVDMYTEPKAIHFAS 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 51:217-226(1987).
-!- CATALYITIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
-!- PATHWAY: Fthanol utilization: second step.
-!- SIMILARITY: RELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-87248080; PubMed-3036652; P. Elliott B., Davies R.W., Pickert M., Gwynne D.I., Buxton F.P., Elliott B., Davies R.W., Lockington R.A., Scazzocchic C., Scaly-Lewis H.M.; "Cloning and characterization of the aida gene of Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Emericella nidulans (Aspergillus nidulans).
Eukaryota, Fungi, Ascomycota, Ferizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
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Live 98, Mismatchos 207,
                                                                                                                                                                                                                                                                                                                                                       01-AUG-1988 (Rcl. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase (EC 1.2.1.3) (ALDDH).
                                                                                                                                                                                                                                                  497 AA
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Pfam: PF00171; aldedh; 1.
PPGSITE; PS00070, ALGEHYDE_GEHYDP_CXS, 1.
PPGSITE; PS00687; ALDEHYDE_DEHYPE_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                          PKI;
                                                                                                                                                                                                                                                                                                                         01-AUG-1988 (Rel. 08, Created)
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P08157;
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                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
186 IAFAKIVDEIGLPRGVFNLVLGRGETVGQELAGNPKVAMVSMTGSVSAGEKIMATAAK-N 244
                                                                             245 ITKVCLELGGKAPAIVMDDADLELAVKAIVDSRVINSGQVCNCAERVYVQKGIYDQFVNR 304
                                                                                                                    258 LKKVTLELGGKSPNIVFDDADIDNAISWANFGIFFNHGGGGGGGGSFILVGEGIYDKFVAR 317
                                                                                                                                                               305 LGFAMQAVQFGNPAERNDIAMGPLINAAALERVEQKVARAVEEGARVAFGGKAVEGKGYY 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- PATHWAY: Ethanol utilization; second step.
-i- TISSUE SPECIFCITY: EXPRESED AT LOW LEVELS IN MANY TISSUES AND AT HIGHER LEVELS IN SALINARY GIAND, STOMACH, AND KIDNEY
-i- SIMILAPITY- RELOWS TO THE ALDEHYDE DEHYDEGGENASES FAMILY.
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                                                                                                                                                                                                                                                                                                                                                 425 KAIKGLKFGETYINRENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQTQVVY 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAD (ADP PART) (RY SIMILARITY)
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15-JUN-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase 6 (EC 1.2.1.5).
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PROSITE; PSOU687; ALDEHYDE DEHYDR_GLU: 1
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NP_BIND 257 2
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Score 719.5; DB 1; Length 512;

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Query Match

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"Molecular cloning, characterization, and potential roles of cytosollo and mitochondrial aldehyde dehydrogenases in ethanol metabolism in Saccharomyces cerevisiae."
J. Bacteriol. 180:822-830(1998).
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Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
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01-077-1996 (Rel. 34, Created)
12-10N-2002 (Rel. 41, Last sequence update)
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34.3%; Pred. No. 5e-41;
                       Mismatehas
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Best Local Similarity
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Mueller-Auer S., Namath A., Nentwich U., Orfnor P., Posarson D., Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Scharfe M., Scharfe M., Scharfe M., Scharfe M., Scharfe M., Scharfe M., Scharfe M., Tellelin H., Unrestanzu L.A., Oshinsky S., Vierndeels F. Vissers S., Viss H., Walsh S. V., Mambutt P., Wadjer F., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H., Hani J.; "The nucleotide sequence of Saccharomyces celevisiae chromosome XVI.", Nature 387:103-105(1997).
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32.5%, Pred No. 5 3e 41,
five 108; Mismatches 202, Tudels 12, Sags
                                                                                                                                                                                                                                                                                                                                                                                                          Meaden P.G., Dickinson F.M., Mifsud A., Tessier W., Westwater J. Bussey H., Midgley M.;
The ALD6 gene of Saccharomyces detevisiae encodes a cytosolic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY, BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                     Norbeck J., Blomberg A.; Metabolis and regulatory changes associated with growth of Sacrharomyces reprevisiae in 1.4 M NaCl Evidence for Osmotic induction of glycerol dissimilation via the dihydroxyacetone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFam; PF00171; aldedh; 1.
PROSITE; PS00070; ALOEHYDE_DEHYDR_CYS; FALSE_NEG.
PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mg(2+)-activated acetaldehyde dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Ethanol utilization; second step. SUBCELLUIAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                       SEĞUENCE OF 1-15, AND CHARACTERIZATION.
MEDLINE=98053564; Pubmed=9392076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR002086; Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                                     Biol. Chem 272.5544-5554(1997)
                                                                                                                                                                           SEQUENCE OF 75-78 AND 481-487.
STRAIN-ATCC 44827 / SKQ2N;
MEDLINE=97190279; PubMed=9038161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 253 NAI
271 271 POJ
305 305 POJ
120 126 L
499 AA, 54283 MW, 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase, NAD, Magnesium.
INIT_MET 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U56604; AAB01219 1; -
EMBL; U39205; AAB68304.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast 13:1319-1327(1997)
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ACT_SITE
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This SWISS FROI entry is depyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial outliffes requires a libersh agreement (See 111p //www.ishesibelb.high and or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   383 YFIRPTVFYDVNEDMRIVKEEIFGPVVTVAKFKTLEEGVEMANSSEFGLGSGIETESLST 442
204 ALYFASLCKKVGIPAGVVNIVPGPGPTTVGAALTNIPPIPKLAFTGSTFVGKSVAVDSSES 263
                                            244 NITKVCLELGGKAPALVMDDADLELAVKALVDSRVINSG<sub>E</sub>VONGAEHVYVQKG1YDQEVN 303
                                                                                    264 NLKKITLELGGKSAHLVFDIANIFKTIPNI, VNGTFKNAGOT GSSGSPIYV QEGIYDELLA 323
                                                                                                                                                                          324 AFKAYLETEIKVGNPFDKANF-QGALTNPGQFFTIMNYIFLGKKFGAKIITGGFKVGFKG 382
                                                                                                                                                                                                                       363 YYYPPTLLLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSOYGLTSSIYTQNLNV 422
                                                                                                                                                                                                                                                                                                             423 AMKAIKGLKFGETYINPEN-FFAMQGFHAGWPKSGIGGADGKHGLHGYLQTQVVYLQ 478
                                                                                                                                                                                                                                                                                                                                                        443 GLKVAKMEKAGTVWINTYNDFDSRVPF-GGVKQSGYGPEMGEEVYHAYTEVKAVRIK 498
                                                                                                                                   3.04 REGEAMDA - VQPGNPAEPNFTAMSPELINAAALEEVEEKVARAVEEGAFVAFFGAFVEGRAGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- CATALYTIC ACTIVITY: Betaine aldehyde + NAD(+) + H(2)0 = betaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Pebryophyta, Inacheophyta;
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heranne aldeligde deligite genase, ettlereplast presursor (EC 1.2.1.8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning of a plant betaine-aldehyde dehydrogenase, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: SUBCELLULAR LOCATION. Chloroplast.
1: SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; 1PR002000.
Plan, PR00171; alded, 1.
PR0SITE; PS00070; ALDEHYDE_DEHYDE_CYS; 1.
PR0SITE; PS00087; ALLEHYDE_LEHYLE_GLU; 1.
Oxidoreduclase; NAD; Chloroplast; Transit peptide.
TRANSIT 1 1 6497 EETAINE-ALDEHYDE DEHYDEOENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cnzyme implicated in adaptation to salinity and drought.";
Proc. Natl. Acad Sri U S A R7:2745-2744(1490).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shu W., Ai W., Chen S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv Savoy hybrid 612;
MEDLINE-90207274; PubMed-2320587;
Weretilnyk E.A., Hanson A.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Re). 16, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, M31480; AAA34025.1; -. EMBL, G69142; AAB41696.1, -. PIR; A35994; A35994 HSSP; P05091; 1CW3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spinacia oleracea (Spinach)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P17202; P93555;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DHAB_SPIOL
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118 FAGQAEALDGKOKAPVTLPMERFKSHVL--ROPLGVVGLISPWNYPLLMATWKIAPALAA 175
                                                                                                                                                                                                                                                                                                                                                     170 GNTIVIKPSEFTTNNAIAFAKIVDEIGLPRGVFNLVLGRGETVGQELAGNPKVAMVSMTG 229
                                                                                                                                                                                                                                                                                                                                                                          57 -- QPEWEALPATERASWLRKISAGIRERASEISALIVEEGGKIQQLAEVEVAFTADYIDY 114
                                                                                                                                                                                                                                                   58 FRRNNWSATSGAHRATYLRAIAAKITEKKDHFVKLETIDSGKPFDEAVLDIDDVASCFEY 117
                                                                                                                                                                                                                                                                                       115 MAEWARRYEGE-----ILQSDRPGENILLFKRALGVTTGILPWNFPFFLIARKMAPALLT 169
                                                                                                                                                                                                                                                                                                                                                                                                                        230 SVSAGEKIMATAAKNITKVCLELGGKAPAIVMDDADLELAVKAIVDSRVINSGQVCNCAE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                           290 KVYVQKGIYDQFVNKIGEAMQAVQFGNPAERNDIAMGPLINAAALERVEQKVARAVEEGA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 RVAFGGKAVE--GKGYYYPPTLLLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408 DYGLTSSIYTQNLNVAMKAIKGLKFGETYINRENFEAMQGFHAGWRKSGIGGADGKHGLH 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSVPV-OHPMYIDGQFVTWRGDA---WIDVVNPATEAVISRIPDGQAEDARKAIDAAFRA 56
                                                                                                                                                                      19; Gaps
                                                                               Query Match 29.4%; Score 718.5; DB 1; Length 497; Best Local Similarity 33.2%; Pred. No. 5.7e-41; Matches 162; Conservative 104; Mismatches 263, Indels 19.
257 257 BY SIMILARITY.
291 291 BY SIMILARITY.
424 424 S -> F (IN REF. 2).
497 AA; 54270 MW; 55088240E635E22F CRC64;
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Search completed: June 24, 2003, 10:14:29 Job time : 10.6475 secs

us-09-830-751-6.rspt

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Genfore version 5.1 6 Copyright (c) 1993 - 2003. Compugen Ltd
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OM protein - protein search, using sw model

June 24, 2003, lugum-15 ; Search time & Each Seconds (Without alignments)
2642 [68 Million rel] updates/sec Run on:

JS-09-830-751-6 Title

A PIGK HGL HISYLOTOVVY LOS 479 1 MSVPVQHPMY LD3QFVTWRG 2446 Perfect score. Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

671580 Total number of hits satisfying chosen parameters:

671580 segs, 206047115 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match U\*

Database :

SPTREMBL\_21:\*

1: sp\_archea:\*
2: sp\_bacteria:\*

sp\_plant:\*
sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_uclassified:\*
sp\_rvirus:\*
sp\_bacteriap:\* sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\* sp\_mammal:\*
sp\_mhc:\*
sp\_organelle:\*
sp\_phage\*\* sp\_archeap:\* 5: 6: 7: 8: 10: 11:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	ORX901 esoberishing			09pi19 campylobact	elliosoloim Ardyno	nestasmont the	og474w0 thermoriasm	Q9rkfl streptomyce	Seiomophesa Smylou	O8y3f2 ralstonia s	084950 escherichia	eltenomies zmmsko	UBz4f8 salmenella	Q9k7p5 bacilius ha	292te2 rhicobium m	the many of the state of the st
	17	088301	COLXMR	C9UM97	Q9F119	242484	29HK01	บช24พบ	Q9PKF1	POTAMS	_ั <b>สห</b> 3₽2	<b>いちもX8ご</b>	CHEMMI	OP24FR	Q9K7P5	2317280	2411.
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	Ouery Match Length DB	4/9	480	480	393	4 R F	493	403	492	483	497	482	£ 7	104	475	484	100
o¥÷	Query Match	66	63.7	63.5	52.3	4.5	36.9	36.9	36.5	36.0	35.7	35.6	35.5	25.	34 K	44.4	. 11
	Score	2426	1557	1552	1279.5	1066.5	€U&	902	894	879 5	872.5	870 5	868.5	858 5	845 5	840.5	47.77
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17   835   34.1   468   16   99K863   18   832   34.0   486   15   99K869   19   817   833   843   848   10   99K869   19   99K878   19   99K878   19   99K878   19   99K878   19   99K878   19   99K878   19   99K787   19   99		78yiq7 brucella me Q92y70 rhizobium m Q98y14 arabidopsis Q987il rhizobium l Q8y8i9 listeria mo			992xq0 rhizobium m Q98ay0 rhizobium l Q9xpm7 ralstonia s 2930q6 rhizobium m Q9wwd5 agrobacteri	QBUB52 agrobacteri QBTH5 GOYZA saliv QBX9W5 escherichia Q9jtn7 neisseria m
835 835 817 817 817 811 811 811 811 811	16 17 17 16	16	51 1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	15 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	10 10 16
	10.08.9	33 F 33,3 488 33,3 488 33,3 488 488	1. 25. CC. C.			
	~			32 797.5 33 797.5 34 796.5 35 795.5 36 795.5		42 784.5 43 783.5 44 782.5 45 781 5

## ALIGNMENTS

InterPro; IPR002086; Aldehyde dehydr

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181 TINNAIAFAKIVDEIGLPRGVFNLVLGRGETVGQELAGNPKVAMVSMTGSVSAGEKIMAT 240
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                                                                                                                                                                                                                                                                                                 61 EALPAIERASWLRKISAGIRERASEISALIVEEGGKIQQLAEVEVAFTADYIDYMAEWAR 120
                                                                                                                                                                                                                                                                                                                                       21 RYEGEIIQSDRPGENILLFKRALGVTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 KGYYYPPTLLLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSSIYTQNL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20175755; PubMed=10710307; MEDLINE-20175755; PubMed=10710307; MEDLINE-20175755; PubMed=10710307; MEDLINE-20175755; PubMed=10710307; MEDLINE-20175755; PubMed=1071, Heideliberg 1. Johtfries A.C., Nolson K.E., Eisen J.A., Ketchum K.A., Phodo D.W., Pedens J.E., Hickey E.K., Nolson W.C., Gwinn M.L., Phodo D.W., Pieterson J.D., Hickey E.K., Mason T., Ciecko A., Parksey D.S., Rair E., Cittone H., Clark E.P., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamarhe-van T., Ginch M.O., Fraser C.M., Moxon E.K., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meniugitidis serugioup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSVPVQHPMYIDGGFVTWRGDAWIDVVNPATEAVISKIPDGQAEDARKAIDAAERAQPEW
                                                                                                                                                                                                                          1 MSVPVQHPMYIDGQFVTWRGDAWIDVVNPATEAVISKIPDGQAEDAKKAIDAAEKAQPEW
                                                                                                                                                    Gaps
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                                                                                                                                                    0
                                                                                                             99.2%; Score 2426; DB 16; Length 479; 99.4%; Prod No 2 40.15%, tive 0; Mismatches 3; Indels 0
                                                                       479 AA; 52238 MW; D49819EA02E5C7CF CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLIED 15, Last sequence update) 01-DEC-2001 (TrEMBLIED, 19, Last annotation update)
               PROSITE; PSOU070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
PROSITE; PSOU687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
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HSSP; P51977; 1BXS.
                                                                                                                              Best Local Similarity 99 4.
Matches 476, Conservative
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Pfam; PF00171; aldedh; 1.
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                                                         Complete proteome. SEQUENCE 479 AA;
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                                                                                                               Query Match
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66 IERASWERKISAGIRERASEISALIVEEGGKIQQIAFVEVAFTADYIDYMAEWARRYEGE 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 GEAMQAVQFONE - AFFANETAMOPLI NAAALEEVERVAFAVEEGAFVAFGEAVERGY 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 YYPPTILLIDVRQEMSIMHEETFGPVI.PVVAFDTI.EDAISMANDSDYGLTSSIYTONI.NVA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 QHPMYIDGQFVTWRCDAWIDVVNPATEAVISKIFFRNJAEDAKKAIDAAEKAQPEWEALPA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 HIFAEIVDAVGLPAGVENVVNGPGAEIGNALSAHPQVDMVSLTGSVEAGROVMEAASANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 TAAMKGVEYGNPAEAFAGALEMGPLIEHKAVKAVAEKVEKAVKÇGAKLVGGKKAEGKGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 FYVTRRLQFGETYINRENFEAMOGFHAGWKKSG1GGAIXGKHGLEEYLOTOVVYLET 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Rasham D., Brown D., Chillingworth T., Tayles R.M., Dayls F., Devilis K., Foltschill T., Hamlis R., Helloyd S., Jagels K., Leather S., Moule S., Muncall K., Quall M.A., Hallouream M.A., Partherford S., Mouneals K., Skelton J., Mahlechead S., Spraft H.G., Harrell B.G., Strain of Neisseria "Complete DNA sequence of a serogioup A strain of Neisseria
                                                                                                                                                                                               Gabs
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                                                                                                                                                                                               7
                                                                                                                                             64.2%; Soure 1857; DB 16; Length 480;
64.2%; Pred. No. 1.2e 98;
                                                                                                                                                                                             63; Mismatches 110; Indels
                                                                                               480 AA; 52256 MW; 35A72F5D1231F107 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT 2000 (TrEMBLrel, 15, Created)
01-0CT-2000 (TrEMBLrel, 15, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
Pfam: PF00171; aldedb; 1.
PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS: UNKNOWN 1.
PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU: UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-22491 / SERGROUP A / SERGTYPE 4A;
MEDLINE-20222556; Pubmed 10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aldehyde dehydrogenase A (EC 1.2.1.22).
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Pfam, PF00171; aldedh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis (serogroup A)
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                                                                                                                                                                 64.28;
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EMBL: AL162753; CAB83774.1;
HSSP; P51977; 1BXS.
                                                                                                                                                                                             301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                             Query Match
Best Local Similarity
Matches 301, Conserva
                                                                         Complete profeome.
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                                                                                               SEQUENCE
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63 VEPGAYLPKTAQGTPEPADELTPTTVAEGGKTKDLARVEVMETADYLDYQAEWARRYEGE 122
                                                                                                                                                                                                                                                                                                                                126 IIQSDRPGENILLFKRALGVTTGILPWNFPFFLIAPKMAPALLTGNTIVIKPSEFTTNNA 185
                                                                                                                                                                                                                                                                                                                                                                                                              186 IAFAKIVDEIGLPRGVFNLVLGRGETVGQELAGNPKVAMVSMTGSVSAGEKIMATAAKNI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 HIFAEIVDAVGLPAGVFNVVNGPCAFIGNALSAHFQVDMVSLTGSVEAGRQVMEAASANI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 TKVCLELGGKAPATVMDDADLELAVKATVDSKVTNSGQVCNCAEKVYVQKGTYDQFVNRL 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 TAAMKGVRYGNPAEAEAGALEMGPLIEERAVKAVAEKVERAVKQGAKLVCGGKRAEGRGY 362
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                                                                                                                                                                                                                                                    66 IERASWLRKISAGIPEPASEISALIVEEGGKIQQLAEVEVAFTADYIDYMAEWARRYEGE 125
                                                                                                                                                                            6 QHPMYIDGQFVTWRGDAWIDVVNPATEAVISRIPDGQAEDARKAIDAAERAQPEWEALPA 65
                                                                                                                                                                                                               3 QLAMYINGRFENDFNGEWRNVLNPSTEEAIAREPKGGKADVDRAVAAARAAQPAWERLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 MKAIKGLKFGETYINRENFEAMQGFHAGWRKSGIGGANGKHGLHGYLQTQVVYLQS 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saps
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reveals hypervatiable sequences.";
Nature 403-665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campylobacter jejuni.
Bacteria; Proteobacteria, epsilon subdivision, Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20150412; FUEMGGT-105848104;
Parkhill J., Wren B W., Mungall K., Ketley J M., Churcher C.,
Basham D., Chillingworth T., Davies k.M., Feltwell I., Hoiroyd S
Jagels K., Karlyshev A V., Moule S., Pallen M.J., Penn C W.,
Quail M.A., Pajandream M.A., Rutherford K.M., van Vliet A.H.M.,
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(4
                                                                                                                                     64; Mismatches 110; Indels
PROSTIE: ESOODO ALLGERYDE_LEHYDK_TYS; UNKNOWN_I.
PROSTIE: PSOUGHY: ALLGERYDE_LEHYDK_GLG; UNKNOWN_I.
Orgidareductaso. Complete practicance.
SEQUENCE: 480 AA, 52255 MW; D204R0707634769 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Aldehyde dehydrogenase C-terminus (EC 1.2.1.22).
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PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
                                                                                            Score 1552, DB 16,
Pred No. 2 78 48.
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Whitehead S., Barrell B.G.;
                                                                                                  63.5%;
                                                                                                                     1960 J. J.
                                                                                                                                     Matches 300; Conservative
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                                                                                                                     Similarity
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91 VEBSSKIQQLAEVBVAFTADYIDYMAEWAPRYBSFIIQSDPPSENILLFKRALSVITGIL 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 VVAFIG BEBALSMANDSPYGELSSTYTQNENVAMKATKGBKFGFTY FINFENFRAMMSFHA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 TAKEDILDEVIDMANDCEYGLTSSIYTQNLDIAMRASHELKFGETYINKENPEAMQGFHA 359
                                                                                                                                                                                                                                                                                                                                                                                                 151 PWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNAIAFAKIVDEIGLPRGVFNLVLGFGE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PWNFPFFLIARKMAPALLTGNTIVIKPSSETPNNAFEFAKLVSQSSLPKGVFNLVAGKGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 EAIKASKICNNSONTATERAVHTSVYDEPVDKFVKAMSKVSVGNTI-KGDFDMGPLVN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 AAALEPVEKKAAKAVEESAKVAFSPKAVSKSYYYPPTILLIJVPREMSIMHEETFSPVLP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 AERAQPEWEALPAIERASWLKKISA3IRERASEISALIVEEGGKIQQLAEVEVAPTADYI 112
                                                                                                                                                                                                                                                                                   1 MQEQGKTRVLASIEINFTADYMDYTAEWARRYEGEIIQSDRANEHIYLYKSAIGVIGGIL 60
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-: SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.

LIGGELYDE : PROMISSING TO THE ALDEHYDE OF ANALYDES FAMILY.
                                                                                                                                                            1, Gaps
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                                                                   52.3%, Score 1279.5, DB 16; Length 393; 63.1%, Pred No. 9 80.80, tive 52; Mismatches 90, Indels 1,
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PPOSITE; PSOOK87; ALDEHYDE_DEHYDE_CIJI; UNKNOWN_1.
exidoreductase; Plasmid.
SEGHEN'E 486 AA; 53309 MW; GHFFEL392E98AGG CPC54;
    SHE AA; 42907 MW; DEDA71000E4E6AA7 7P764;
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01-08C-2001 (TrEMBLrel. 19, Last sequence update)
01-MAP-2002 (TrEMBLrel 20, Last annotation update)
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                                                                                                                                                            Matches 245, Conservative
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                                                    113 DYMAEWARRYEGELIQSDRPGENILLFRRALGVITGILPWNFPFFLIARKMAPALLIGNT 172
                                                                                                        115 EYACDGARSIEGDIIPSDNPAEHIMIHKIPRGVVVAITAWNFPLALAGRKLGPALVAGNS 174
                                                                                                                                                               173 IVIKPSEFTTNNAIAFAKIVDEIGLPRGVFNLVLGRGETVGQELAGNPKVAMVSMTGSVS 232
                                                                                                                                                                                               233 ACEKTMATAAKNITKVCLELGGKAPATVMDDADLELAVKATVDSRVINSGQVCNCAERVY 292
                                                                                                                                                                                                                                                                                                        293 VQKGIYDQFVNRLGEAMQAVQFGNPAERNDIAMGPLINAAALERVEQKVARAVEEGARVA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                          295 VHESTYNEFMERFMEKVKGLKLGNPMDA-ATTIGPKVNAKEVAHMEHLVTKSVEEGATVA 353
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55 AERAQKQWKKVPARKRADLLRTFAAEIKANKNQLAELI,VREQGKLLAVAKMEVEVTASFI 114
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19, Last annotation update)
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Best Local Similarity 88.4%; Pred. No. 9.3e-
Matches 182; Conservative 100, Mismatches
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EMBL; AL445065; CAC11938.1; -.
HSSP; P05091; 1CW3.
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                               24.9 CLELGGKAPATVMDDADLELAVKATVDSRVTNSGQVCNCAERVYVQKGTYDQFVNRLJEA - 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 FFLPT11GNADGKSK1FQEETFAPV1GAPK1SSVFFMYDLANDSKYGLASYLFTKDPN11 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 SKITYKAKELIEENRKELENTITIGENGKPVKEAAFEUWTINGMQYYAFWAMKLNGSVVE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [29] SDRPGENTLLFKRALGVTTGTLPWNFPFFLTARKMAPALLTGNTTVTRPSEFTTNNATAF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 GTTNHRKIFOYKUPYGTVVALTPWNEPAGWVARKLAPALLTGNTVILKPSSDTFGSAEWI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 MYIDGQEVTWRGDAWIDVVNPATEAVISKIPGGQAEDARKAIDAAERAQPEWEALFAREGE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawamoto I.,
                                                                                                                                                                                                185 VRKEVEAGVPKGVI,NETTGEGSFLODYTVEHKKVNI,ITMFGSTATGGRIMOKASANMAKI.
                                                                                                                                     189 - AKTVDETGL/PRGVENLVLGRGETVGQEL/AGNEKVAMVSMTGSVSA/BETMATAAKNTTEV
                                                                                                                                                                                                                                                                                                                                      24.5 ILELGGGKAPFMVMKDADMDNALKTIJMAKYWNAGQSCTAAFRLYVHEDTYDTFMSRFVEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SdPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 MKATKGLKFGETYTNRENFEAMOGFHAGWRKSGTGGADGKHGLHGYLOTOVVYL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 PEASEPTEPOFT VANAPOPPASOCYHTOPOWTODACHOSKYOTSPYTKIKNIYV 475
                                                                                                                                                                                                                                                                                                                                                                                                     309 MOAVOFGNPAERNDIAMGPLINAAALEPVFOKVARAVFFGARVAFGGK AVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawashima T., Amano N., Koike H., Mukino S. L., Hiquchi S., Kawamo Kawashima T., Amano N., Koike H., Mukino S. L., Hiquchi S., Kawamo Ninoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.; Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium.?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaecta; Thermoplasmata; Thermoplasmatales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493 AA; 54801 MW; EBECCE8HB292CD54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pram: PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96; Mismatches 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.10 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.5 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPK002086; Aldehyde_dehydi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed-11121031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-00T-2001 (TrEMBLE). 18, 01-00T-2001 (TrEMBLE). 18, 01-MAK-2002 (TrEMBLE). 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.4%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aldehyde dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermoplasma volcanium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TV1050 OR TVG1076124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCB1_TaxID=50339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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185 VKKFIQAGVPKGALNYITGRGSVIGDYIVEHKKVALITMIGSTSTGQRIMQKASANMAKL 244
                                                                          249 CLELGGKAPAIVMDDADLELAVKAIVDSRVINSGQVCNCAERVYVQKGIYDQFVNRLGEA 308
                                                                                                       245 MEELGGKAPPMVWKDADINNALKTLIMAKYWNAGGSCIAAERLYVHEDIYDTFINKFVEL 304
                                                                                                                                                           309 MQAVQFGNPAERNDIAMGPLINAAALERVEQKVARAVEEGARVAFGGKAVE----GKGY 363
                                                                                                                                                                                                   305 SKKIVVGDPSRAD---MGPLINTTALKGTEEVVEEAKESGARILYGGSKPDLSGPYKNGY 361
                                                                                                                                                                                                                                             364 YYPPTLLLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSSIYTQNLNVA 423
189. AKTVDEIGLPRGVENLVLGRGFPVGQRLAGNPKVAMVSMTGSVSAGEKTMATAAKNTTKV-24.8
                                                                                                                                                                                                                                                                                  362 FFLPTIIDNVDQKSKIFQEEIFAPVIGARKVSDVEEMYSLANDSKYGLASYLFTKDFNLI 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A set of ordered cusmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(2) / M145;

BRILLEY S D., Charter K F, Cerdeno-Tarraga A -M, Challis G L,
Bentley S D., Chare K D, Harris D E., Quail M A., Kieser H,
Harper D., Bateman A, Brown S, Chandra G., Chen C.W. Collins M.,
Fromin A, Fraser A, Goble A., Hidalgo T., Hornsky T., Bowarth S,
Huang C -H., Kieser T, Larke L, Murthy L., Gliver K, G'weil S.,
Rabbinowitsch E., Rajadleam M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell R G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                        422 FEAAERIREGELYINMPGPEASQCYHTGPRUJGQAGEGSRYGII.FYLKIKNIYV 475
                                                                                                                                                                                                                                                                                                                              424 MKAIKGLKFGETYINRENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQTQVVYL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)..', Nature 417\cdot141\cdot147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redembach M., Kieser H.M., Demapaite D., Eighner A., Gullum J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY. BRIONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cerdeno A.M., Parkhill J., Rarrell R.G., Pajandream M.A. Submitted (NoV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes, Actinobacteria, Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-JUN-2002 (TrEMBLrel, 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002086; Aldehyde_dehydr.
Pfam; PF00171; aldedh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative aldehyde dehydrogenase.
SCO3486 OR SCE65.22.
Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY,
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70 SWLPKISASIHERASEISALIVEEGGKIQQLAEVEVARTARYIRYMAEWAKPYEGEIIQS 129
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                                                                                                                                                                                                                                                                                                                                                                    130 DEPGENILLEKKALGVITGILPWNFPFFLIAPKMAPALLTGNTIVIKPSEFTINNAIAFA 189
                                                                                                                                                                                                                                                                                                                                                                                                             139 E-PGRSLGVREEPIGVVAAILPWNFPVAIFARKVAPALMAGNAVVLKPSELTPLSALALA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 KIVOPIGLPRGVENI/VIZIRGETVRQELABNPKVAMVSMIGSVSAGEKIMATAAKNIIKVC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 FEGERALWEGGLISVVARBSKERDRALVIHFOVARVIMEGSIRGGREILAQVADQIIEVS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 LELGGKAPAIVMDDADLELAVKAIVDSPVINSGQVCNCAFPVYVQKGIYNQFVNRLGEAM 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 PPTLLLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLTSS1YTQNLNVAMK 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 APTVL/FNVPPEMPIAPPEVFGPVL/PIIPFPAEAEVVSAANSTAYGLTAYVYTPPL/SPAMP 436
                                                                                                                                                                                             10 YIDGÇEVTWRĞDAWIDVVNPATEAVISKIPDGQAEDARKAIDAAERAQPEWEALPAIERA 69
                                                                                                                                                                                                                                      19 FVAGEYELDSSHGTLPVINPANGQLVAEVPSSSSSTVDRAVTAAVAAQREWGRRSHVARA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 1569. PAO1;
MEDLINE-20437337; PubMed-10984043;
Strover C. W. Pham X.-Q. T., Errafin A. L., Miroquchi S.D., Warronor P., Strover C. R., Pham X.-Q. T., Errafin A. L., Miroquchi S.D., Warronor P., Garber R. L., Golfry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Paier M.H., Hannork R. W., Lorry S., Olson M.V.;
"Complete genome sequence of Pseudomonas deruginosa PAO1, an
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 AIKGLKFGETYINRENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQTQVYLQ 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, gamma subdivision, Pseudomonadaceae;
                                                                                                                                                    Indels
                                                               492 AA; 52173 MW; 1CF94E55C73036FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01 MAR 2001 (TrEMBLrel. 16, Created)
01-MAP-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last ancotation update)
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PROSTIE: PS00070; ALUEHYDE_DEHYDE_CYS; UNKNOWN_1.
PROSITE: PSOUGTO: ALGEHYDE_DEHYDE_CYS; UNKNOWN_1.
PROSITE, PSOGGR7, ALGEHYDE_GEHYDE_GLD, GARNOWN_1
Oxidoreductase.
                                                                                                      36.5%; Scure 894; 64 16;
38.9%; Pred. No. 3.8e-53;
iive 92, Mismatches 191,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPP902986; Aldehyde_dehydr.
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EMBL; AE004464; AAG03654.1; -.
                                                                                                                                               Matches 184, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opportunistic pathogen.";
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                                                                                                                               Local Similarity
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                                                                  SEQUENCE
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497 AA; 52690 MW; CP41ECPD999PB7C1 CRC64;

SPOUPNORS

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70 SWLRKISAGIRERASEISALIVEEGGKIQQLAEVEVAFTADYIDYMAEWAPPYEGEIIQS 129
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                                                                                                                                                                                                                                                                                                                                            130 DRPGENILLEKRALGVTTGILPWNFPFFLIARKMAPALLTGNTIVIKPSEFTTNNAIAFA 189
                                                                                                                                                                                                                                                                                                                                                                                       134 HQPDKRIIVIKQPIGVTAAITPWNFPSAMITFKAGPALAAGGTMVLKFASGTPYSALALA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                190 KIVDEIGLPRGVFNLVLGRGETVGQELAGNPKVAMVSMTGSVSAGEKIMATAAKNITKVC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 LELGGKAPATVMDDADLELAVKATVDSRVINSGQVCNCAEKVYVQKGTYDQFVNRLGEAM 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 LELGGNAPFIVFDDADLDAAVEGALISKYRNNGGTCVCANRLYVQUGVYDAFVDKLKAAV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 QAVQFGNPAERNDIAMGPLINAAALERVEQKVARAVEEGARVAFGGKGYYYYPPIL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 LLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLFSSIYTQNLNVAMKAIKG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 LVDVPKNALVSKDETFGPLAPVFRFKDEAEVIAMSNDTEFGLASYFYAPPLARVFPVAEQ 432
                                                                                                                                                                                                                 14 YVDGAWYDADNGQTIKVNNPATGEIIGSVPKMGAAETRRAIEAADKALPAWPALTAKERA 73
                                                                                                                                                                        10 YIDGQFVTWRGDAWIDVVNPATEAVISRIPDGQAEDARKAIDAAERAQPEWEALPAIERA 69
                                                                                                                               1; Gaps
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable succinate-semialdehyde dehydrogenase oxidoreductase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salanoubat M., Genin S., Artiquenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cartolien L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siquier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
                                                                                    DB 16; Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 LKFGETYINRENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQTQVVYL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 LEYGMVGINTGLISNEVAPFGGIKASGIGREGSKYGIEDYLEIKYLCL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ralstonia solanacearum (Pseudomonas solanacearum).
Bacleria; Proteobacteria; beta subdivision; Kalstonia group;
                                                                                                                               187; Indels
                                        483 AA: 51622 MW; 1ED1643DCB83075C CRC64;
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PROSITE; PS000672; ALDEHYDE_DEHYDE_CYS; UNKNOWN_1.
PROSITE; PS00667: ALDEHYDE_DEHYDE_GIJ; UNKNOWN_1.
Oxidoreductase; Complete proteome.
PROSITE: PS00687: ALDEHYDF_DEHYDR_GLIT: IINKNOWN_1
                                                                                 36.0%; Score 879.5; DB 1
39.3%; Pred. No. 3.7e-52;
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                                                                                                                               96; Mismatches
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Nature 15:497-502(2002)
EMBL; AL646057; CAD13556-1;
InterPro; IPR002086; Aldehyde_dehydr.
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                                                                                                                             184; Conservative
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                                                                                 Query Match
Best Local Similarity
                      Complete proteome.
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                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                       139 DETPAPOGDRETVVNKEPTGVLAATTEWNFPTAMMTRKVGPALAAMVARALETPYS 198
                                                                                                                                                                                                                                                                                                                                                  185 ATAFAKIVDETGLPRGVENEVIGRGETVGGELAGNPRVAMVSMTGSVSAGERIMATAARN 244
                                                                                                                                                                                                                                                                                                                                                                                         199. ALAFAELAARAGVPAGLIJSTVTGDAQGTGGELTTANPVVHKIJSFTGSTAVGRIJJMRQCADD. 258
                                                                                                                                                                                                                                                                                                                                                                                                                                 24.5 ITKVCLELGGKAPAIVMIDADI FLAVKATVDSPVINS/32V/N/AEFVYVQKGTYDQFVNR 304
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                                                                                                                                7.8
                                                                                        DVVNPATEAVISKIPDGQAEDARKAIDAAERAQPEWEADP 64
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MEDLINE-21156231: PubMed-11258796;
Hayashi T., Makino K., Ohnishi W. Kurokawa K., Ishii K., Yokoyama K.,
Han C. G., Obtsubo E., Nakayama K., Murata T., Tanaka M., Tohe T.,
Tida T., Takami H., Honda T., Sasakawa C., emasawata N., Yasunada T.,
Kuhara S., Shiba T., Hattori M., Shinaqawa H.;
                                                                                                                              19 WRTQAFLAGAWTDADDGSTRDVTDPATGRVICTVPAMGAAFTRRALEAAQAAQRAWRKVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 KCYYYPPTILLDVRQEMSIMHEETFGPVLPVVAFDTLEDAISMANDSDYGLISSIYTQNL
                                             19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.21 NVAMKATKGLKFGETYTINPENFEAMOGPHACWPKSGTGGANGREBIJFGTQTQVV 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli ol57:H7.";
Nature 409:529-533(2001).
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MEDLINE-21074935; PubMed-11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Postal G., Havkett L., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Pimalanta E.L., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaese,
35.7%; Score 872.5; DR 16; Length 497;
                                          182; Conservative 100; Mismatches 174; Indels
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                      Pred. No. 1.2e 51;
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                        48.38;
                                                                                        18 WKGDAWI ---
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                        Best Local Similarity
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      Query Match
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71 WERKISAGIRERASEISALIVEBGGRIQAEVEVAFTADYIDYMAEWARPYEGEIIQSD 130
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                                                                                                                                                                                                                                                                                                                                11 IDGOFVTWRGDAWIDVVNPATEAVISPIPEGGAEDAFKATDAAEPAGPEWEALPATEHAS 70
                                                                                                                                                                                                                                                                                                                                                            STRAIN-LT2 / ScScidiz / Alco 700720; MEDLINE=21534948; PubMed=11677609; McClelland M , Sanderson K E , Spleth J , Cilfron S W , Latrelille P., Courtney L , Porwollik S , All I , Dante M , Du F , Hou S , Layman D , Leonard S , Nguyen C , Scott K , Holmes A , Grewal N , Mulvaney E , Ryan E , Sun H , Florea L , Miller W , Stoneking T , Nhan M , Waterston R , Wilson R K ;
                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
"Complete genome sequence of enterchemotriagic Escherichia coli
0157-H7 and genomic comparison with a laboratory strain K-12.",
DNA Pes. 8:11-22(2001)
EMBL: ARONS4145, AAST768 1: -.
                                                                                                                                                                                                                                              35 (%, Seere 870 %, DR 16, Lyngth 482; 39.3%; Pred. No. 1.5e-51; Live 92; Mismatches 187; Indels 1;
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01-MAR-2002 (TrEMBLrel 20, Last sequence update)
01-JUN-2002 (TrEMBLrel 21, Last ansotation update)
Succinate-semialdehyde dehydrogenase I, NADP-dependent (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 KFGETYINRENFEAMQGFHAGWRKSGIGGADGKHGLHGYLQ 471
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                                                                                                                    PFam: PF00171; aldedh: 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
                                                                                                       InterPro; IPR002086, Aldehyde_dehydr.
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Matches 181, Conservative
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"Complete genome sequence of Salmonella enterica serovar Typhimurium

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[97] KIVDEIGLPPGVFNLVLGPGETVGLELAGNPKVAMYSMTGSVSAGEKIMATAAKNITKVC 249
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                                                                                                                                                                                                                                                                                           10 YIDGGEVIWEGDAMIOVVNPATEAVISEIPEGGAEDARKAIDAAFRAGPEWEALPAIERA
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01-MAR-2002 (TrEMBLrol. 20, Last sequence update)
01-JUN 2002 (TrEMBLrol. 21, Last amnotation update)
5.colladte schriddehyde dehydrogense (EC 1.2.1.16).
9172911
                                                                           Pfam, PF00171, aldedh, 1.
PRGSITE, PS00070, ALGEHYDE_DEHYDE_CYS, UNKNOWN_1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
                                                                                                                                                                                                      35.5%; Score 868.5; DB 16;
39.4%; Pred. No. 2.1e-51;
Live 91, Mismatches 188.
           Nature 413.852.856(2001).
EMRL; AEGUM827; AAL21676-1;
InterPro; IPP002086; Aldehydo_Johydr
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                                                                                                                                                                                                                                                 182, Conservative
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70 SWLRKISAGIRERASEISALIVEEGGKIQQLAEVEVAFTADYIDYMAEWARRYEGEIIQS 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
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MEDLINE=20512582; Pubmed+11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki P., Masui N
Puji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                    Length 482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    91; Mismatches 189; Indels
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SEQUENCE 482 AA; 51894 MW; FEF850C52F818DC7 CRC64;
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01-007-2000 (TrEMBLrel. 15, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                DB 16;
                                                                                                                                                                            PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN I., PROSITE; PS00687: ALDEHYDE_DEHYDR_GLU; INKNOWN_I
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                                                                                                                                                                                                                                                                                                                                                            35.1%; Score 858.5; 39.2%; Pred. No. 1e-
enterica serovar Typhi CT18.";
Nature 413.848-852 (2001).
EBHBL; ALG27276; CAD05900.1; -
InterPro; IPR002086; Aldehyde_dehydr.
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NCBL_TaxID=86665;
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127 IQSDRPGENILLFKRALGVTTGILPWNFPFFLJARKMAPALLTGNTIVIKPSEFTTNNAL 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 BAMQAVQFGNPAERNDTAMGPLINAAALEKVEGKVAKAVEEGAKVAEGGRAVEGK (3YYY 465
                                                                                                                                                                                                                                                                           67 ERASWERKISAGIRERASEISALIVEEGGKIQQIAEVEVAFTADY DYMAEWARRYEGEL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 KUCLELGGKAPATUMDDADLELAVKATVDSRVINSGQVCNCAERVYVQKGTYTQFVNRLG 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 MYTDGQFVTWRGDA - - WIDVVNPATEAVISRIPOGQAEDARKAIDAAERAQPEWEALFAI 66
                                                                                                                                                                                                                                    6 LYIDG---TWTGDLLDTFDVKNPATGEVVGVMPNGGKAEAAAA1EAAQRAFLKWRKY1AA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 KTVELPREAGEPKOVVNLVPGDAKETOPEMISHEHVEKLIFFIGSIAVOKLIMKUSAGRMI.
                                                                                                                                                       Sales
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; aipha subdivision; Rhizobiaeeae group;
Ehizobiaeeae; Siborhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 AIKGLKFGETYINRENFEAMOGFHAGWRKSGIGGAISCHGLHGYLOTOVV 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.6%; Score 845.5; DB-16; Length 475; 39.1%; Pred. No. 7.7e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TIEMBLE). 19, Last sequence update)
01-MAR-2002 (TEBMBLE). 20, Last annotation update)
Probable succinate-semialdehyde dehydrogenase (FT 1.2.1.16).
65-85-81 OR KR0014 OR SMC02780.
                                                                                                                                                   84; Mismatches 195; Indels
                                                               475 AA; 51437 MW; 9AH1A2EE8PE9C117 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002086; Aldehyde_dehydr.
Pfam: PP00171; aldedh; IPPROSTTE; PS00070; AldeHyDE_DEHYDR_CYS; UNKNOWN].
PROSTIE; PS00687; ALDEHYDE_DEHYDR_CLU; UNKNOWN].
Pfam; PF00171; aldedh; 1.
PROSTTE; PS00070; ALDEHYDE_DEHYDR,CYS; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
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                                                                                                                                                   Matches 184, Conservative
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76 LRRWFELMIENKDDLGRILTMEQGKPLAEATGEIVYGASFIEWFAEEARRVYGDLVPGHQ 135
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                                                                                                                                                                                                                                                                                              132 PGENILLEKPALGVTTGILPWNFPFFLIAPKMAPALLTGNTIVIKPSEFTTNNAIAFAKI 191
                                                                                                                                                                                                                                                                                                                                                                                192 VDEIGLPRGVFNLVLGRGETVGQELAGNPKVAMVSMTGSVSAGEKIMATAAKNITKVCLE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 LGGKAPAIVMDDADLELAVKAIVDSRVINSGUVUNCAERVYVUKGIYDQFVNRLGEAMQA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 VQFGNFAERNDIAMGPLINAAALERVEQKVARAVEEGARVAFGGKAVEGKGYYYPPTLLL 371
                                                                                                                         20 GDAW-----IDVVNFATEAVISKIFDGQAEDARKAIDAAEKAQPEWEALPAIERASW 71
                                                                                                                                                Ouery Match 34.4%; Score 840.5; DB 16; Length 484; Best Local Similarity 37.4%; Pred No. 1 72-49; Matches 174; Conservative 97; Mismatches 186; Indels 9;
SQ SEQUENCE 484 AA; 51866 MW; AAC2988AZ9D5D498 CRC64;
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Search completed: June 24, 2003, 10:17:13 Job time · 40 6606 secs

375 DVTQAMAVAREETFGPVAPLFRFKDESDVIAQANDTEFGLASYFYAKDLARVFRVAEALE 434

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OM protein - protein search, using sw model

Tune 24, 2003, 10-02-25; Search time 40,2175 Seconds (Without alignments) 1696 383 Million cell updates/soc Run on.

 $US = \bar{0}\bar{9} - \bar{8}3\bar{0} - 751 - \bar{8}$ 

STS BYGGTKGLLVSYSDKFFGLE 512 1 MTNNPPSAQIKPGEYGFPLK.. Perfect score

Sednence:

908470 seqs, 133250620 residues Searched:

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Scoring table:

Total number of hits satisfying chosen parameters:

Minimum OB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 08

A\_Geneseq\_101002 Database

/SIDS2/gcgdata/geneseg/genesegp-embl/Aal990 nAT.\* /SIDS2/gcgdata/geneseg/genesegp-embl/Aal990 nAT.\* /SIDS2/gcgdata/genescg/genesesp-embl/AA1991.DAT:\* /SIDS2/gcgdata/genescg/genescap-embl/AA1992\_FAT:\* /SIDS2/gcgdata/genescg/genescgp-embl/AA1993.DAT:\* /SIDS2/gcgdata/geneseg/geneseap.embl/AA199.DAT.\* /SIDS2/gcgdata/geneseg/geneseap.embl/AA2001.DAT.\* /SIDS2/gcgdata/geneseg/geneseap.embl/AA2001.DAT.\* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\* DAT: \* PAT: \* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:\* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT·\* /SIDS2/gegdata/geneseq/geneseqp.emb1/AA2002.DAI.\* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983 nat:\*/SIDS2/gcgdata/geneseqp-embl/AA1984.bAT:\*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:\* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1982.bAT.\*/SIDS2/gcgdata/geneseg/genesegqp-embl/AA1983 bAT.\* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:\* /SIDS2/qcqdata/geneseq/geneseqp-emb1/AA1980.DAT:\* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:\* /S1DS2/gcgdata/geneseg/genesegp-emb1/AA1995 /S1DS2/gcgdata/geneseg/genesegp-emb1/AA1996 /SIDS2/gcgdata/geneseq/geneseqp.embl/AA1981 14: 15: 16: 19:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	E. coli aldehyde d	C qlutamicum prote	Corynebacterium ql	V.cholerae VPI pha	Novel human diagno	Novel human diagno	Enterococcus faeca	Staphylococcus aur	Staphylococcus epi	Novel human diagno
Q1		AAG92818	AAB79351	AAB49208	ABG25490	ABG29625	AAU34957	AAW89793	ARP39696	ABG27689
DB	C1	C3	22	ر: د:	C1	C1	22	18	53	C1
Length	512	206	206	206	1302	1393	496	508	510	371
% Query e Match Length DB I	100.0	64.1	64.1	65.9	56.3	56.3	44.4	40.8	40.4	40.2
Score	2673	1714.5	1714.5	1682	1505.5	1505.5	1186.5	1090.5	1080	1074
Result No.		C1	m	4	5	9	7	8	6	10

Human aldehyde deh Prosophila melanog Human ALDHS protei Human ALDHS protei Yeast aldehyde deh Sequence of aldehy Arabidopsis thalia Arabidopsis aldehy	a produce de constante de const	Staphylococcus and Staphylococcus and Lorsia Lenuicolia Aldahyde-dehydroqe Rhodococcus erythr Aldehyde deydroqe Rhodococcus erythr S. epidermidis ope Barley betaine ald	Staphylonorus api Ruman ovarian anti Pseudomonas aerugi Human aldehyde deh Human dehyde deh Ruman dehyde odenas Cladosporium herba Arabidopsis thalla Human protein SEQ
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## ALIGNMENTS

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AAR74926 standard; Protein; 512 AA.
                                                                                                  26-JUN-2001 (first entry)
                                                           AAB74926;
AAB74926
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RESULT 1

Aldehyde dehydrogenise, glyerrol dehydratuse, 3 HF, glyerrol; feedstock, 3 hydroxypropionic acid, genetic engineering; glucose; bacterial host, absorbable provibetic device; surgical suture; beta-lactam; acrylic acid; trifluoromethylated alcohol; diol; polyhydroxyalkonate; copolymer; lactic acid. E colialdebyde debydrogenise ildR protein sequence 352 ID NO:8. 

Escherichia coli.

WO200116346-A1.

38-MAR-2001.

30-AUG-2000; 2000Wn-4523878

9401S-0151440. kū - AUG - 1999.

(WISC ) WISCONSIN ALUMNI RES FOUND.

Suthers PF, Cameron DC,

WPI; 2001-315988/33.

N-PSDB; AAF82084

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3-Hydroxypropionic acid preparation, for use e.g. as monomer, by fermenting recombinant microorganisms expressing genes for suitable
                                                                                               enzymes in the presence of glycerol or glucose
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26-SEP-2001 (first entry)

AAC92818;

Claim 5; Page 46-48; 63pp; English.

The present invention describes a method for the production of 3-hydroxypropionic acid (3-HP). The method comprises fermenting a recombinant microorganism in the presence of a source of glycerol (1) or glucose, where the microorganism: (1) expresses genes for non-native enzymes which catalyse the production of (3-HP) from (1); (ii) carries genetic constructions for the expression of a glycerol dehydratase (GDHT) and aldehyde dehydrogenase (4BH) capable of catalysing the production of (3-HP) from (1); or (iii) carries a genetic construct an ADH capable of catalysing the production of (3-HP) from (1); or (iii) carries a genetic construct an ADH capable of catalysing the production of (3-HP) from (1); a first and a monomer, and is useful e.g. in the production of absorbable prosthetic devices and surgical sutures or for incorporation into beta-lactams, production of actylic acid or formation of trifineromethylated alcohols Incorporation of genes encoding two enzymes makes the host organisms able to produce (3-HP) from (1). The biotechnological method of preparing (3-HP) is potentially cheaper than chemical synthesis. The present sequence represents the E. coli aldehyde dehydrogenase aldb, which is used in the exemplification of the present invention. or diols, polyhydroxyalkonates and copolymers with lactic acid

512 AA; Sednence

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61 KRDIDLALDAAHKVKDKWAHTSVQDRAAILFKIADRMEQNLELLATAETWDNGKPIRETS 120
                                                                                                                                                                                 61 KRDIDLALDAAHKVKDKWAHTSVQDRAAILFKIADRMEQNLELLATAETWDNGKPIRETS 120
                                                                                                                                                                                                                         121 AADVPLAIDHFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWK 180
                                                                                                                                                                                                                                               181 MAPALAAGNOVVLKPARLIFPLSVLLLMETVGDLLPPGVVNVVNGAGGVIGEYLATSKPIA 240
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                                                                                             Gaps
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100.0%: Score 2673; DB 22; Length 512; 100.0%: Pred. No. 1.3e-264;
                                         Indels
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                                     Mismatches
                                     0,
                                       Conservative
                     Best Local Similarity
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   Query Match
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sequences from the Corporators at manager or navious appropriate superior that the corporators are useful for identifying the mutation point of a gene derived from a mutant of corporatorm bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from corporatorm bacterium, and identifying a homologue of a gene derived from corporatorm bacterium, corporatorm bacterium, are useful for producing amino acids, nucleic acids, vitamins, see derived and organic acids, particularly Liysiae. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formal directly from the European Patent office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 RYPASCIRAQEGGISEVOSETVAYHEHEPLGVVGQIIPWNFPLLMASWKMAFALAAGNCV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 VERPARLIPLISVILLIMELYGOLLIPPGVVNVVNGAGGVTGEYLALSKELAKVAFTGSTEVG (25)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 HAAADAWGKTSVAERALILHRIADRMEEHLEELAVAETWENGKAVRETLAADIPLAIDHE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 RYFFAGATRAQEDRSSQTDHNTVAYHFNEPTGVVGQTTPWNFPTLMATWKLAPALAAGNAT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 PGEYGFPLKLKARYDNF1GGEWVAPADGEYYQNLTPVTGQLL/CEVASSGKRD1DLALDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 PGTEGSTVNYEKRYENY1GGKWVPPVBGQY1, BN1 SPVTGEVI CEVARGTAAD VELLDAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mizoguchi H, Ando S, Hayashi M, ochiai K, Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of nucleotide and protein
                                                                                                                  Colymeform bacterium, amino acid synthesis, vitamin, saccharide,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; SEQ ID NO: 6572; 246pp + Sequence Listing; English.
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82; Mismatches 105;
                                                                          C glutamicum protein fragment SEQ ID No: 6572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                    99,JP-0377484.
                                                                                                                                                                                                                                                                                             18-DEC-2000; 2000EF-0127688
                                                                                                                                                                                                                                                                                                                                                         2000JP-0159162.
                                                                                                                                                                                                                                                                                                                                                                          2009JP-0280988
                                                                                                                                                                          Corynebacterium glutamicum.
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nes 313: Conservative
                                                                                                                                       organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Senoh A,
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Tateishi N,
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252 QQTMQYATQNTTPVTLELGGKSPNTVFADVMDEEDAPFDKALEGFALFAFNQGEVTTPS 411

AAG92818 standard; Protein; 506 AA.

RESULT 2 AAG92818

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247 KLINRAASDKITEVILELGGSKSESIFESIVISSAGARAKAVBSFAMFALNGSEVCTCFS 300
                                                                                           RALVQESIYERFMERALREVESIRSGNPLDSVIQMGAQVSHGQLETILNYLDIGKKEGAD 371
                                                        307 RALVHESTADFFI.FLGVKRVQNIKLGNPLDTETMMGAQASQEQMDKISSYLKIGPEEGAQ 366
                                                                              372 VLTGGRRKLIEGELKUSYYLEPTILFGQNNMKVFQEETEGPVLAVTTFKTMEEALELAND 431
                                                                                                                           TQYGLGAGVWSRNGNLAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKQSGIGRETHKMML 491
                                                                                                                                      Corynebacterium glatamicum, carbor metabolism and energy production. SMP protein, sugar metabolism and oxidative phosphorylation protein, fine chemical production; organic acid, proteinogenic amino acid, monproteinogenic amino acid, putine base, pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                      Corynobarterium glutamicum SMP protein sequence SPG ID NO 200
                                                                                                                                                                      492 EHYQQTKCLLVSYSDKPLGLF 512
                                                                                                                                                                                                                                                  AAB79351 standard; Protein; 506 AA.
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acid, a diol, a carbohydrate, an aromatic compound, a vitanin, a cofactor, a polyketide, or an enzyme. The presence of (1) or SMP proteins (11) encoded by them are used for disquesting the presence of activity of Corynebacterium diphtheriae in a subject. (11), (11), (11) or host ceils containing them are used to map genomes of organisms related to the gradient in dentity and localise C. giutamicum sequences of interest, in evolutionary studies, in determining SMF protein regions required for function, in modulating SMF protein regions required for function, in modulating SMF protein regions required metabolism of sugars, and in modulating high, energy molecule production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 HKVKDKWAHTSVQDRAATUFKTADRMEQNIELLATAPTWUNGKPTRETSAADVPLAIDHP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 HAAADAWGKTSVAEPALILHPIADPMEEHLEEIAVAETWENGKAVPETLAADIPLAIDHF 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleoside, a lipid, a saturated or unsaturated fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 VMKEAEQTHASILYLINIIGDLIPESVLNIVNSDAGEAGAALSGSNFISKIAFTGSTEVA
                                                                                                                                                                                                                                                         New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids,
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                                                                                                                                          Schroeder H, Zelder O, Haberhauer G;
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62.5%; Pred. No. 2.2e-166;
Live 82; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 450-452; 1246pp; English.
99DE-1042095.
99DE-1042123.
99DE-1042125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated bacteriophage encoded by a pathogenicity island of a pathogenic bacterium, useful for generating bacteriophage-base vaccines or vectors, e.g. to treat allergies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a pathogenicity island of a pathogenic bacterium. The bacteriophage may be used in pharmaceuticals e.g. for generating an immune response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention relates to an isolated bacteriophage encoded by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage; pathogenicity island; vaccine; allergy.
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63.3%; Pred. No. 4.8e-163;
tive 67; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V.cholerae VPI phage conserved gene AldA protein.
                                                                                                                                                                                                                                                                                                              AAB49208 standard; Protein; 506 AA.
                                                               492 EHYQQTKCLLVSYSDKPLGLF 512
                                                                                                            486 NHYQQTKNLLVSYDPNPTGLF 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 3; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYMA-) UNIV MARYLAND BALTIMORE.
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Matches 309; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-122703/13.
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                                                                                                                                                                                                                                                                                                                                                                                     AAB49208;
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                                                                                                                                                                                                                                           RESULT 4
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319 AKIJERVALIKQGNPLDTETQIGAQVSKRQYDKIJGYIQIGKDGGAEJJFGGHPNNQENY 378
                                                                                                                                                       259 STIELGGGKSPNIYFPDIFSHEDQYLDKCIESALLAFPNQGEVCTCPSRILVHESIYEKFL 318
                                        325 FPATPPVESTPSGNPLDSVTGMGAQVSHGQLETILNYTD1GKKEGADVLTGGKRKLLEGE 384
                                                                                                                                  385 EKDGYYLEPTILFGONNMRVFQEEIFGPVLAVTTFKTMFFALELANDTGYGLAAGVWSRN 444
                                                                                                                                                                                                                    445 GNIAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKQSGIGRETHKMMLEHYQQTKCLLUSY 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving (11). (11) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as melecular weight markers and as a food supplement. (11) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucieotide sequences have applications in diagnostics, forenside mapping, indentification of mutations responsible for genetic disorders or other traite to access biodiversity and to produce other types of data and products dependent on bNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PPR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymereotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypoptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; tood supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #25481.
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                                                                                                                                                                                                                                                                                                              505 SDKPLGLF 512
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960 QNLTTFVPDTHQIAIRNTKACSIFVSFALRTTHSC--AISHSSLEDPPAILFKIADRMEQ 1017
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                                                                                                                                                                                                                                                     NLELLATAETWDNGKP1KETSAADVPLAIDHFRYFASCIRAQEGGISEVDSFTVAYHFHE 154
                                                                                                                                                                                                                                                                                                                    160 FLGVVGGIIPWNFPLLMASWKMAPALAAGNCVVLKPAELIPLSVLLLMEIVGDLEPGVV 219
                                                                                                                                                                                                                                                                                                                                                                                   220 NVVNGAGGVIGEYLATSKPTAKVAFTGSTEVGQQIMQYATQNIIFVTLELGGKSPNIVFA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 DVMDEEDAFFDKALEGFALFAFNQCEVCTOFSPALVQFSIYEPFMEFALFAFKIFSIFSGNF 339
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amino acid sequences. ARGENIGO-ARGENIGO represent nevel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patient did not appear in the printed specification, but was obtained in electronic format directly from WIPO at frowho.int/pub/published_pot_sequences.
                                                                                                                                                                                         43 QNLT---PVTGQLLCEVASSGKRDIDLALDAAHKVKDKWAHTSVQDRAAILFKIADRMEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                             PB 22, Leagth 1302,
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                                                                                                                             56.3%, Score 1505.5, DB 22
89.1%; Pred. No. 2.6e-144;
                                                                                                                                                         7, Mismatches
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                                                                                                                                            Local Similarity 89.13
nes 302, Conservative
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                                                                                             1302 AA;
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23-AUG-2000;
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                                                                                                                             Query Match
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1051 QNETTFVPDTHQIALHNTKACSIFVSFALRTTHSC--ALSHSSLEDPPAILFKIADRMRQ 1108
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                                                                                                          The invention relates to isolated polynuclectide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polypeptide (11) sequences. (1) is useful as hybridisation probes, and gene mapping, and in recombinant production of (11). The polynucleotides are also used in diagnostics as expressed sequence tages for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat district states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical discorders involving aberrant protein expression or biological activity discorders involving aberrant protein expression or biological activity the polypeptide and polynucleotide sequences have applications in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess brodiversity and to produce other types of data and produce therefore other types of data and produce dependent on DNA and amino acid sequences. ABG20401-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
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Pred. No. 2.9e-144;
7; Miscatribes 25;
Ciaim 20; SEy 1D No 59984; luspp; English.
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89.1%;
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\begin{array}{c} \mathbf{x} \times \mathbf{x} \Rightarrow \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{x} \circ \mathbf{
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to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discoverty of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruqinosa and Enterococcus facelis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 ISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGNCVVLKPARLTPLSVL 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibiotics, comprise sequences of antisense nucleic acids
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21-MAP-2001; 2001Wo US09180
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                                                                                                                                                                                                                                                                                    16-FEB-2001;
                                                                      21-MAR-2000;
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                                                                                             443 ENGNLAYKMGRGIQAGBVWTNCYBAYPAHAAPCGYRGSCIGRETHKMMLEBYQQTKCLLV 50.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences found their transments) are useful as primers or probes for isolating homologues of any of the 5191 Stantous DNA sequences contained on the computer readable medium.
                                            367 GLOKGAFLAPTILANGTNIMOVAQERIFGPVATVIKERTERVIRLANDSEYGLOGAVES 4.26
                                                                                                                   invention. The INA sequences encoding the Staurous proteins are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read only memory (RAM) or 10 RAM. Homelogy searches using the Staurous that sequences allows putative functions to be assigned so that protein encoding or regulatory regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a Staphylococcus aureus protein sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode actious have been identified and these polypeptides can be used in a vaccine composition against Scaurens infection. The polypeptides can also be used in a kit for the imminodetection of Scauteus in a sample. Scaureus is implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer readable medium; vaccine; S.aureus Infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in numerous human diseases, including cellulitis, eyelid intections, I
poisoning, esteomyelitis, skin and surgical wound intections, scalded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide(s) and proteins derived from Staphylococeus aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus protein SEQ ID #5241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 23; Page 3242-3244; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                      AAW89793 standard; Protein; 508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0009861.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-1999 (first entry)
                                                                                                                                                                                        503 SYSDKPLGLF 512
                                                                                                                                                                                                                                     487 VTKEEADGLY 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-S, aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxic shock syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                     AAW89793;
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508 AA;

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146 VNDIDKDTMSIVRHEPIGVVGAVVAWNFPMLLAAWKIAPAIAAGNTIVIQPSSSTPLSLL 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRAAILFKIADRMEQNLELLATAETWDNGKPIKETSAADVPLAIDHFKYFASCIRAQEGG 144
                                                                                                                                                                                                           145 ISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGNCVVLKPAKLFPLSVL 204
                                                                                                                                                                                                                                                                             205 ILMEIVGDILPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVGQQIMQYATQNILP 264
                                                                                                                                                                                                                                                                                                                                                                                   266 ALCELGGKSANTIL------DDANLDLAVEGLQLGTLFNQGEVCSAGSRULVHFKTYDQL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 VPRLQBAPSNIKVGNPQDBATQMGSQTGKDQLDKTQSYIDAAKESDAQILAGGHK-LIEN 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 GEDRGPPFEPTLIAVPDNHHKLAQEELFGPVLGVIKVKDDQEATDTANDSEYGLAGGVFS 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 RNGNLAYKMGRGIQAGPVWTNCYHAYPAHAAFGGYKQSGIGRETHKMMLEHYQQTKCLLV 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
                                                                     25 YDNEIGGEWVAPADGEYYQNLTPVTGQLLGEVASSGKRDIGGALDAAHKVKDKWAHTSVQ 84
                                                                                                     26 YGLFINGEFVKGSSDETIEVTNPATGETLSHITRAKDKDVDHAVKVAQEAFESWSLTSKS 85
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis ORF amino acid sequence SEG ID NO:4541.
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                                    Ġ,
     DB 18, Length 508;
tch 40.8%, Score 1090.5, DB 18, Lengt) al Similarity 43.5%, Pred. No. 2e-102; 213; Conservative 101; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP39696 standard; Protein; 510 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-055779P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus epidermidis.
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N-PSDB; ABN92241.
Query Match
Best Local Similarity
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08-NOV-1997;
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                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 TSPVINSETVAYHPHEPLGVVGQTTPPWNFPLLMASWKMAPALAARRIVVVLKPABLLTPLSVL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 VNEIDGNTMSLVVNEFVGVVGTVVAWNFPILLASWKLGPALAAGNIVVIQPSSSTFLSLI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 VITELGGKSPNIVFAOVMPEEDAFEPFALEGFAT FRENGGRVTTPSPATVQESIYERF 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 ITLELGGKSANIIF-----DDANLEQVIEGVQLGILFNQGEVCSAGSKLLVQSSIYNEL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 MERATREVESTRSGNFLI/SVTOMCADVSHOCI,PTTLNYTDTGKREG-ADVLTGGPPKILE 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440 TTD1HFALNVARAMETSEIWINTYNQIPASAPERSYRKSSISHEVYKDAIKNYQQVKNIF 499
                                                                                      ARNAUS, A to ABNAUS represent. Staphylococous apidermidis open reading frame (OPE) machele acid sequences which encode the amino acid sequences given in ARESTIZ4 to ARESTIGO The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections The sequences can be used to screen for compounds able to interfere with the S. epidermidis life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 YDNFIGGEWVAPADGEYYQNLFPVFGQLLCEVASSGKKDIDLALDAAHKVKDKWAHTSVQ 84
                                                                                                                                                                                                                                                  cycle or inhibit S, epidermidis infection.
N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 YOLF INNEFLASOSOSTITVSNPANCEDLARVARACKRIVORAVÇAAHDAFDSWSKISKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 EPKEKEAFENIKVGPPFDEDIKMSAOTGPEOLDKIESYIKIAEEDPKANILTGGHP-1TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (83) GPL/KINSYYLEP/TTL-FRGINNMRVFGEFTFGPVLAVTTFKTMFEALELAND/TQYGLGAGVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 ELMELVGPLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVGQIMQYATQNIIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 SPNGNLAYKMGPGTGAGPVWTNOYHAYPABAAFGGYKQSGTGFFBBKMMLEHYQQTKGLL
polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, chromosome mapping, gene mapping, gene therapy, forensic:
food supplement, medical imaging, diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Intela
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.4%; Score 1080; DB 23; Best Local Similarity 43.8%; Pred. No. 2.4e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            101, Mismatches 165,
                                             Disclosure; SEQ ID 4541; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #2/680.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Character Value
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                                                                                                                                                                                                                                                                                                                                                                      510 AA;
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Homo saprens.

Human aldehyde dehydrogenase ALDHZ protein sequence SEQ ID NO:4

26-JUN-2001 (first entry)

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, ollgomens, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy Lechniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 FNQGEVCTCPSRALVQESIYERFMERAIRRVESIRSGNPLDSVTQMGAQVSHGQLETILN 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fip wipo int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and to produce other types of data and products dependent on DNA and amino acid sequences. ARG00010-ARG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensits, yene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 58048; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C, Tang YT;
                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                         2000US-0540217.
2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS91876
W0200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biodiversity
                                                                                                                                                                                                                         31-MAR-2000;
                                                                                                                                                                                                                                                            23-AIIG-2000;
                                                                         11-OCT-2001
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AAB74924 standard; Protein; 500 AA

AAB74924

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present sequence represents the human aldehyde dehydrogenase ALDHZ, which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 HSGREENPLADETERDRITYLAALETLINGKPYVISYLVELEMVELETLEVYAGWADEVHOR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 ISEVDSETVAYHEHEPLGVVGQ11PWNFP1LMASWKMAPALAAAGN°VVUKFARDTFLSVL, 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an ADH capable of catalysing the production of (i HP) from (1). I HP is a monomer, and is useful e.g. in the production of absorbable prosthetic devices and surgical sutures or for incorporation into beta-lactams,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 FIGGEWVAPADGEYYONIJPVTGOLIJJEVASSGKRDIDLALD- AAHKVKDKWAHISVU 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 FINNEWHDAVSRKTEPTVNPSTGEVICQVAEGDKEDVDKAREGREGAFQIJJSPWRRMDAS BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3-hydroxypropionic acid (3-HP). The method comprises fermenting a recombinant microordanism in the presence of a source of algorithm of glucose, where the microordanism: (i) expresses genes for non-native enzymes which catalyse the production of (3-HP) from (1); (ii) carries genetic constructions for the expression of a alycerol dehydratase (GDHT) and aldehyde dehydrogenase (AMH) capable of catalysing the production of (3-HP) from (1); or (iii) carries which expresses the dham gene from Klebsiella pneumoniae and a gene for which expresses the dham gene from Klebsiella pneumoniae and a gene for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             production of acrylic acid or formation of trifluoromethylated alcohols of ducis, polyhydroxyalkonates and copolymers with lastic acid. Incorporation of genes encoding two enzymes makes the fest organisms able to produce (3-HP) from (1). The biotechnological method of preparing (3-HP) is potentially cheaper than chemical synthesis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fermenting recombinant microorganisms expressing genes for suitable
                                                                                      feedstock; 3 hydroxypropionic acid; denetic enginecting; almoses barterial host; absorbable prosthetic device; surgical surune; beta-lactam; acrylic acid; triffuoromethylated alcohol; diol; polyhydroxyalkonate; copolymer; lactic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-Hydroxypropionic acid preparation, for use e.g. as monomer, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for the production of
                                                                   Aldehyde dehydrogenase; glycerol dehydratase; 3 HP; glycerol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.7%; Score 954; DB 22; Length 500;
42.0%; Pred. No. 2.40 8B;
ive 84; Mismatches 176; Indels 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzymes in the presence of allycerol or alucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 32-35; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                             99US-0151440.
                                                                                                                                                                                                                                                                                                                                               30-AUG-2000; ZOÖUWO-USZ3878.
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                                                                                                                                                                                                                                                      WO200116346-A1.
                                                                                                                                                                                                             Homo sapiens.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Brosophila. The invention is useful in developmental biology and in Plucidating cell signalling and
                                                                       263 IPVTLELGGKSPNIVFADVMDEEDAFFDKALE: GFALFAFNQGEVCTGPSRALVQESIY 320
                                                                                                                                                                                                                                                                                                        205 ILMETVGPL-TPPGVVNVVNGAGGVIGEYLATSKETAKVAFTGSTEVGQQIMQYA-TQNT 262
                                   204 YVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVAFTGSTEIGRVIQVAAGSSNL 263
                                                                                                       264 KRVTLELGGKSPNIIMS-----DADMDWAVEDAHFALF-FNQGDCCCAGSKTFVQEDIY 316
                                                                                                                                          321 ERFMERAIRRVESIRSGNPLDSVTGMGAGVSHGGLETILNYIDIGKKEGADVLFGGRRKL 380
                                                                                                                                                                                                                381 LEGELKU-GYYLEPTILFG--QNNMRVFQEEIFGPVLAVTTFKTMEEALELANDTQYGLG 437
                                                                                                                                                                                                                                    438 AGVWSRNGNI AYKMGPGIQAGPVWTNCYHAYPAHAAFGGYKQSGIGPFTHKMMLEHYQQT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo int/pub/published_pet_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more yenes from Diosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                          317 DEFVVRSVARAKSRVVGNPFFSKTEDGFQVDETQFKKILGYINTGKQEGAKLLCGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; celi signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID No 7212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  520 AA
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                                                                                                                                                                                                                                                                                                                                                          498 KCLLVSYSDK 507
                                                                                                                                                                                                                                                                                                                                                                                            490 KTVTVKVPQK 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 LLMELVGUL LITCVVNVVNGAGOVIGBYLATSKRIAKVAPTGSIRVGQI-MOYATQNI 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 LEGELKDGYYLEFTILFG QNNMRVFQEETFGFVLAVTTFKTMEEALELANDTQYGLGAG 439
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                                                                                                                                                                                                                                                                                 43 FINNEWHKSKSGKIFETINPITAEVIAEIGGADKEDIDIAVGAAFNAFKLGSPWPPMDAS 102
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                                                                                                                                                                                                              28 FIGGEWVAPADGEYYONLTPVTGQLLCEVASSGKKDIDLALDAAH----KVKDKWAHTSVQ 84
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binding affinity, drug targeting, alcoholism, alcohol induced disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 EPFMERATRRVESTRSONFLESVIGMGAGVSHÖQLETTINYTEFGKRGADVITGGRPKL
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                                                                                                     41.6%, Pred. No. 6.6e-88,
tive 86, Mismatches 179;
                                                                   35.5%; Score 949; DB 22;
41.6%; Pred. No. 6.6e-88;
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                                                                                                     Local Similarity 41.6%
nes 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500 LLVSYSDK 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511 VIVKVAQK 518
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520 AA;
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   Sequence
                                                                          Query Match
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N-PSDB; ABA99282, ABA99283.

New genetic variants with polymorphisms in the aldehyde dehydrogenase 5 (ALDH5) gene, useful for studying the function of ALDH5, and for expressing ALDH5 protein which is useful in screening drugs for

treating ALDH5-related diseases

Claim 30; Page 72-74; 96pp; English

human aldehyde dehydrogenase 5 (LDH5) gene containing polymorphic sites.

The polymorphic ALDH5 variant is useful in studying the effect of the variation on the biological activity of ALDH5 and on the binding affinity of candidate drugs targeting ALDH5 four the treatment of alcoholism and alcohol-induced disorders. Polymorleotides comprising a polymorphic gene variant or fragment may be used for therapeutic purposes. ALDH5 protein isoforms may be used in assays to measure the binding affinities of one or more candidate drugs targeting the ALDH5 protein soforms may be used in assays to measure the binding affinities of one or more candidate drugs targeting the ALDH5 protein may be used to generate antibodies. Haplotyping method can be used by scientists to validate ALDH5 as a candidate candidate candidate associated with ALDH5 activity, and in the design of clinical trials of candidate drugs for treating a specific condition or disease predicted to be candidate drugs for treating a specific condition or disease predicted to be associated with ALDH5 activity. Information on polymorphisms on the ALDH5 activity information on polymorphisms on the ALDH5 drugs for treating a specific condition or disease predicted to be associated with ALDH5 activity. Information on polymorphisms on the ALDH5 drugs for the plant of the biological trials of the ALDH5 drugs for the plant of the biological trials of the ALDH5 drugs. ALDH5 as well as in identifying drugs targeting this protein for the treatment of disorders related to its abnormal expression or function. The products of the invention have antialcoholic activity. This sequence represents the human ALDH5 protein described in the disclosure of the This invention describes a novel isolated genes and haplotypes of the invention.

517 AA: Sequence

5460 35 0%; Srore 936; DR 23; Length 517; 42.0%; Pred. No. 1.4e-86; Inde s Mismatches 182 . œ Conservative Local Similarity 205; Query Match Matches

28 FIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKPDTDLALDAAH --- KVKDKWAHTSVQ 84 40 FINNEWQDAVSKKTFPTVNPTTGEVIGHVAEGDRADVDRAVKAAREAFRLGSPWRRMDAS 99 q

100 ERGRIJANIJADLVERDRVYLASLETLDNGKPPOFSYALDIJJEVIKVYRYPAGWADKWHGK 159 DRAAILFKIADRMEQNLELLATAETWDNGKPIPETSAADVPLAIDHFRYFASCIRAQEGG 144 ò g

145 ISEVDSETVAYHFHEPLGVVAQIIPWNFPLLMASWKMAPALAAGNCVVLKPARLTFLSVL 204

qq ò

9 9 5 qq 9 qq ò q

160 TIPMHGQHFCFTRHEPVGVCGQIIPWNFPLVMQGWKLAPALATGNTVVMKVAEQTFLSAL 219 205 LLMEIVGDI. I.PPGVVNVVNGAGGVIGEYI.ATSKRIAKVAFTGSTEVGÖQIMQYA-TQNI

263 IPVTLELGGKSPNIVFADVMDEEDAFFDKALEGF - ALFAFNQGEVCTCPSFALVQESTY 320

ERFMERATRRVESTRSGNFLDSVTQMGAQVSHGQLETTLINYIDIGKKEGALIVLTGGREKKL. 380 333 NEFLERTVEKAKORKVGNPFELDTÖÖGPQVOKEOFEPVLGYTOTGOKEGAKLLGGGEP-- 390 181 LEGELKDGYYLEPTILFG-ONNMRVFQEEIFGPVLAVTTFKTMEEALELANDTQYGLGAG 439 -FGE--RGFFIKPTVFGGVQDDMRIAKEEIFGPVQPLFKFKKIEEVVERANNTRYGLAAA 447 440 VWSRNGNLAYKMGRGIQAGPVWTNOYHAYPAHAAFGGYKQSGIGRETHKMMLEHYQQTKC 499 

500 LLVSYSDK 507

q ó

508 VIIKVPQK 515

ALDHS; human; polymorphism; haplotype; aldehyde dehydrogenase 5; binding affinity; drug targeting; alcoholism; alcohol induced disorder; Human ALDH5 protein polymorphic variant. Location/Qualifiers AAM49517 standard; Protein; 517 AA. /label- Aia, Val /label= Val, Ile 'label" Leu, Arq label - Asp, Asp /label: Val, Ala /label- Mot, (first entry) Misc-difference 276 Misc-difference 176 Misc-difference 470 Misc-difference 107 Misc-difference 86 Misc-difference WO200192279-A2. antialcoholic. Homo sapiens. 13-MAY-2002 AAM49517; RESULT 14 AAM49517 

(GENA-) GENAISSANCE PHARM INC. 29 MAY 2001; 2001WO US17253. 26-MAY-2000; 2000US-207508P. 06-DEC-2001

Sanchis A; Duda A, Finkel K, Kazemi A, Messer C,

WPI; 2002-122054/16.

New genetic variants with polymorphisms in the aldehyde dehydrogenase 5 (ALDH5) gene, useful for studying the function of ALDH5, and for expressing ALDH5 protein which is useful in screening drugs for treating ALDH5-related diseases

Disclosure; Fiq 3; 96pp; English.

This invention describes a novel isolated genes and haplotypes of the human aldehyde dehydrodenase 5 (ALMS) erne containing polymorphic sites. The polymorphic ALMS variant is useful in studying the effect of the variation on the biological activity of ALMS and on the binding affinity of candidate drugs targeting ALMS to the treatment of ALDHS as well as in identifying drugs targeting this protein for the treatment of disorders related to its abnormal expression or function. The products of the invention have antialcoholic activity. This sequence represents the human ALDHS polymorphic variant protein described in the disclosure of the invention. protein. ALDHS proteins may be used to generate antibodies. Haplotyping method can be used by scientists to validate ALDH5 as a candidate target for treating a specific condition or disease predicted to be associated with ALDH5 activity, and in the design of clinical trials of alcoholism and alcohol-induced disorders. Polynucleotides comprising a polymorphic gene variant or tragment may be used for therapeutic purposes. ALDHS protein isoforms may be used in assays to measure the candidate drugs for treating a specific condition of disease predicted to be associated with ALMES activity. Information on polymorphisms on the ALDHS gene can be applied for studying the biological tanction of binding attinities of one or more candidate drugs targeting the ALDHS professes where the ALDHS brokesses were the ALDHS brokesses were the ALDHS brokesses were the contracting the ALDHS brokesses were the contractions and the contractions are the contractions.

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                                                                                                                                                                                                                                                                          263 IPVILELGGKSPNIVFANVMDFFDAFFDKALEGF--ALFAFNQGFVGTGPSRALVQESIY 320
                                                                                                                                                                                                                                                                                                                                                                                                           321 EPFWEPATPPVESIPSGNPLDSVTQMGAQVSHGQLETILNYIDIGKKEGADVLFGGKRKL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 NEFLERTVEKAKORKVGNPFELDTQQGPQVDKEQFERVLGYIQLGQKEGAKLLCGGER-- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 LEGEL-KDGYYLEFTILFG-QNNMRVFQEETFGPVLAVTTFKTMEEALELANDTQYGLGAG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 ERGRILLNXI.ADI.VERDPVYI.ASI.FTLDNGKPFQESYALDI.PEVIKVYRYFAGWADKWHGK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 VWSRNGNLAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKQSGIGRETHKMMLEHYQQTKC 499
                                                                                                                                                                                    DRAATLFKIADRMEQNLELLATAETWDNGKPIRFTSAADVPLAIDHFRYFASCIRAQEGG 144
                                                                                                                                                40 FINNEWQDAVSKKTFPTVNPTTGEVIGHVAEGDPADVDRAVKAAREXFRLGSPWRRMDAS 99
                                                                                                               28 FIGGEWVAPADGEYYÖNLTPVTGQLLCEVASSGKKDIDLALDAAH---KVKDKWAHISVQ 84
                                                                                                                                                                                                                                                      145 ISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGNCVVLKPARLTPLSVL
                                                                                                                                                                                                                                                                                                                         205 LIMEIVGDI-IFFGVVNVVNGAGGVIGEYLAISKRIAKVAFIGSTEVGUGIMQYA-IQNI
                                                                                                                                                                                                                                                                                                                                               220 YLASLIKEAGFPGVVNIITGYGPTAGAAIAQHXDVDKVAFTGSTEVGHLIQKAAGXSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     feedstock; 3 hydroxypropionic acid; genetic enginecing; glucose; bacterial host, absorbable prosthetic device; surgical surure; beta-lactam; acrylic acid; trifluoromethylated alcohol; diol,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast aldehyde dehydrogenase ALD4 protein sequence SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aldehyde dehydregenase; glycerol dehydratase; 3-HP; glycerol;
                                                 Length 517;
                                                            Local Similarity 42 0%; Prod No 1 40-86;
Les 205; Conservative 80; Mismatches 183; Indels
                                             35.0%, Score 936, DB 23, 42.0%; Pred No. 1 4#-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polyhydroxyalkonate; copolymer; lactic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB74923 standard, Protein, 495 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cameron DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       500 LLVSYSDK 507
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            Sequence
                                                                                                                                                                                    85
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                                             Query Match
                                                                              Matches
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55 EGREDDVEEAVQAADRAFSNGSWNGIDPIDRGKALYRLAELIEQDKNVIASIETLDNGKA 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 GFAL-FAFN"GEVOLGPSKALVQESIYERFMERATRRVESTRSGNPLDSVTQMGAQVSHG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 MASWKMAPALAAGNCVVLKPARLTPLSVLLLMETVGDL-LPPGVVNVNGAGGVTGRYLA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 NILLGIYYNSGEVGCAGSEVYVEESIYDKFIEEFKAASESIKVGCPFDESTFGGAGISQM 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 QLNKILKYVDIGKNEGATLITGGERL-----GSKGYFIKPTV-FGDVKEDMRIVKEEIFG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 PVLAVTTEKTMEEALELANDTQYGLGAGVWSPNGNLAYKMGPG1QAGRVWTNCYHAYPAH 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 PVV?VTKEKSADEVINMANDSEYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFHHA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                             3-hydroxypropionic acid (3-HH). The method comprises formenting a recombinant microcrapism in the presence of a source of glycorol (1) or glucose, where the microcrapism (1) expresses genes for non-native enzymes which catalyse the production of (3-HP) from (1); (1) carries genetic constructions for the expression of a glycerol dehydratase genetic construct of the expression of a glycerol dehydratase production of (3-HP) from (1); or (11) carries a genetic construct which expresses the dhas gene from Klebsisella procumoniae and a gene for an Alb capable of catalysing the production of (3-HP) from (1). 3-HP is a monomer, and is useful e.g. in the production of (3-HP) from (1). 3-HP is production of acidical prospection into beta lactams, production of acidic acidic formation of filling monethylated aluchols or diols, polyhydroxyalkonates and expenses with lactic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Incorporation of genes encoding two enzymes makes the host organisms able to produce (3-HP) from (1). The biotechnological method of preparing (3-HP) is potentially cheaper than chemical synthesis. The present sequence represents the yeast aldebyde dehydrogenase ALD4, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23° TSKPIAKVAFTGSTFVSQQIMQVATQNIIRVTLELGGKSPNIVFAFVMFFFDAFFFKAFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSHLPMTVPIKLPNGLEYEQPTGL-----FINNKFVPSKQNKTFEVINPSTEEEICHIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 MWAWKIAPALVIGNIVVLKIAESIFLSALYVSKYIFQAGIPIGVINIVSGFGKIVVEAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          854 QLETTLINY I DIGKK PGADVLÆGGRRKLJÆGET,K PGYYLÆPTTLFG - - QNNMRVFQEETFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                  combinant migroorganisms expressing genes for suitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . ₩.Z
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for the production of
                                                                                                                                  3-Hydroxypropionic acid preparation, for use e.g. as monomer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.0%; Scott 935; DR 22; Length 495; 41.1%; Pred. No. 1.7e-86; ive 84; Mismatches 183; Indels 2
                                                                                                                                                                                                                        enzymes in the presence of glycerol or glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 VPEGGENASGLGREMSVDALQNYLQVKAV 490
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                                                                                                                                                                                                                                                                                                                    laim 5, Page 26-28, 63pp; English
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200; Conservative B
2001-315988/33
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                                      N-PSDB; AAF82081.
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115

57

411

Search completed: June 24, 2003, 10:13:47 Job time: 42.2175 secs

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GenCore version 5.1 6
Copyright (c) 1993 - 2003 Compugen Ltd
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OM protein - protein search, using sw model

Pun on: June 24, 2003, 10-13 55, Search time 14 1793 Seconds (without alignments) 1062 435 Million cell updates/sec

Title: US-09-830-751-8 Perfect Score 2673

Sequence: 1 MTNNPPSAQIKPGEYGFPLK ...HY@@tkGllvSYSHKPLGLF 512

Scoring table. BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: Saged\_Batelbas\_AA;;
1: Cqq2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
2: /cqq2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
3: /cqq2\_6/ptodata/1/iaa/6A\_C'MH pep:\*
4: /cqq2\_6/ptodata/1/iaa/6A\_C'MH pep:\*
5: /cqq2\_6/ptodata/1/iaa/PCTUS\_C'MH pep:\*
6: /cqq2\_6/ptodata/1/iaa/PCTUS\_C'MH pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ			COLUMNICA	
Result		Query				
NO.	Score	Match	Match Length	B :	ID	Description
1	1080	40.4	510	4	US-09-134-001C-4541	Sequence 4541, Ap
C1	P 5.7	C.	153	4	2 \$62-122-60-SA	2, Arr
ю	847	31.7	485	4	US-09-651-941-9	2
4	847	31.7	485	4	US-09-955-597-9	Sequence 9, Appli
ഗ	847	31.7	508	4	US-09-655-270A-9	6
ပ	845	31.6	506	4	US-09-134-0010-4383	438
7	752	28.1	497	<del>-</del> +	US-08-513-841-2	
8	752	28.1	164	.1	US - U8 - 535 - 834 - 2	: 4
6	752	28.1	497	C ŧ	US 08-942-673-2	C i
10	752	28.1	10.4	~;	US-09-118-317 2	ر ،
11	731.5	27 4	488	4	175-09-134-0015-4246	424
75	604	11	7 1. 7	7	118 114-1 44-1001C 4388	Sequence 4388, At
13	593.5	2.5	518	4	US-09-134-001C-4451	4457,
14	583	21.8	482	-;	US 09 155-183-4	
15	578.5	21.6	487	4	-09-351-224E-	
16	380 5	14 2	464	4	118-08-134-001C-4701	Sequence 4701, Ap
17	267	10.0	133	Н	US-08-346-611-2	
18	267	10 O	133	C 1	US-08-794-494 2	c ì
19	177 5	ع. ع	551	4	08-08-855-061-5	Sequence 2, Appli
30	106	C . 4	<u>ر</u> د	÷	US - 09 - 612 - 964 - 2	C į
21	98.5	3.7	637	<b>,</b>	US-08-235-838-14	14
CI CI	38.5	3.7	637	C 1	US-08-465-473B 14	7
23	97.5	3.6	711	_	US-08-235-838-7	7, 1
Ç.4	37.5	<u>ئ</u> ج	711	C-3	TS-08-465-473B-7	7, 1
(C)	44	۶.	601		RS-08-333-358 14	Sequence 14, Appl
38	25	3.6	[09		US-08-463-694-14	Sequence 14, Appi
27	62	3.6	601	_	US-08-694-501-14	Sequence 14, Appl

~	94	ж Э.2	72	4	US-09-655-270A-33	Sequence 33, Appl
۵.	ر د ج	5.5	5588	~	US-09-036-987A-6	, A
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7	c G	L- ۳۰	1257	c.	H3-08-7-0-152A-2	Sequences 2, Appli
~	91.5	3.4	484	Н	US-08-030-06-8	Sequence 8, Appl
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4	С <u>Б</u>	4	202	4	HS-09-923-654-2	7
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36	89.5	۳. ش	1385	r-1	US-07-675-772-2	
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38	89.5	3.3	1385	<del>-</del> -1	US-08-158-232-2	Sequence 2, Appl
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Ö	89.5	.* .*	7.85 1.85	-	115-08-316-301A-2	r i
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'n	89.5	3.3	1385	4	US-09-076-137-2	Sequence 2, Appl
4	89.5	3.3	1385	นา	PCT-US92-03624-2	Sequence 2, Appl
ın	89.5	3.3	1385	9	5281530-1	Patent No. 5281530

## ALIGNMENTS

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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC'
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 VNEIDQNTMSLVVNEPVGVVGTVVAMNFPILLASWKLGPALAAGNTVVIQPSSSTPLSL( 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 VTLELGGKSPNIVFADVMDEEDAFFFKALEGFAL FAFNQGEVCTOFSFALVQESIYDKF 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 MERALPRVESTRSINFLLISVTSMSAZVSHOGDETTI,NYTD FORRETTANLTGORRILLE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 LEKEKEAPENIKVGOPEDDIKMSAQTGPBQLDKIESYIKIABEDDKANILIGGHP-1TD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 DRAATLEKIADEMEQNLELLATAETWONGKPIRETSAADVPLATDHFRYFASCIRAQEGG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 LLMEIVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAPTGSTEVGQQ1MQYATQNIIP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 YGLETNNEPDASISGETLTVSNPANGELLAKVAPAGKKTVFKAVGAAHDAFLSWSKISKE 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 ISEVDSEIVAYHEHEFLJVVGQIIPWNFFLLMASWKMAFALAAGNJVVLKFAFLIFLSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 ELAKIFGEVLPKOVVNVLTGKSSESSPATFHHEGVFKLSFTSSTTV YSVAQASAERIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 40.4%; Score 1080; DB 4; Length 510;
Best Local Similarity 43.8%; Prod No. 1.70-108;
Matches 215; Conservative 101; Mismatches 167; redels 10, Sups
                                                                                                                                                                  TITLE OF INVENTION. ....
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PPIOP APPLICATION NUMBER: US 60/054,964
FRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
                        ; Sequence 4541, Application US/09134001C; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4541
                                                                                                                                                                                                                                                                                                                                                                          PEDGE FILLING DATE: 1997-08-NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4541
                                                                                          GENERAL INFORMATION:
US-09-134-001C-4541
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440 TIDIHRALNVARAMRIGRIWINTYNOIPAGAPEGGYRKSGIGREVYRDAIRNYQQVRNIF 499
383 GELKDGYYLEPT1L-FGONNMRVFQEE1FGPVLAVTTFKTMEFALELANDTQYGLGAGVW 441
                                           880 NGLDKGYFFEPTIIEINDNKHQLAQEEIFGPVVVVEKFDDEQEAIEIANDSEYGLAGGIF 439
                                                                                       442 SRNGNLAYKMGRGIQAĞRVWINCYHAYPAHAAFGGYKQSGIGKETHKMMLEHYQQIRCIL. 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 GKLYSNAYLNDLAGCIKTLRYCAGWADKIQGQ-GRTIPIDGNFFTYTRHEPIGVCGQIIP 188
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Riccardo Dalla-Favera and APPLICANT: Alessandro Massimo Gianni TITLE OF INVENTION: A Retroviral Vector Capable of Transducing the TITLE OF INVENTION: Addebyde Dehydrogenase-1 Gene and Uses of Said TITLE OF INVENTION: Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 1%; Score 857 5; DR 4; Longth 521; 38.7%; Pred. No. 2.9e-84; ative 83, Mismatchës 197, Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/09/221,294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                             : Sequence 2, Application 05/09221294
; Patent No. 6268138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM 330 466 DX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
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amino acid
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                                                                                                                                                                                                                               500 IDTSNQTKGLY 510
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US-09-221-294-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
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703 VO
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                                                                                                                                                     303 DEDNAVE----FAHROVEYHQQQCCIAASRIFVEESIYDEFVRKSVERAKKYILGNPLTP 358
                                                                                                                                                                                                          343 VTQMGAQVSHGQLET11.NY1D1GKKEGADVLTGGRRKLLEGEL, KIMMYLEPT11.LG (ON 400)
                                                                                                                                                                                                                                                                                                                401 NMRVFQEELFGFVLAVTTFKTMEFALELANDFQYGLGAGVWSRNGNLAYKMGRG1QAGRV 460
                                                                                                                                                                                                                                                                                                                                            229. IGEYLATSKRIAKVAFTGSTEVOQQIMOYA. TQNITPVTLELGGKSPNIVFADVMDEEDA. 287
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PRIOR APPLICATION NUMBER: 60/152,545
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Patent No. 6355470
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NUMBER OF SEQ 1D NOS: 28
SOFTWARE: Microsoft Office 97
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Matches 185; Conservative
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                                                                                          4.26 RALREAQTLIDAGNVWINSWGVLNPASPYRGEGGSGYGSGLGGGAALESFTKEKSI 479
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APPLICANT: RAINER, RUSS
TITLE OF INVENTION' Genes Encoding Picric Acid Degradation
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CURRENT FILING DATE: 2001-09-17
PRIOR PAPLICATION NUMBER- 60/152,545
PRIOR FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
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Patent No. 6329151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 IGGEWVAPADGEYYÇNLTPVTGGLLGEVASSGKPDIDLALDAAHKVKDKWAHTSVQDPAA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 IGDQLTPSSTGATFDSINPADGSHLASVAEATAADVARAVEAAKAAARTWQPMRPAQPTP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CMGANISM: Phodocoreus erythropolis HL PM-1
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PPLOF APPLICATION NUMBER: US h0/7054,954
PRIOR FILING DATE: 1997-11-08
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Patent No. 5380370
                                                                                                                                                                                                                                                                                               1999-February-19
MBER: 60/152,542
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                                                                                                                                                                                                                                             60/120,702
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APPLICANT: Lynn Doucette-Stamm et al
                                                                                                                                               Microsoft Office 97
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NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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67 ALDAAHKY--KDKWAHTSVQDRAAILFKIADRMEGNLELLATAFTWDNGKPIRETSAADV 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 -- EIDHCIACFEMAAGAARMIJHGDFFNNIGEGIJFGMVIJREFFGVGIJITPWNFPFMILFE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 KMAPALAAGUCVVLKPARLTPLSVLLLMETVGDL-LPPGVVNVNGAGGVTGFYLATSKR-23H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 IAKVAFTGSTEVGQQ-IMQYATQNIIPVTLÆLAGKSPNIVFADVMDEDAFFDKALÆGFA-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 LEAFINGGEVCTCPSRALVOBSTYERFMERATRRVESTRSGNPLDSVTOMGAQVSHGDLEL 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 ILINYTIDIGKKEGADVLITYORRKILLE) ELKIOTYTLETTILET UNNMKVEQHELFSTVI. 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 SLPLKPREFGF------PIDGEWRAGKD--FFDRSSPAHDVPVTRIPRCTREDLDE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 IDMLSFTGSTCVGKSCTHAAADSNLKKLGLELGGKNPTVVFALSNAK DAVAFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.1%; Score 752; DR 1; Longth 497; 37.1%; Pred. No. 8e 73; ive 80, Mismatches 197; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..497
IDENTIFICATION METHOD: experimentally
                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 18-909-0 PCT TELECOMMUNICATION INFORMATION:
                                                                     APPLICATION NUMBER: JP 241851/1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               475 GGYKOSGIGRETHKMMLEHYDOTK 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gluconobacter oxydans
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; Patent No. 5834263
                                                                                                                                                                 24,518
                        FILING DATE: 08 MAR-1993 PRIOR APPLICATION DATA:
                                                                                         FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     703-413-3000
                                                                                                                                                                                                                                                                                                                                                    497 amino acids
                                                                                                                                       NORMAN F. OBLON
                                                                                                                                                                                                                                                   TELEFAX: 703-413-2220
THLEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: mat peptide LOCATION: 1..497
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                 PEGISTRATION NUMBER:
       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORCANISM:
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US-08-696-834-2
                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN:
                                                                                                                                           NAME:
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APPLICANT: Suzuki, Hiromi
TITLE OF INVENTION: No 5754481el L.sorbose Dehydrogenase and No. 5753481el L.sorb
TITLE OF INVENTION: Dehydrogenase Obtained from Gluconobactet .xyydus 7-100
                                                                                                                                                                                                                              78 WAHTSVODRAAILFKIADRMEQNLELLATAETWDNGKPIRETSAADVPLAIDHFRYFASC 137
                                                                                                                                                                                                                                                                                                                       138 IRAQEGG-----ISEVDSETVAYHFHEPLGVVGQ1IPWNFP1.1.MASWKMAPALAAGNCV 191
                                                                                                                                                                                                                                                                                                                                                 192 VLKPARLIPISVLLLMETVGDL-LPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 GQQIMQYATQNIIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNGGEVCTCP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 WSLETSEVRGKKVRAVADKIKENREELAKLETLDTGKTLEE-SYADMDDIHNVEMYFAG- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 VMKPSEITPLTTIRVFFLMEEVGFPKGTINLVLGAGSEVGDVMSCHEEVDLVSFTGGIET 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 SRALVQESIYERFMERAIRRVESIRSGNPLDSVTQMGAQVSHGQLETILNYIDIGKKEGA 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 TIALGGKRPERE-DLQAGLFFEPTVITDCDTSMRIVQEEVFGPVVTVEGFADEEBAIRLA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 NDTQYGLGAGVWSRNGNLAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKQSGLGRETHKM 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 KLKARYDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDAAHKVKD--K 77
                                                                                                                                                                                16 KLSNR--QYIDGEWVESSNKNTRDIINPYNQETIFTVAEGTKEDVERAILAARRSFENGE 73
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      iSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.: 1755 Jefferson Davis Highway, Suite 400
Arlington
                                             31.6%; Score 845; DB 4, Length 506; 87.8%; Pred. No. 6.3e-83;
                                                              Best Local Similarity 37.8%; Pred. No. 6.3e-83;
Matches 190; Conservative 105; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette, 3.50 inch, 1.44 Mb storage
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FILLING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5753481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Niwa, Mineo
APPLICANT: Saito, Yoshimasa
APPLICANT: Ishii, Yoshinori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MS-DOS Editor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virginia
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US-09-134-001C-4383
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67 ALDAAHKV--KDKWAHTSVQDRAAILFKIADFMEGNLELLATAETWENGKPIPFTSAANV 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 PLAIDH----FRYFASCIRAQESG-ISEVDSETVAYHFHEFLGVVGQIIPWNFFLLMASW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 -- EIDHCIACFEMAAGAARMLHGDTFNNIGEGLEGMVLKEPIGVVGLITPWNFPFMILZE 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                             APPLICANT: Hayashi, Hiromi
TITLE OF INVENTION Method for Producing 2 Keto-Leadenic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
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                                                                                                                                                                                                                       Oblon, Spivak, McClelland, Maier & Neustadt,
                                                                                                                                                                                                                                                                                                                                                                                                  Diskette - 3.50 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                1755 Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DENTIFICATION METHOD: experimentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 28612/1994
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER 18708/696,834
FILING DATE: 24-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glucomobacter oxydans
GENEPAL INFOPMATION:
APPLICANT: Niva, Mineo
APPLICANT: Saito, Yoshimasa
APPLICANT: Ishii, Yoshimori
APPLICANT: Yoshida, Masaru
                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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TELERAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHAPACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              497 amino acids
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Matches 187; Conservative
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1.,497
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                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: No. 586129201 ; serbose Debydrogenase and No. 58612936
TITLE OF INVENTION: L'sorbosone Debydrogenase Obtained from Gluconobacter
TITLE OF INVENTION: oxydans T-100
                                       298 LFAFNQGEVCTCPSPALVQESTYEPFMEPATPPVESTPSGNPLDSVTQMGAQVSHGQLET 357
                                                            358 ILNYIDIGKKEGADVLIGGREKKILEG - ELKEGRYYLEPTILEG-GNUMFVEGEEIFGFU 414
                                                                                                                                        415 AVITEKTMEEALELANITQYGIGAGOWSKNSNIAYKMGKGIQAGKOWINCYHAYPAHAAF 474
                                                                                                                                                                                                                                   400 ASPHFDTVDEAIAIANDTVYGLAASVWSKDIDKALAVTPPVPAGPFWVNTIMSGGPETPL 459
231 IDMESFTSSTGVSKSCIHAAAADSVLYPLGLEFGGFNPTVVFADSNFFDAA--DAVAFG-- 286

    Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
1755 Jefferson Davis Highway, Suite 400

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 241851/1993
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           475 GGYKQSGIGRETHKMMLEHYQQTK 498
                                                                                                                                                                                                                                                                                                  HS/08/942,673
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MS-DOS Editor
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; Sequence 2: AFPLication US/08942673
: Fatent No. 5861.92
: GENERAL INFORMATION:
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PEFFERME / TOWNER INFORMATION:
TELECOMMUNICATION INFORMATION:
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Saito, Yoshimasa
Ishii, Yoshinori
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TELEX: 248855 OPAT UR
INPORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoshida, Masaru
Suzuki, Hıromi
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MOLECULE TYPE: peptide
OPIGINAL SOUPCE:
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MEDIUM TYPE: Diskett
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OPERATING SYSTEM:
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APPLICANT:
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L-sorbosone Dehydrogenase Obtained from Gluconobacter
oxydans T-100
                                                                                                                                                                                                     80; Mismatches 197; Indels 40; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 -ISFNTGQCCVSSSRLIVERSVAEKFERLVVPKMEKIRVGDPFDPETQIGAITTEAQNKT 345
                                                                                                                                                                                                                                                                                                                                                                                       56 AVAAAPPAFENGSWAGLAAADPRAAVII.KAAGILREFRDDIAYWEVLENGKPISQAKG--- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                  125 PLAIDH----FRYFASCIPAQEGG-ISFVDSETVAYHFHEPLGVVGQIIPWNFPLLMASW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 KMAPALAAGUCVVLKPARLTPLSVLLLMEIVGDL-T-PPGVVNVVNGAGGVIGEYLATSKE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 RAPFILASGCTLVVKPAEVTSATTLLLAEILADAGLPKGVFNVVTGTGRTVGQAMTEHQD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 LFAFNQGEVCTCPSRALVQESIYERFMERAIRRVESIRSGNPLDSVTQMGAQVSHGQLET 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 ILNYIDIGKKEGADVLTGGRRKLLEG--ELKDGYYLEPTILFG-ONNMRVFQEEIFGPVL 414
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                                                                                                                                                                                                                                                                                                                                          67 ALDAAHKV--KUKWAHTSVQDRAAILFKIADRMEQNLELLATAETWDNGKPIRETSAADV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 IAKVAFTGSTEVGQQ-IMQYATQNIIPVTLELGGKSPNIVFALVMDEEDAFFDKALEGFA 297
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                                                                                                                                                                                                                                                  7 SAQIKPGEYGFPLKLKARYDNPIGGEWVAPANGEYYQNIJFPVTGQLIJJFVASSGKRDIDI. 66
                                                                                                                                                                                                                                                                                             8 SLPLKPREFGF------FIDGEWRAGKD--FFDRSSPAHDVPVTKIPRCTREDLDE 55
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STREET: 1755 Jefferson Davis Highway, Suite 400
CITY: Arlington
                                                                                                                                                          28.1%; Score 752; DB 2; Length 497; 37.1%; Pred. No. 8e-73;
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                                        NAME/KEY: mat peptide
LOCATION: 1..497
IDENTIFICATION METHOD: experimentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 GGYKQSGIGRETHKMMLEHYQQTK 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 GGFKOSGWGREAGLYGVEEYTOIK 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09118317
Patent No. 6197562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Niwa, Mineo
APPLICANT: Saito, Yoshimasa
APPLICANT: Ishii, Yoshinori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yoshida, Masaru
APPLICANT: Suzuki, Hiromi
                                                                                                                                                          Query Match 28.1%
Hest Local Similarity 37.1%
Matches 187; Conservative
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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STRAIN: T-100
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239. TAKVAPTGSTEVGQO-IMQYATGNI IPVTLELÄÄKSPNI VFADVMDEEDAPEDKALEGFA. 297.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 KMAPAGAAGNCVVLKPARDTITLSVILLMETVGDL TJITGVVNVVRGAGGVIGFYLATEKRE 238
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IDENTIFICATION METHOD: experimentally
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FILING FATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
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                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/118, 317
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: UK 9404700.9 FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Gluconobacter oxydans
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|8 | SLPLKPREFGF
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SOFTWARE: MS-DOS Editor
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Matches 187; Conservative
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                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                         FILING DATE:
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APPLICANT: Type Pougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES PELATING TO STAPHYLOGOCC
TITLE OF INVENTION: EPIDERMIDIS POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EFIDERMILIS FOR LIAGNOSTICS AND THEKAPEUTICS FILE REFERENCE: GTC-007
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Matches 145, Conservative 103; Mismatches 204,
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29.4%; Pred. No. le-56;
                                                                              CURRENT APPLICATION NUMBER: US/09/134,001C
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                                                                                                                                PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR PILLING TATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779
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PRIOR APPLICATION NUMBER: US 60/064,964
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                              ORGANISM: Staphylococcus epidermidis
                                                                                                    1998-08-13
                                                                                                                                                                                                           1997-08-14
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SEQ ID NO 4388
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1994-08-13
PRIOP APPLICATION NUMBER: US 50,064,964
PRIOP FILING DATE: 1997-11 08
PRICE APPLICATION NUMBER: US 60/055,779
PRICE FILING DATE: 1997:08:14
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Patent No. 6380370
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Patent No. 6380370
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ORGANISM: Staphylococcus epidermidis
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                                                                                                                                                                                                                     20 KLKARYDN----FIGGEWVAPADGEYYONLTPV-TGQLI,CEVASSGKRDIDI,AI,DAAHKV 74
                                                                                                                                                                                                                                                                32 KVKAQLGQDIPLVINGEKLTKTD--TFNSVNPANTSQLIAKVSKATQDDIEKAFESANHA 89
                                                                                                                                                                                Gaps
                                                                                                                                                                             35;
                                                                                                                                 Length 518;
                                                                                                                                                                           83; Mismatches 202; Indels
                                                                                                                              22.2%; Score 593.5; DB 4,
34.0%; Pred. No. 1.5e-55;
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EARLIER APPLICATION NUMBER: GB96/06187
                                                             ORGANISM: Staphylococcus epidermidis
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NUMBER OF SEQ ID NOS: 14
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APPLICANT: Rhodes, Michael J.C.
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                                                                                                                                                      Best Local Similarity 34.08
Matches 165; Conservative
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                                                                                  US-09-134-001C-4451
SEQ ID NO 4451
                LENGTH: 518
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                                          TYPE: PRT
                                                                                                                              Query Match
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21.8%; Score 583; DB 4; Length 482;

Query Match

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DVPLA1DHFRYFASCTRAUF 14.2
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                                                                                                                                                                                                                                                                                                                                                                143 - GGTSEVDESSETVAMPHEHEPEGOVGGTTPWNEPELMASWMANEALAAGNCOVT KRANTERL - 201
                                                                                                                                                                                                                                                                                                                                                                                               202 SVLILMETVGOL-LIPAVVNVNGA --- GOVTGEYLATSEKTARVAFTGSTEVOQCTMQY - 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 ATONITEVILELEGISKSPNIVEALVMIGERAFERALIGGEALFA ENGGEVOLOPSKALVO (16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.0. SARHLKPALLELIGGKAPLLVL-----DDADLEAAVQAAAFGAYFNGGQTCMSTERLLVD 29.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 ESTYERFMERAIRRVESTRSONPLDSVTOMGAQVSHGQLETTLNYTDTGKKEGADVLTGG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 PRELLEGELKRIZPTEPT LEGON - NMKVEGELFGEVLAV LEKIMERALELANDLOYG - 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 O---LEGSI-----LQPTLLIXQVDASMKLYREESFGPVAVVLKGFGFEALLGLANDSEFG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 LGAGVWSRNGNLAYKMGRGIQAGRVWTNCYHAYP-----AHAAFGGYRQSGTGRETHKMM 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 DAAHKV--KDKWAHTSVQDRAATLFKTADRMEONLELLATAETWDNGKFTRETSAADVFL 126
                                                                                                29 TGGEWVAPADGEYYONLI PVTGQLLJTEVASSGKRDTDLALDAAHKVRDKWAHTSVQDRAA 188
                                                                                                                                                                  8 IGGQSCPARDGRTFERRNPVTGELVSRVAAATLEDADAAVAAAQQAFPAWAALAPNERRS 6.7
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                                      97; Mismatches 189; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82; Mismatches 206; Indels 51; Caps
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Best Local Similarity 33.5%; Pred, No. 5.80-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 ILFKIADRMEQNLELLATAETWONGKPIRETSAA···
32.4%; Pred. No. 1.9e-54;
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CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ 1D NOS: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09351224E
Patent No. 6388171
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                                      158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 171; Conservative
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APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 IEHFTOLR 469
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Best Local Similarity
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                                      Matches
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55 AASVQAVKKGPWKKFTGAQRAACMLKFADLAFKNAEKLARLESI,PTGRPVSMITHFDIPN 114	AIDHFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIFWNFPLLMASWKMAPALA 186	MYSVERYYAGWADKIAGKTFPEDNGKPNWRY EPMGVCAGIASWNATFLYVGWKIAPALA 173	KPARLTPLSVLLLMEIVGDL-LPPGVVNVVNGAGGVIGEYLATSKRIAKVAFT 245	AGOSFIFKASEKSPLGVLGLAPLFAEAGFPPGVVQFLTGA-PVTGEALASHMDIAKISFT 232	ŒIMQYAIŒNIIPVILEIGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQ 303	RSVGGGRAVKQ-ATLKSNMKRVTLELGEK-PTIVFNEAPLERGSGESAKDFSKF 284	304 GEVOTOPSPALVQ-ESIYEPFMEPAIPRVESIPSGNPLDSVTQMGAQVS 351	GQTWVPPSCLLVQMSNLAEKFHGVPHGSFR3GTQFWLGQFWFFFFFFFFFFFFF 336	LNYIDIGKKEGADVLTGGRKKLLEGELKDGYYLEPTILFG-QNNMRVFQEEIF 410	KSQYDRVIGNIDVG-KDIAQLLIGVGKKGDRGFAIEFIIFVNPKFGSKIWFEEIF 390	TEKTMEBALELANDTQYGLGAGVWSRNGNLAYKMGRGIQAGRVWTNCYHAYPA 470	GPVLSIKTFKTEEEAIEIANDTTYGLASVIYTKSLNRCLRVSSALETGGVSINFPFIPET 450	KOSGIGRETHKMMLEHYQQTKCL 500	
AASVQAVKKGPWK	AIDHFRYFASCIR	MVSVFRYYAGWAD	AGNCVVLKPARLT	AGOSFIFKASEKS	GSTEVĢĢĢĢIMĢYĀ	RSVGGGRAVKQ-A	GEVOTOPSPALVQ	GQIWVPPSCLLVQ	HGOLETILNYIDI	KSQYDRVLGNIDV	GPVLAVITEKTME	GPVLSIKTFKTEE	HAAFGGYKQSGIG	TPFGGMKŲSGSG
52	127	115	187	174	246	233	304	285	352	337	411	391	471	451
qq	Qy	qq	Οy	qq	Οy	qq	Qy	pp	Qy	QQ	Qy	qa	Qy	qa

Search completed: June 24, 2003, 10:31:44 Job time: 16.1793 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compagen 1.1d.
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OM protein - protein search, using sw model

June 24, 2003, 10 17.21, Search time 24 7492 Seconds (without alignments) 2238.528 Million cell updates/sec Run on

US-09-830-751-8 Perfect score:

HYDOTKOLLVSYSPKPLGUF 512 1 MTNNPPSAQIKPGEYGFPLK.. Sequence:

Gapop 10 0 , Gapext 0 5 BLOSUM62 Scoring table:

417779 seqs, 108206813 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing. Minimum Match 0%

Published\_Applications\_AA:\* Database :

1: /cgn2\_6/ptodata/2/pubpaa/USO8\_NEW\_FUB.pcp:\*
2: /cgn2\_6/ptodata/2/pubpaa/TCO\_NEW\_FUB.pcp.\*
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10: /cgn2\_6/ptodata/2/pubpaa/USO9\_NEW\_FUB.pcp.\*

/cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*/cgn2\_6/ptodata/2/pubpaa/US10\_FUBCOMB.pep:\* /rgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUR\_prp.\* /cgn2\_6/ptodata/2/pubpaa/US60\_PURCOMR\_p-p.\* 10:

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	\$ Query Match	% Query Match Length	DB	ΠD	Description
-	1714 5		303	10		
-	C . + T / T		000	٠,	7/20.070.00/ 60.00	seducince estrict Ap
C‡	1186.5	44.4	496	0.1	HS-04-815-242-10550	Sequence 10550, A
3	1090.5	<b>4</b> ∩ α	50R	-1	US-08-781-986A-5241	Sequence 5241, Ap
4	946.5	35.4	492	6	US-10-268-518-4	Sequence 4, Appli
<b>ن</b> .	986	35.0	493	ı,	US-10-175-696-21	Sequence 21, April
Ą	926	ر ج	493	10	US-09-823-901-9	
7	919	34.4	501	σ	US-09-344-882-22	Sequence 22, Appl
30	919	34 4	501	Ġ.	48-10-293-865-22	
σ.	918	34.3	538	σ	US-09 344-882-20	
01	915	34 3	7.38	σ	IIS-10-203-865-20	Sequence 20, Appl
11	908	33.9	512	9	75-A9-9£1 403-12	12,
12	905	ታ ታ	512	σ,	15-10-268-518-2	A.
13	905	ત્રસ વ	115	σ	US 10 205-823-14	7
14	892 5	33 4	534	6	US-09-344-882-24	24
15	892 F	33.4	534	œ.	HS-10-293-865-24	7
16	873	32.7	406	10	HS-09-815-242-5644	26.
17	873	32.7	496	10	US-09 815-242-12657	Sequence 12657, A
18	87U	12 F	4 9 5	σ,	US-09-847-208-11	Sequence 11, Appl
19	844.5	31.6	518	'n	08-09-919-039-143	

72 BEVEREKWAHTSVQDRAATLFKIADEMEGNLELLATAETWDNGKPIRETSAADVPLAIDHF 131 

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Sequence 12102, A Sequence 17, Appl Sequence 5, Appl Sequence 4, Appl Sequence 4, Appl Sequence 10057, A Sequence 1235, Ap Sequence 10264, A Sequence 1735, App Sequence 1148, Ap Sequence 1348, Ap Sequence 3, Appli Sequence 3, Appli Sequence 4, Appli	Sequence 12, Appli Sequence 12, Appl Sequence 28, Appl Sequence 6482, Ap Sequence 4837, Ap Sequence 2, Appli Sequence 2, Appli
10 08-09-815-242-12102 9 US-1U-1/5-696-17 10 US-09-813-901-5 9 US-1U-1/5-696-17 10 US-09-815-242-13057 10 US-09-815-242-13459 10 US-09-815-242-13459 10 US-09-915-242-13459 10 US-09-915-242-14047 10 US-09-915-242-14047 10 US-09-925-302-736-16-16-16-16-16-16-16-16-16-16-16-16-16	9 IIS-04-8R2-644-5 9 US 10-272-419 L2 1 US-09-7-8-5-6-5482 9 US-09-7-8-5-6-5-482 9 US-09-7-8-5-6-4037 9 US-09-7-8-8-8-99 10 US-09-816-7-60-2
4 4 4 4 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4884 498 521 4533 802 802
	21 6 21 5 21 5 20 1 18 5 17 8 17 8
88 88 8	5778 5 5778 5 574.5 538.5 444.5 474.5
G 4 G 4 G 4 C 4 C 4 C 4 C 4 C 4 C 4 C 4	8 6 4 4 4 4 4 4 9 8 9 9 9 9 9 9 9 9 9 9 9 9

### ALIGNMENTS

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12 PREYGFFIKLKARYONFIGGEWVAFADGEYYUNLIFVIGGLLGEVASSGKEDIDLALDAA 71
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Best Local Similarity 62.5%, Fred. No. 7.1e-152,
Matches 313, Conservative 82, Mismatches 105,
                                                                                                                                                                                                                                                                                                                                            APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
ITILE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/737484
PRIOR PILING DATE: 2000-12-18
PRIOR PELLING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-16
PRIOR PLILING DATE: 2000-04-07
FRICH APPLICATION NUMBER: JF 00/159162
PRIOR PLILING DATE: 2000-04-07
FRICH APPLICATION NUMBER: JF 00/159162
PRIOR PLILING DATE: 2000-04-07
FRICH APPLICATION NUMBER: JF 00/159162
NUMBER: OF SEQ ID NOS: 7059
SOFTWARE: PALENTING NOS: 7059
                                    Sequence (572) Application US/397348655
Publication No. US20020197695A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM. Corynebacterium glutamicum
                                                                                                                                                   MIZOGUCHI, HIROSHI
                                                                                                              APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSH
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                        APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YÖKÖL, HAKUHIKO
APPLICANT: TATEISHI, NACKO
APPLICANT: SENOH, AKIHIRO
                                                             Fublication No. 3820(GENERAL INFORMATION:
US-09-738 626-6572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-03 738-015-0574
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252 QQIMQYATQNIIIVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVCTCPS 311
                                                                                                                                                                                                                                                                  372 VLTGGRRKLLEGELKDGYYLEPTILFGQNNMRVFQEETFGPVLAVTTFKTMEEALELAND 431
                                                                                                                                                                                                                                                                                                                                                                                                                                              132 RYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGNCV 191
                                                                                                                                                      192 VLKPARLTPLSVLLLMFIVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVG 251
                                                                                                                                                                                                                                                                                                                                  312 RALVQESTYERFMERATRRVESTRSGNPLOSVTQMGAQVSHGQLETTLNYTFTGKKEGAL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 TQYGLGAGVWSRNGNLAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKQSGIGRETHKMML 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10550
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PPICK FILING DATE: 2000-05-23
PPICK APPLICATION NUMBER: 60/20/, 27
PRIOR ELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR APPLICATION NUMBER: 60/257
PRIOR APPLICATION NUMBER: 60/257
PRIOR APPLICATION NUMBER: 60/257
PRIOR APPLICATION NUMBER: 60/257
PRIOR APPLICATION NUMBER: 60/269, 308
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Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492 EHYQQTKCLLVSYSDKPLGLF 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486 NHYQQTKNLLVSYDPNPTGLF 506
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; ORGANISM: Enterococcus faecalis
US-09-815-242-10550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, H. Howard
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US-09-815-242-10550
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44.4%; Score 1186.5; DB 10; Length 496;

Query Match

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85 DRAATLEKTADRMEGNLELLATAETWONGKPTRETSAADVPLATDHERYFASCTRAJEGG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 VEALKEKFEQVINGFPWEKDVEMGAQINEHOLEETLKYVETGVKEGATLITGGGR 13EN 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 ELKDGYYLEPTILF-GONNMKVFQEEIFGPVLAVTTFKTMEEALELANDTOYGLGAGVWS 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 GLDKGAFLAPTLLANGTNTMCVAQFF1FGPVATV1KFETFEEV1RLANDSEYGLGGAVES 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          443 RNGNLAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKOSGIGRETHKMMLEHYQQTKCLLV 50.2
                                                                  25 YDNFIGGEWVADARGFYYÖNI TPVTGÖLL CPVASSGKRUTULALDAAHKVKDKWAHTSVO 84
                                                                                                               14 YQLYINGEWTTGSGNKMIASYNPSNGEKLAEFVDATNADVDRAVEAAQEAFQTWKDVDVV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5255
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE. Diskette, 3.50 inch, 1.4Mb storaqe COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
Best Local Similarity 48.68; Pred. No. 1.90-102;
Matches 238; Conservative 79; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Gerome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER, US/08/781,986A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/BOCKET NUMBER: PH248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE, Human Genome Scien
STREET: 9410 Key West Avenue
Cllt: Kockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 30,446
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 ATLELGGKSAN: IF
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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320 VPRLGEAFSNIKVGNPQDEATQMGSGTGKDQLDKIQSYIDDAAKESDAQILAGGHR-LTEN 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 ISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGNCVVLKPARLTFLSVL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 LLMEIVGDLIPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVGGIMQYATQNTIP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 EVAKIFQEVLPKGVVNILTGKGSESGNAIFNHDGVDKLSFTGSTDVGYQVAEAAAKHLVP 265
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                                                                                                                                                                                                                                                                                                                                                              26 YGLFINGFFVKGSSDETIFVTNPATGETLSHITRAKDKDVDHAVKVAQEAFESWSLTSKS 85
                                                                                                                                                                                                                                                                                                                   25 YDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDAAHKVKDKWAHTSVQ
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                             DB 1; Length 508;
                                                                                                                                                                                                                        Query Match 40.8%, Score 1090.5; DB 1; Length Best Local Similarity 43.5%; Pred No. 1 G_{\rm e}-93; Matches 213; Conservative 101; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Huntel, John Joseph TITLE OF INVENTION: 9136, A HIMAN ALDENYDE DEHYDPOGENASE TITLE OF INVENTION: FAMILY MEMBER AND USES THEREFOR FILE REFERENCE: MP101-234PIRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4 0
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CURRENT FILING DATE: 2002-10-10
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, Sequence 4, Application US/10268518
; Publication No US20030100034A1
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                                                                   508 amino acids
TELEFAX: (301) 309-8512 INFORMATION FOR SEQ IN NO: 5
                                        SEQUENCE CHARACTERISTICS.
                                                                                                                single
                                                                                                                                                         ; MOLECULE TYPE: protein US-08-781-986A-5241
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                                                                                                              STRANDEDNESS:
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LENGTH: 492
                                                                   LENGTH
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                                                                                                                                                                                                                                                                       201 LSVLLLMEIVGDL----LPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVGÖÖLMÖ 256
                                                                                                                                                                                                                                                                                                                                                                                                                     257 -YAFONIIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAF-NOGEVCTCPSKAL 314
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                                                                                 32 EWVAPARGRYYQNLTPVT-GQLLCFVASSGKRDTDLALDA---AHKVKDKWAHTSVQDRA 87
                                                                                                                                                                                                                                                   144 --- GISEVDSETVAYHFHEPLGVVGQIIPWNFPLUMASWKMAPALAAGNCVVLKPAPLTP
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                                                                                                                                                                                                         51 PILPKLANLIEEREDELAALETUSLGKPLAEAKSDTEVGRAIDETRYYAGWAPKLMGEPP
                                            Gaps
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APPLICANT: RUGOLph-Owen, Laura A.
TITLE OF INVENTION- NOVEL HUMAN ENZYME FAMILY MEMHERS AND USES THEREOF
FILE REFERENTE: 10448-1970,01
                                       33;
35.4%; Score 946.5; DB 9; Length 492;
45.3%; Pred No 550-80;
                                          79; Mismatches 160; Indels
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PRIOF FILING DATE: 2001-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICE FITING NATE: 2001-06-15
PRICE APPLICATION NUMBER: PCT/US01/19319
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2000-03-31
NIMPER
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PRIOR APPLICATION NUMBER: 09/823,901
PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-03-31
APPLICATION NUMBER: 09/862,658
FILING DATE: 2001-05-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Sequence 21, Application US/1017696
| Publication No. US20030092658A1
| GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488 -- KMMLEHYQQTKCLLV 502
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                   45.38;
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                 al Similarity 45,38
225; Conservative
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Query Match
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88 ALLFKIADRMEGNLELLATAETWDNGKPIRETSA-ADVPLAIDHFKYFASCIKAQEG--- 143
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                                                                                                                                                                                                                                                                                                               Ouery Match 35.0%; Score 936; DB 9; Length 493; Best Local Similarity 45.2%; Pred No 5.34-79; Matches 225; Conservative 79, Mismatches 160; Indels 34;
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                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                        ; OTHER INFORMATION: consensus sequence US-10-175-696-21
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/211,727
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Patent No. US20020001807A1
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                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                             PRIOR FILING DATE: 2000-06-15
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APPLICANT: Meyers, Rachel
                                                                      NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                LENGTH: 493
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                                                                                                                      SEQ ID NO 21
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AFFLICANT: Lutziger, Isabelle
APPLICANT: Web, Table June
TITLE CE INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Acetyl CoA Levels in Plants
                                                                                                                                                                                                                                                                                        144 ---GISEVDSFTVAYHFHEPLGVVGOTTPWNFPLLMASWKMAPALAAGNCVVLKPARLTP 200
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                                                                                  35.0%; Score 946; DR 10; Length 494;
45.2%; Pred. No. 5.4e-79;
                                                                                                                           79; Mismatches 160; Indels
                                                                                                                                                                        32 EWVAPADGEYYQNLIPVI - GQLDCEVASSOKEDIDLALDA
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PRIOF APPLICATION NUMBER: US (0,0040,717
               , OTHER INFORMATION, consensus sequence US 09-823-901-9
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Patent No. US20020162137A1
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Schnable, Patrick S
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Matches 225; Conservative 7
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Allred, Carolyn C
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Wurtele, Eve S
Oliver, David J
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FEATURE
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TYPE: PRT

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83 RAKLINKFADLIEENIEELAKLDAVDGGKIPQIGKYADIPATAGHFRYNA-----GAA 135
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                                                                                                                                                                 28 FIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDAAHKVKD--KWAHTSVQD 85
                                                                                                                                                                                                               23 FINGQFIDAASGKIFETIDPRNGEVIATIAEGDKEDVDLAVNAAKYAFUHGFWFKMTGFE 82
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PEPLICANT: Wen, TSUL-Jung
TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Acetyl CoA Levels in Plants
                                                                                                                     36; Gaps
                                                                     34.4%; Score 919; DB 9; Length 501; 39.4%; Pred. No. 2.1e.77;
                                                                                         Best Local Similarity 39.4%; Pred. No. 2.1c·77;
Matches 196; Conservative 100; Mismatches 165; Indels
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CURPENT APPLICATION NUMBER- US/10/243,845
CURRENT FILING DATE: 2002-11-13
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PRIOR PILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/090,717
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APPLICANT: Ke, Jinshan
APPLICANT: APPLICANT: Johnson, Jerry L
APPLICANT: Allred, Carolyn C
''''I'ANT: Fatland, Beth
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Schnable, Patrick S
ORGANISM: Arabidopsis Thaliana
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NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 3.1
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APPLICANT: Wurtele, Eve S
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Oliver, David J
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; ORGANISM: ALC
US-09-344-882-22
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LENGTH: 501
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TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Acetyl CoA Levels in Plants
FILE REFERENCE: 201574
CUBRENT APPLICATION NUMBER. US/201/344,882
CUBRENT FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                    86 KAALLEKIALIKMENI ELLATAETWINIKPI PETSAAI VELATIHERYEASI IRAQEGGI 145
                                                                                                                                                                                                                                                                                                             146 SEVDSETV-----AYHFHEPLGVVGQ11PWNFPLLMASWKMAPALAAGNCVVLKPAR 197
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                                                                                                                                             28 FIGGEWVAPADGEYYQNLTPVTGQLLGEVASSGKPDIDLALDAAHKVKD--KWAHTSVQD 85
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                                                                                                   Indels 36;
                                                         Ouery Match 34.4%; Score 313, 5B 9, Length 501; Best Local Similarity 39.4%; Pred. No. 2.1e-77; Matches 196; Conservative 100; Mismatches 165; Indels
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ER- US 60/090,717
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Patent No US:00:2016:137A1
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Oliver, David J
Behal, Robert
Schnable, Patrick S
Ke, Jinshan
Johnson, Jerry L
Allred, Carolyn C
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Lutziger, Isabelle
Wen, Tsui-Jung
ORGANISM: Arabidopsis Thaliana
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                   US-10-293-865-22
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ORGANISM: Arabidopsis Thalland

US-10-293-865-20

TYPE: PMT

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62 INGNPVDSASGKTFPTLDPPTGEVIAHVAEGDAEDINRAVKAARTAFDEGPWPKMSAYER 121
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APPLICANT: Wen, Tsui-Jung
TITLE OF INVENTION: Materials and Methods for the Alteration of Engyme and
                                                                                                                                  Gaps
                                                                         44.3%; Score 918; DB 9; Length 538; 41.1%; Pred. No. 2.9e-77; tive 90; Mismatches 170, Indels
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PRIOR APPLICATION NUMBER: US 09/344,882
PRIOR FILING DATE: 1999-06-25
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APPLICANT: Oliver, David J
APPLICANT: Behal, Robert
APPLICANT: Schable, Patrick S
APPLICANT: Ke, Jinshan

// ORGANISM: Arabidopsis Thaliana
US-09-344-882-20
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GENERAL INFORMATION:
APPLICANT: Nikolau, Basil J
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APPLICANT: Allred, Carolyn C
APPLICANT: Fatland, Beth
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NUMBER OF SEQ ID NOS: 38
                                                                                                 Local Similarity 41.1%
nes 202; Conservative
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LENGTH: 538
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                                                                                                                                                      87 AATLEKTADRMEÖNLELLATAETWONGKPIRETSAADVPLATDHERYFASCIIKAQEGGIS 146
                                                                                                                                                                                              122 SRVLLRFADLVEKHSEELASLETWONGKPYQQSLTAETPMFARLFRYYAGWADKTHOLFT 181
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TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
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34.3%; Score 918; DB 9; Langth 538;
41.1%; Pred, No. 2.9c 77;
tive 90; Mismatches 170; Indels
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SOFTWARE
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; GENERAL INFORMATION:
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WINTERHAGER, ELKE
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                    Best Local Similarity 41.19
Matches 202; Conservative
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                                                                                                     61 KRDIDLALDAAHKVKDK---WAHTSVQDRAAILFKIADRMEGNLELLATAETWDNGKPIR 117
                                                                                                                                                                                                      118 ETSAADVPLAIDHFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMA 177
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3 NNPPSAQIKPGEYGFPLK-LKARYDN-FIGGEWVAPADGEYYQNLTPVTGQLLCEVASSG 60
                                                  10 NGQPDG--KPPALPRPIRNLEVKFTKIFINNEWHESKSGKKFATCNPSTREQICEVEEGD 67
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TILLE OF INVENTION: 9136, A HUMAN ALGEHYDE DEHYDEGGENASE
TITLE OF INVENTION: FAMILY MEMBER AND ISES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 AFGGYKQSGIGRETHKMMLEHYQQTKCLLVSYSDK 507
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CORPENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/329,809
PRIOR FILING DATE: 2001-10-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10268518 Publication No. US20030100034A1 GENERAL INFORMATION:
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Matches 201; Conservative
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OPGANISM: Homo sapien
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APPLICANT: Gannavarapu, Manujuata APPLICANT: Gannavarapu, Manujuata APPLICANT: Gorbatcheva, Bella APPLICANT: Gorbatcheva, Bella APPLICANT: Gorbat Sebastian APPLICANT: Hamatkar, Shubhangi APPLICANT: Wonscy, Angela M. APPLICANT: Glatt, Karen APPLICANT: Glatt, Karen APPLICANT: Anderson, Dustin APPLICANT: Anderson, Dustin APPLICANT: APPLICANT: APPLICANT: APPLICANT: THE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
                                                                                                                                       296 FALFAFNGGEVCTCPSPALVQESIYERFMEPAIPPVESIPSGNPLDSVTQMGAQVSHGQL 355
                                                                                                                                                                                                                                                                     306 ---VEFNWGQCCTAASRVEVEERVYSEEVRESVEYAKKRPVGDFDVKTEWGPQTDQKQF 362
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                                               188 VWKLAPALCCGNTMVLKPAEQTPLTALYLGSLIKEAGFPPGVVNIVPGFGPTVGAAISSH 247

    NNPPSAQTKPHEYGFPLK-LKAPYINN-FTGGEWVAPAFHTYYQNLTPVTGQLLATBVASSG-KG

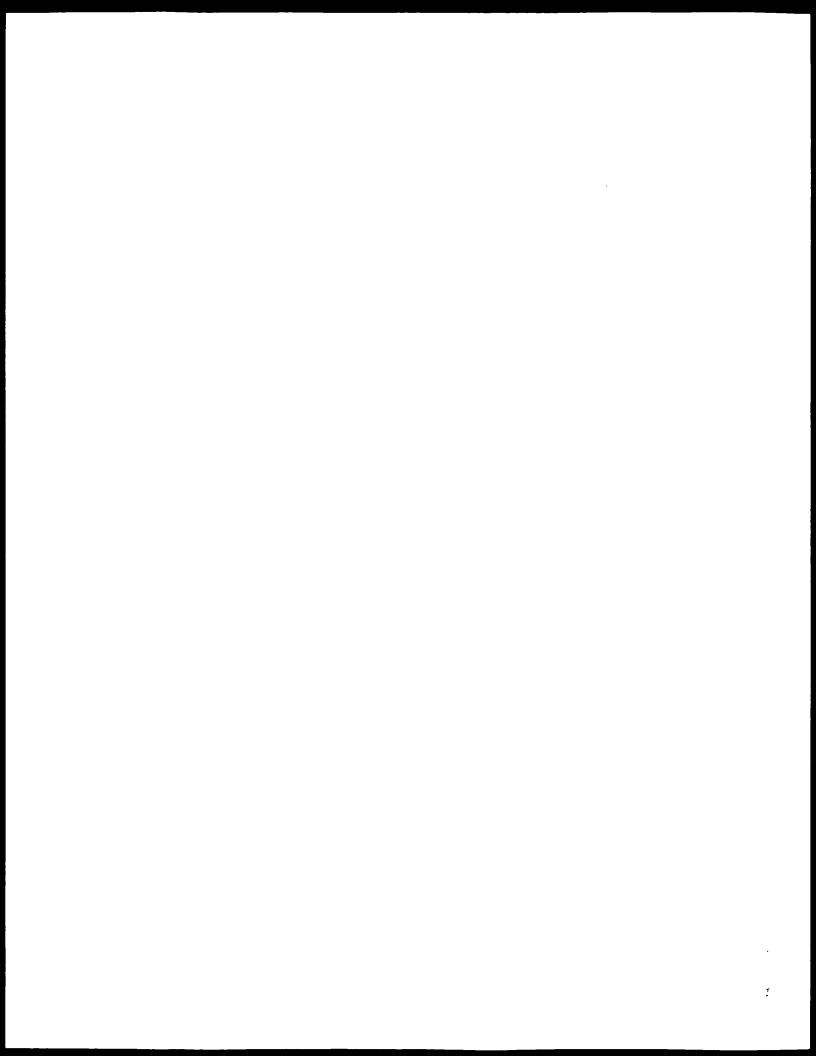
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                                                                                                        237 KPIAKVAFTGSTEVGQQIMQYATQ-NIIPVTLELGGKSPNIVFADVMDEEDAFFDKALEG
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PPTOR PTILING DATE: 2001-088-22
PETOR FILING DATE: 2001-08-25
PRIOR PTILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60,741,746
PRIOR FILING DATE: 2001-12-11
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PRIOR APPLICATION NUMBER: 60/307,982
FRIOR FILING DATE: 2001-07-25
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; Publication No. US20030108963A1
; GENERAL INFORMATION:
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LENGTH: 512
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61 KRUIDLALDAAHKVKDK---WAHTSVQDRAAILFKIADRMEGNI.ELLATAETWDNGKPIR 117
                          68 KPDVDKAVEAAQVAFQRGSPWRKLDALSRCRLLRQLADIJVERDKATLAALETMDTGKPFL 127
                                                                        .18 ETSAADVPLAIDHFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMA 177
                                                                                                 178 SWKMAPALAAGNCVVLKPARLTPLSVLLLMETVGDL-LPPGVVNVVNGAGGVIGEYLATS 236
                                                                                                                                                                                  188 VWKLAPALCCGNTMVLKPAEQTPLTALYLGSLIKEAGFPPGVVNIVPGFGPTVGAAISSH 247
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                                                                                                                                                                                                                                                 248 PQINKIAFTGSTEVGKLVKBAASRSNLKRVTLELGGKNPCIVCADA--DLDLAVECAHQG 305
                                                                                                                                                                                                                                                                                           296 FALFAFNQGEVCTCPSRALVQESIYERFMERAIRPVESIRSGNPLDSVTQMGAQVSHGQL 355
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                                                                                                                                                                                                                                                                                                                                                                                             363 DKILELIESGKKEGAKLECGG-----SAMEDKGLFIKPTV-FSEVTDNMRIAKEEIFGP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                       413 VLAVTTEKTMEEALELANDTQYGLGAGVWSRNGNLAYKMGRGIQAGRVWTNCYHAYPAHA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and TITLE OF INVENTION: Acetyl CoA Levels in Plants
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40.7%; Pred. No. 7.1e-75;
tive 86; Mismatches 181; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 AFGGYKQSGIGRETHKMMLEHYQQTKCLLVSYSDK 507
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IMER: US 60/090,717
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Patent No. US20020162137A1
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Oliver, David J
Behal, Robert
Schnable, Patrick S
Re, Jinshan
Johnson, Jerry L
Allred, Carolyn C
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Wen, Tsui-Jung
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NUMBER OF SEQ ID NOS:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-344-882-24
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LENGTH: 534
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                                147 EVOSETVAYHFHEPLGVVGQTTPWNFPLLMASWKMAPALAAGN°VVLKPARLTPLSVLLL. 205
                                                                                                                                                       207 METVGDL-LPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVGOCIMOYATO NITP 264
                                                                                                                                                                                                                                                                                                       238 GKLIHEAGLIPEGVVNIVSGFGATAGAALASHMEVEKVAPTGSTEVGKITLELASKSINIKA 297
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TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Accept to a Levels in Plants
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PRIOR APPLICATION NUMBER: US 09/344,882
PRIOR FLING DATE: 1999 06-25
PRIOR APPLICATION NUMBER: US 60/090,717
PRIOR FILING DATE: 1998_06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/10294865
Publication no. US/20040106090A1
GENERAL INFORMATION:
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Oliver, David J
Behal, Robert
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SOFTWARE: Patentin Ver. 3.1
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US-10-293-865-24
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AAILEKIADERREGNI ELLATAETWON:KPIPETSAAUVPLAIDHERYEASCIRAGEGGIS 146 :	EVDSETVAYHFHEPLGVVGQITPWNFPLLMASWKMAPALAAGNCVVLKPARLTPLSVLLL 206 	MEIVGDL-LPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVGQQIMQYATQ-NIIP 264 	VTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVCTCPSRALVQESIYFR 322 	FWERALPPVESIPSGNPLDSVTQMGAQVSHGQLETILNYIDIGKKFGADVITGGRPKLLE 382  - - - - - - - - - - - - - - - - - - -	383 GELKDGYYLEPTILFG-ONNMRVFQEEIFGPVLAVTTFKTMEEALELANDTQYGLGAGVW 441	SENGNLAYKMSEGIQAGEVWINCYHAYPAHAAFGGYKQSGIGRETHKMMLEHYQQTKCLL 501 	502 VS 503 526 TS 527
87 A	147 E	207 N	265 v         298 v	323 F	383 6	442 S 466 T	502 V 526 T
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Search completed. June 24, 2003, 10:37:07 Job time: 25.7492 secs



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GenCore version 5.1 6
Copyright (c) 1993 - 2003 compagen Ltd
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OM protein - protein search, using sw model

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US-09-830-751-8

HYQQTKCLLVSYSDKPLGLF 512 1 MTNNPPSAQIKPGEYGPPLK Perfect scure: Sequence.

BLOSUM62 Scoring table:

4569144 seqs, 644733110 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Maximum DB seq length: 2000000000 Minimum DR seq length: 0

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 08

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## SUMMARIES

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		_		8581,	9101,	2360	2769	3375	17072, Å
		Description		Sequence	Sequence	Sequence	Sequences	Sequence	Sequence
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1545	,		Sequence 8001, Ap	12218,	Sequence 4614, Ap	13/1,	11572,	31772,	1/140,		31013,	4508,	Sequence 7105, Ap		17869,	31773,	92377,	23469,	20615,	6997,	21741,		4948,		Sequence 10758, A			Sequence 14000, A			Sequence 10148, A	218,	Sequence 170, App	Sequence 6572, Ap	74075	23, App	3547,	55849. A
-60-360-039-1	/ R T	60-360-039-	- 09-791-537-	-60-360-036-	4-680-038-09-	-60-360-039-	**************************************	-09-791-537-317	-nu-360-039-1714	144-142	-741-547-310	4-60-360-044-4	-698-69-	-10-015-127-1	-60-360-038-17	-09-791-537-5177	-09-791-537-9237	-60-360-03	.60-360-03	-03-328-35	-60-360-03	09-791-53	-09-791-53	-09-252-99	09-791-537	60-03	09-791-537	÷ 4	-537	-74]-547-4890	489-033A	505 740 ·	-09-603-124B-27	÷	-537-740	3-5-6-	43.7	01-0863]-558
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## ALIGNMENTS

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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
FILE OF INVENTION: METHODS OF USE THEREOF
FILE PERFERENCE: 261/210
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44 KM; Pred No i 5e-255;
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                                                                                                                                                                                                           CUPPENT APPLICATION NUMBER: US/09/791,537 CUPPENT FILING DATE: 2001-02 22
                                        : Sequence 8581, Application US/09791537
: GENERAL INFORMATION:
                                                                                                                                                                                                                             CUPRENT FILING DATE: 2003-02 22 NUMBER OF SEQ ID NOS: 153055 SOFTWARE: Patentin version 3.0
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APPLICANT: HINKE, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: SLATER SSION OF MICROBIAL PROTEINS IN FLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
FULE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NORES: US/60/360,039
CURRENT FILING DATE: 2022-02-21
NUMBER OF SEQ ID NOS: 47374
                                     27. KVAPTGSTEVIGIGI MEYATENTI PVTT BIJ CIK SPNITE ADVMDE DA PFDKALD GEALFA - 330
                                                                                                                                341. YIDIGKKEGADVLTGGPRILLEGFLKIKIYYI PPTILEOQNNMPVEQEFI FODVI AVTTEK. 420
                                                                                                                                                                                                                                                                                                                                                            4.21 TMEEALELANDTQYGLGAGVWSRNGNLAYKMGRG1QAGRVWTNCYHAYPAHAAFGGYKQS 480
                                                                                                                                                                                                                                                                                                                                                                                              61 KRDIDLALDAAHKVKDKWAHTSVQDRAATLFKTADRMEGNLELLATAFTWDNGKPTRFTS 120
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                                                                                              FNQGEVCTCPSRALVQESTYERFMERATRRVESTRSGNPLDSVTQMGAQVSHGQLETTLN
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                                                                                                                                                                                                                                                                                            991 YIDIGKKEGADVLTGGRRKLLEGELKDGYYLEPTILFGONNMRVFOEETFGPVLAVTTFK
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Pred. No. 1.6e·265;
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; GENERAL INFORMATION:
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Best Local Similarity 99.89
Matches 511, Conservative
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                           AADVPI.AIDHFRYFASCIRAQEGGISEVDSFTVAYHFHEPI.GVVGQIIPWNFPLLMASWK 180
                                                                                                                             MAPALAAGUCVVIKPARLTPLSVILIAMFIVGDLLPPGVVNVVNGAGGVIGEYLATSKRIA 240
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CURRENT APPLICATION NUMBER: US/09/791,537
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NUMBER OF SEQ ID NOS: 153055
SOFTWARE. Patentin version 3.0
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511; Conservative
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US-09-791-537-9101
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FITTE OF INVENTION: ADDAME FOR DIAGNISTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
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                 FILE REFERENCE: 107196.135
CUPPENT AFFLICATION NUMBER: US/OM/LNJ, 6410
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REPERENCE: 84-10 ($2052)A CURPENT APPLICATION NUMBER - 18760,446,039 CURPENT APPLICATION NUMBER - 18760,446,039 SEQ. ID. NOS: 47374
                                                  1999-02-18
BER: US 60/094,145
                                                                                                    PRICK APPLICATION NUMBER: US 60/074,787
PRIOR FILING DAFF: 1998-02-18
NUMBER OF SEQ ID NOS: 11326
SEQ ID NO 9978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1707z, Application US/bu3bu039; GENERAL INFORMATION:
                                                                                                                                                                                                                   ORGANISM: Enterobacter cloacae
                                                                                        1998-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Goldman, Barry S. APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C.
                                                                                                                                                                                                                                                                                                            Matches 483; Conservative
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                                                                     PRIOR APPLICATION NUMBER PRIOR FILING DATE: 1998-
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                                                                                                                                                                                                                                                                                            Similarity
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HS-60-360-039-17072
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                                                                                                                                                                                  CENGTH, 546
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VENTION: NUCLEIC ACID AND AMIND ACID SEQUENCES RELATING TO ENTPROPARTER
                                                                                                                                                                                                                               APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACIER
TITLE OF INVENTION: CLOAPAE FOR DIAGNOSTICS AND THERAPEUTICS
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                 421 IMEEALELANDIQYGUGAGVWSRNGNLAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKQS 480
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1ive 17; Mismatches 12, Indels 0
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                                                                                          511 GIGRETHKMMLEHYQQTKCLLVSYSDKPLGLF 542
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CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                   OPGANISM: Enterobanter cloadae
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 11324
SEQ ID NO 9975
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TITLE OF INVENTION: EXPRESSION OF MICHORIAL PROFEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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                                                                                                                  1 MTNNPPSAQIKPGEYGFPLKLKAPYDNPIGGEWVAPADGEYYQNITPVTGQLLCEVASSG 60
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Length 546;
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TITLE OF INVENTION: EXPRESSION OF MICHOBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                            82 SVQDRAAILEKIADRMEQNLELLATAETWDNGKPIRETSAADVPLAIDHFRYFASCIRAQ 141
                                                                                                                                                                                                                                                                                     202 SVLLLMEIVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVGQQIMQYATQN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 LIPVTLELGGKSPNIFFDDVAREDDDYLDKALEGFTMFALNQGEVCTCPSRALVQESIYE 315
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                                                                                                                                                                                                                                                                                                                                                                                                       136 EGSISELDHDTIAYHFHEPLGVVGQIIPWNFPLLMACWKLAPALAAGNCVVLKPAEQTPA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 RFMERAIRRVESIRSGNPLDSVTQMGAQVSHGQLETILNYIDIGKKEGADVLTGGRRKLL 381
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                                                                                                                                                                 22 KARYDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDAAHKVKDKWAHT 81
                                                                                                                                                                                                                16 KARYDNFIGGOWVAPADGRYFDNSSPIHGRKICETARSQAIDIERALDAAHAAKAGWART 75
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                                                                     71.8%; Score 1918; DB 27; Length 506; 71.7%; Prod No. 4.4e-188; tive 57; Mismatches 82; Indels 0
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CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15459, Application US/60366039 GENERAL INFORMATION:
; OKGANISM. Caulobacter crescentus
US-60-360-039-17072
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
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APPLICANT: Chen, Xianfeng
                                                                                           Loral Similarity
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US-60-360-039-15459
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APPLICANT: STATCE, STOVEN C. TITLE OF INVENTION: EXPRESSION OF MICROHIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROFERIES
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                                                                                                                             125 EGGISEIDSDTIAYHFHEFLGVVGQIIPWNFFLLMACWKLAPALAAGNCVVMKPAKQTFA 184
                                                                                                                                                                                                                  185 STIVIMEVIGDIJPBGVIAVVNGFGDFAGKPIASNPRIAKTAFTGFTTTGRIJMQYASON 244
                                                                                                                                                                                                                                                              262 TIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVCTCPSRALVQESIYE (21
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                                                                                   [4.2] EGGISEVOSEIVAYHEBELGVVGQLIPWNEPGLMASWKMAPALAAGNIVVULPARITIT.
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71.98, Pred. No. 5.4e 188;
Live 58, Mismatches 80, Indels 0;
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// GENERAL INFORMATION:
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Hinkle, Gregory J.
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; Sequence 8001, Application US/09791537 ; GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
TITLE OF INVENTION: FXPRESSION OF MITPHORIAL PROMPTINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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.85 SILVLMEVIGDIJ.PPGVI.NVVNGFGI.EAGKPLASNPRIAKIAFTGETTTGRIJMQYASQN 244
                                                                   262 IIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVCTCPSRALVQESIYE 321
                                                                                                   365 DGELSDGFYVKPTVFKGHNKMRVFQEEIFGPVVSVTTFKDEADALAIANDTLYGLGAGVW 424
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GENERAL INFORMATION:
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APPLICANT: Chen, Xianfeng
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185 VSYSPKALGFF 495
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US-60-360-039-16210
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
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442. SPNSNLAYKMSKSTQAGPVWTNZYHAYPAHAARGGRYKQSGTGRETHKMMLEHYQQTKCLL, 501
                                                                                                              16 KQQYENYIGGAWVPPAGGEYFESTTPITGKPFTRVPRSGQQDVDAALDAAHAAKAAWART 75
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Live 67; Mismatches 73, Indels 0.
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Query Match
                                                                                                        TYPE: PRT
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APPLICANT: Hinkle, Gregory J.
APPLICANT: STATET, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A.
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven G.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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                                                                                                                                                                                                                                                                                                                                                                                                                         63; Mismatches
                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: 18,560,739
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 505
                    : Sequence 12218, Application US/60360039
: GENERAL INFOHMATION:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                          ORGANISM: Mesorhizobium loti
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                                                          APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
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US-60-360-039-12218
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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Blackle, Gregory J.
APPLICANT: Blackle, Gregory J.
APPLICANT: Blackle, Gregory J.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROTEINES
FILE PEFFERENCE: 38-10/520523A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILLING DATE: 2002 02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 YATQNTIPVTLELGGKSPNTVFADVMDEEDAFFDKALEGFALFAFNGGEVCTCPSRALVU 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 FPLKI KAPYDNFIGGFWVAPADGFYYGNLTPVFGOLLGEVASSCKFFITDLALDAAHKVKD 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.9%; Score 1894; DB 27; Length 506;
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                                                                                                                                                                                                                                                                                                                                               11.1018
                                                                                                                                                                                                                                                                                                                 Pred. No. 1,3e+185;
                                                                                                                                                                                                                                                                                                                                            62; Mismatches
                     CURRENT APPLICATION NÜMBER: US/06/360,039
CURRENT FILLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS, 47374
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                                                                                                                                                                                                    ORGANISM: Burkholderia fungorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497 TRCLLVSYSDKPLCLF 512
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FILE REFERENCE: 38-10(52052)A
                                                                                                                                                                                                                                                                                                                    70.68;
                                                                                                                                                                                                                                                                                                                                               350; Conservative
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                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                               SEQ 1D NO 4614
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Mismatches
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CUFPENT FILING DATE: 20r1-02-22
NUMBER OF SEQ ID NOS: 153055
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; Sequence 31772, Application US/09791537
; GENERAL INFORMATION
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APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
ITLE OF INVENTION: EXPRESSION OF MICFORDIAL PROPEINS IN PLANTS FOR PROPEINS
TITLE OF INVENTION: LANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURPENT APPLICATION NUMBER: US/60/360,039
CURPENT FILING FORE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11572
                                                                                                                                                                                                                      371 ERNALGGELSKGYYVKPTVFRGNNKMRIFQEEIFGPVVSVTTFRNEEBALEIANDTLYGL 430
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                                                                                                                           77 KWAHTSVQDRAAILFKIADRMEQNLELLATAETWDNGKPIRETSAADVPLAIDHFRYFAS 136
                                                                                                                                                              71 AWGKTSAADRANILNRIADRMEANLQRLAVAETIDNGKPLRETTAADIPLAIDHFRYFAG 130
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                                                                                                                                                                                                                                                                                                                                                257 YATQNIIPVILEIGSKSPNIVFADVMDEBDAFFDKALEGFALFAFNLEVCTCPSPALVQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                      317 ESIYERFMERAIRRVESIRSGNPLDSVTQMGAQVSHGQLETILNYIDIGKKEGADVLTGG 376
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                                                      17 FPLKLKARYDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDAAHKVKD 76
                                                                                         13 FP--YKKQYANFIGGEWVKPVGGEYFDNVSPITGEAFTSIPRSRFADVFLALDAAHRAKT 70
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                 Indels
 Pred. No. 1.3e-185;
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 Best Local Similarity
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APPLICANT: Debe, Derek
PEPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                  56 DIEKALDAAHAAKDAWGKTSAAVPALTLNPIADKMEENLDLLALAETWDNGKPIRETTAA 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 RKTLTGDLKDGYYIQPTVFEGNNKMRIFQEEIFGPVVSVTTFKTVEEALEIANDTVYGIG 420
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                                PKILLEGELKIGSYYLEPTILFGONNMRVFORETFGPVLAVTTFKTMEEALELANDTGYGIG 437
138 IRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGNCVVLKPAR 197
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                                                                                                                                 198 LIPLSVLLLMEIVGDLLFPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVGQQIMQY
                                                                                                                                                                                                 181 OTPASILIVMELIEDLLPPGVLNIVNGTGLEAGKPLAQSNRIAKIAFTGSTSVGKEIMRY
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Search completed: June 24, 2003, 10:30:44 Job time: 188.362 secs

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GenCore version 5.1 6
Copyright (c) 1993 - 2003 Compagen Ltd
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OM protein - protein search, using sw model

June 24, 2003, 10:14:35; Search time 55.428 Seconds (without alignments) 2375.712 Million cell updates/sec Pun on:

US-09-830-751-8

HYQQTKOLLVSYSDKPLGLF 512 1 MTNNPPSAQIKPGEYGFPLK. Perfect score: sednauce.

BLASHM62 Scoring table

1171708 soqs, 257189365 residues Searched.

Gapop 10 0 , Gapext 0 5

Total number of hits satisfying chosen parameters:

length: 2000000000 Minimum DB seq length: 0 Maximum DB seq length: 20

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Pending\_Patents\_AA\_New:\* Database :

/cgn2\_6/ptcdata/2/paa/PCT\_NFW\_COMB.prp:\*
/cgn2\_6/ptcdata/2/paa/U806\_NEW\_COMB.prp:\*
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/cgn2\_6/ptcdata/2/paa/U808\_NEW\_COMB.prp:\*
/cgn2\_6/ptcdata/2/paa/U808\_NEW\_COMB.prp:\* /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMH\_pep.\*/cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Query Score Match Length	Query Match Lengt	Lengt	- 4	DB	Q!	Description	<i>c</i>
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	506	٥	US 10 369-493 14000	Sequence	14000,
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### ALIGNMENTS

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                                                                                            APPLICANT: Cameron, Douglas C.
IIILE PER INVENTION: Production of 3-Hydroxypropionic Acid in Recombinant
IIILE OF INVENTION: Organisms
FILE PEFERENCE 960296.96617
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100.0%, Pred. No. 1.7e-236,
tive 0, Mismatches 0, Indels 0
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CURRENT APPLICATION NUMBER: US/09/830,751
CURRENT APPLICATION NUMBER: 0.00-08-30
PPIOP APPLICATION NUMPER: 60.7151,440
PRIOP FILING DATE: 1999-08-30
PPIOP FILING LATE: 1999-08-30
PPIOP FILING LONG: 23
NUMBER OF SEQ ID NOS: 23
                                       Sequence 8, Application US/U9830751; GENERAL INFORMATION: APPLICANT: Suthers, Patrick F. APPLICANT: Cameron, Douglas C.
                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Escherichia coli
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Bost Local Similarity 100.
Matches 512, Conservative
RESULT 1
US-09-830-751-8
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481 GIGRETHKMMLEHYQQTKCLLVSYSDKPLGLF 512
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PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT, Cao, Yongwei
APFLICANT, Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
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Matches 511; Conservative
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LENGTH: 542
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                                      361 YIDIGKKEGADVLTGGRRKILEGELKDGYLEPTILFGONNMRVFQEEIFGPVLAVTTFK 420
                                                          421 TMEEALELANDTQYGLGAGVWSRNGNLAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKQS 480
                                                                                                                                              301 FNQGEVCTCPSRALVQESIYERFMERAIRRVESIRSGNPLDSVTQMGAQVSHGQLETILN 360
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NUMBER OF SEQ 1D NOS: 78614
SOFTWARE: PatentIn version 3.1
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0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                              Sequence 43103, Application US/10282122A GENERAL INFORMATION:
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PRIOR PAPLICATION INMBER: 60/230, 335
PRIOR APPLICATION INMBER: 60/230, 347
PRIOR ELING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12.2
PRIOR FILING DATE: 2001-12.2
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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PRIOR FILING DATE: 2000-05-26
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Yamamoto, Robert
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Zyskind, Judith
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE PEFERENCE: 38-10/52052)4
CURRENT APPLICATION NUMBER: US/10/369,493
                            91 KRDTDLALDAAHKVKDKWAHTSVQDRAATLFKTADRMEGNLELLATAFTWDNGKPTRETS 150
                                                                                                  121 AADVPLAIDHERYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGGIIPWNFPLLMASWK 180
                                                                                                                                                                 151 AADVPLATUHFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIFWNFPLLMASWK 210
                                                                                                                                                                                                                                181 MAPALAAGNÇVVLKPARLTPLSVLLLMETVGDLLPPGVVNVVNGAGGVTGEYLATSKKTA 240
                                                                                                                                                                                                                                                                      241 KVAFTGSTEVGOQIMQYATONIIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFA 400
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0; Gaps
                                                                                                                                     99.8%; Score 2668; DB 6; Length 542; 99.8%; Pred. No. 5.4e-236; ive 0; Mismatches I; Indels (
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211 MAPALAAGNGVVLKPAPITPLSVLJLMEIVSDLLPPGVVNVVNGAGGVIGEYLATSKRIA 270
                                              241 KVAFTGSTEVGÇÇIMÇYATÇNIIPVTLELGGKSFNIVFADVMDEEDAFFDKALEGFALFA 300
                                                                                                                                       301 FNQGEVCTCPSRALVQESIYERFMERAIRPVESIRSGNPLDSVTQMGAQVSHGQLETILN 350
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NUMBER OF SEQ ID NOS: 78614
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CURPENT APPLICATION NUMBER: US/10/282,122A
CURPENT FILING DATE: 2003 02 20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELLING DATE: 2000-03-21
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOP FILING DATE: 2000-10-23
PRIOR PRICTON UNMER: 60/253,525
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR FILING DATE: 2001-02-09
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PRIGE FILING DATE: 2000-05-26
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APPLICANT. Zamudio, Carlos
APPLICANT. Malone, Cheryi
APPLICANT: Haselbeck, Robert
APPLICANT. Ohlsen, Kari
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Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-75409
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Trawick, John
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Sonre 2589; DB 6; Length 512;

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Query Match

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                                                             1 MTNNPPSAQIKPGEYGFPLKLKAPYDNFIGGEWVAPALGERYPQNLIPVTGQLLAEVASSG 60
                                                                                  AFFLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                  0; Gaps
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95.7%; Fred. No. 8.8e-229;
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TIMMENI AFFLLGALLEN NUMBER: US/10/282,122A
CURRENT FILING DATE: 2903 02 20
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PRIOR FILING DATE: 2000-05-23
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR AFFLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
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Forsyth, R.
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APPLICANT: Zamudio, Carlos
AFFLICANT: Malone, Cheryl
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                     SEQ ID NO 9975
LENGTH: 546
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                                                                                                                       PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wiapper or PALM.
NUMBER OF SEQ ID NOS: SEQ ID NOS: SOFTWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                              96.0%; Score 2567; DB 6; Length 534; 94.5%; Pred. No. le-226,
tive 17, Mismatches 11; indels
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PRIOR FILING TARE: 1944-17-24
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR FILING DATE: 1998-02-18
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                          PRIOR APPLICATION NUMBER: 60/26/,636
PRIOR FILING DATE: 2001-02-09
PRIOK APPLICATION NUMBER: 60/269,308
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Matches 484, Conservative
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94.3%; Pred. No. 4.6e 226;
Live 17; Mismatches 12; Indels
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PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR APPLICATION NUMBER: 60,206,948
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ORGANISM: Enterobacter cloacae
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Carr, Grant
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APPLICANT: Cao, Yongwei

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .22 ADVPLAIDHFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKM 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    482 IGRETHKMMLEHYQQTKCLLVSYSDKPLGLF 512
                                                                                 PRIOR FILING DATE: 2000-09-09
PRIOR PAPLICATION NUMBER - 67/242, 578
PRIOR PAPLICATION NUMBER - 60/253, 625
PRIOR PILING DATE: 2000-11-23
PRIOR APPLICATION NUMBER - 60/257, 931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER - 66/257, 931
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: X-any amino acid
US-10-282-122A-72955
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NIMBER: 60,230,335
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 60,230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (11)..(11)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Salmonella paratyphi
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1 SEQ ID NO 72955
                                                                                                                                                                                                                                                                                                                PRIOF FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 88.0%
Matches 397; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY - MISC_FEATUPE
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldmain, Bairy S.
APPLICANT: Goldmain, Bairy S.
APPLICANT: Goldmain, Bairy S.
TILLE OF INVENTION: EXPRESSION OF MICHORIAL PROJEINS IN FLANTS FOF PFOCTORION OF TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILLE REPRENCE: 38-10(52.052)8
FILLE REPRENCE: 38-10(52.052)8
CUPRENT APPLICATION NUMBER US,710/346,493
CUPRENT FILING DATE: J053-02-28
FILLE APPLICATION NUMBER OS 56/346,039
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                       PRIOR FILLING DATE: JUUL 02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17072
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US-10-369-493-15459
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CURPENT APPLICATION NUMBER: US/10/459,493

; Sequence 17072, Application 05/10489494; GENERAL INFORMATION:

US-10-369-493-17072

RESULT 8

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Harry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                           82 SVQDRAAILFKIADRMEQNLELLATAETWDNGKPIRETSAADVPLAIDHFRYFASCIRAQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                     STTDRSNVILKIADRIEQNLELLAYAETWDNGKPVRETLNADVPLCVDHFRYFAGAIRAQ 124
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                                                                                                                                                                                                                                                                                                                                                              5 KPRYDNFIGGAWVAPQGGQYFDNTTPITGKVFTSIARSTAPDIEAALDAAHAAKEAWGKT 64
                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                           71.7%; Score 1917; DB 6; Length 495; 71.9%; Pred. No. 4.7e-167; tive 58; Mismatches 80; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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CURRENT FILLING DATE: 2003-02-28 PRIOR APPLICATION NUMBER- US 60/360,039 PRIOF FILING DATE: 2002-02-21
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                                                                                                                                                        ; ORGANISM: Xanthomonas campestris
US-10-369-493-15459
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SEQ 1D NO 15827
LENGTH: 495
                                                                                                                                                                                                                                                  Best Local Similarity 71,99
Matches 353; Conservative
                                                                     NUMBER OF SEQ ID NOS. 47374
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                                                                                          SEQ 1D NO 15459
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                                                                                                                                       TYPE: PRT
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APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICRORIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROFERTIES
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                                                                                                                                                                                                                                                                                                                                                                                                                       185 SILVUMEVIGDILLPGVINVVNGFGLEAGKFLASNPKIAKIAFIGETTIGKLIMQYASQN 244
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                                                                                                                                                                                         82 SVQDRAAIIJFKIADPMFQNI.ELIJATAFTWINGKPIPFTSAADVPIJAIDHFRYFASCIRAO 141
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                                                                                                                                           5 KPRYDNFIGGAWVAPQGGQYFUNTTP1TGKVFTS1ARSTAPD1EAALDAAHAAKEAWGKT 64
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71.9%; Pred. No. 4.2e-167;
Live 58; Mismatches 80; Indels (
    Length 495;
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11 Similarity 71.9%; Pred. No. 4.7c 167;
353; Conservative 58; Mismatches 80;
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FILE REFERENCE: 38-10(52052)H
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003 02-22
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PRIOR FILLING DATE: 2002-02-21
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
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Matches 353, Conservative
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NUMBER OF SEQ ID NOS: 47374
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                        Best Local Similarity
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                                                                                142 EGGISEVDSETVAYHEHEPLGVVGQIIPWNEPLIMASWKMAPALAAGGNCVVLKPAPLTPL 201
                                                                                                                                                            SVLILMETVGDLLPPGVVNVVNGACCVIGEYLATSKRIAKVAFTGSTEVGQQ1MQYATQN 261
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82 SVQDRAAILFKIADRMEQNLELLATAETWDNGKPIRETSAADVPLAIDHFRYFASCIRAQ 141
                                                                                                                                                                                                                                               262 IIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVCTCFSRALVQESIYE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITPA.034A
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; GENERAL INFORMATION:
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PPTOF FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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PRIOR FILLING DATE: 2000-09-06
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APFLICANT: Öhlsen, Kari
APPLICANT: Zyskind, Judith
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Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-50457
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APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
TILLE OF INVENTION: EMPERSION OF MICHORIDAL PROTEINS IN PLANTS FOR PRODUCTION OF
TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52952)B
CURRENT APPLICATION NUMBER: US/10/369,493
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                                                                                                                                                                                                                                                                                                                 17 FPLKLKARYDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDAAHKVKD 76
                                                                                                                                                                                                                                                                     Gaps
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SED ID NOS+ 78614
SOPTWARE: PatentIn version 3.1
                                                                                                                                                                                                                71.6%; Score 1915; DB 6; Length 567; 72.0%; Pred. No. 9.1e-167;
                                                                                                                                                                                                                                                                60; Mismatches
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PRIOP APPLICATION NUMBER: US 60/2460,039
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AFFLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12218
                                                                                                                                           ORGANISM: Burkholderia mallei
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US 10 369-493-12218
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                                                                       SEQ ID NO 50457
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                                                                                                                          5 EFSRPVKAPFDKRYGNFIGGKWTEPRSCRYFENHSPVNGQLLCHVARSDADDIEAALDAA 64
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71.3%; Score 1905; DB 6; Length 505; 70.3%; Pred No 6 20-166; ive 63; Mismatches 84; Indels
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURPENT FILING PATE: 2004-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 49350. Application US/10282122A
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PRIOR FILLING DAFE: 2000-03-21
PRIOR FILLING DAFE: 2000-05-12
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PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER- 60/242,578
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cherry!
APPLICANT: Hasclbeck, Robert
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Forsyth, R.
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APPLICANT: Zyskind, Judith
APPLICANT: Wall, Dariel
                                         352; Conservative
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Carr, Grant
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Best Local Similarity
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APPLICANT: Chen, Xianfeng
TTLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 48-10(52052)8
FORENT APPLICATION NUMBER, 02312,469,493
CURRENT FILLNG DATE: 2003-02-28
PRIOR APPLICATION NUMBER: 03 60/7460,049
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
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. Sequence 4614, Application US/10369493
: GENERAL INFORMATION:
                 PPIGE FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,941
                                                                PRIOR FILLING DATE: 2000-12 22
PRIOR APPLICATION NUMBER: 50,7267,636
                                                                                                             PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269, 308
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/254,625
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
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                                                                                                                                                                                                                                                        SEQ ID NO 49350
LENGTH: 506
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197 RLTPL.SVLLLMEIVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVGQQIMQ 256
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                                                                                                                                                                  Gaps
                                                                                                                              70.9%; Score 1894; DB 6; Length 506; 70.6%; Pred. No. 6.4e-165; Live 62; Mismatches 82; Indels
                                                                              ORGANISM: Burkholderia fungorum
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NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4614
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Matches 350; Conservative
                                                                                   ; ORGANISM: BULKED
US-10-369-493-4614
                                                                  TYPE: PRT
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Search completed: June 24, 2003, 10:35:24 Job time : 57.428 secs

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# Genrore version 5-1-6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Ture 24, 2003, In least, Search time 19 597; Seconds (Without alignments) 2512.144 Million cell updates/sec Run on.

115-09-830-751-8 Perfect score:

HYQQTKCLLVSYSDKPLGLF 512 2673 1 MTNNPPSAQIKPGEYGFPLK Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length։ 0 Maximum DB seq length։ Հոսասասարդ

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

PIR\_73:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

NO. SCORE 1 2658 2 2651 3 2651 4 2589 5 1910	1	Match Length DB	В	ID	00000
1 2668 2 2651 3 2651 4 2589 5 1918		֡			pescription
2 2651 3 2651 4 2589 5 1918 6 1910		542		S47809	aldehyde dehydroae
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6 1910		506	7	B87693	aldehyde dehydroge
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-	70.9	505	<b>~</b> 1	AG2849	aldehyde dchydroge
8 1895		540	C1	E97626	chloroacetaldehyde
		206	C 1	A83735	aldehyde dehydroge
10 1849.5		515	c a	H75589	aldehyde dehydroge
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12 1802		206	c a	F83142	probable aldehyde
13 1798		507	C1	F70827	probable aldehyde
14 1791	67.0	206	۲3	н83396	probable aldehyde
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		905	C1	T09437	probable aldehyde
		541	C1	A82276	aldehyde dehydrage
10		495	C1	C89778	hypothetical profe
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1		501	C1	T31265	aldehyde dehydroge
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		517	-	DEHUE2	aldehyde dehydroge
		503	c a	T39216	ald-hyde dehydroge
26 953		520	,	809030	aldehyde dehydroge
		200	_	\$00364	
28 949	35.5	517	_	A40872	aldehyde dehydroge
76		519		SE72AE	produble aldehyde

61 KPETELALDAAHKVKDKWAHTSVQFFAAILFKIADFMEGNLFILATAETWENSKPIPEIS 110

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probable aldehyde	protein F54D8.3 [1	aldehyde dehydroge	aldchide dehidroge	aldehyde dehydroge	aldehyde dehydroge	rf2 nuclear restor	aldehyde dehydroge	glycine betaine al	hypothetical prote	glyrine hetaine al	aldehyde dehydroge	aldehyde dehydroge	probable aldehyde	probable aldehyde	obudoble oldehove
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#### ALIGNMENTS

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CATORO CATORO	
Salebourge dehydrogonage //NDD/ (FC 1 2 1 3) aldR [eimilarit] - Derhorichia (c) ( c)	
C. Species: Escherichia	3
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002	
C; Accession: 547809; B57259; F65158	
R; Plunkett, G.	
submitted to the EMBL Data Library, March 1994	
A: Reference under: S4/666	
A. A. Arcession: S4 Avov A. Status: breliminary	
A; Molecule Lype: DNA	
A.Cross-references: EMRL HOSG139, NIE 9466582, FIBN AAR18565 1, FIB 9312476	
R;Xu, J.; Johnson, R.C.	
J. Bacteriol. 177, 3166-3175, 1995	
Arities aidB, an Rocs dependent gene in Escherichia coli encoding an aidehyde dehydr	/dr
A) Peterando Lumbert A37239, Multitaskes490, PMIII:7700013	
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A. Bosse, D. J. & Man, B. & Shao, V.	· :
Science 277 1453-1462 1997	
A, Title. The complete genome sequence of Escherichia coli K.12.	
A; Reference number: A64720; MUID:97426617; PMID:9278503	
A; Accession: F65158	
A;Status: preliminary; nucleic acid sequence not shown; translation not shown	
A, Molecule type: DNA	
A, Residues: 1 542 ::BLAT:	
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A) Experimental Source: Strain Fig. Substrain Maisty	
COMMETCS.	
A.Venue, alob A.Start codon: GTG	
Control formally: aldebyde delydrodenase (NAD+): aldebyde debydrodenase homology	
C. Keywords NAD, axidoraductase	
F.93-352/Demais, aldebyde debydrevenase hamelegy ALDD	
F.298,337/Active site. Glu, Cys #status predicted	
F:454/Binding site. NAD (Cys) #status predicted	
Observ Match 39 88, Novy Pofes, PR 1, Depart 5429	
Pred No. 8.5e-198:	
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	91 121 151 181 2211 271 271 301 361 391	REDIDLALDAAHKVOKWAHTSVODRAALLEKTADRMEONLELLATAETWOKKPIRETTS 150  AADVPLAIDHERYFASCIRAGEGGISEVDSETVAYHEHEPLGVVGOTTPWREPLLMASWK 180  HILLIHTHITHITHITHITHITHITHITHITHITHITHITHITH	Oy 241 KVAFTGSTEVGQOIMQYATQNIIPVTLELAGGKSPNIVEADAWNDEEDAFEDKALEGFALFA 400  1111111111111111111111111111111111
q d d d	451 481 511	THEFALELLANDIOYGLGAGVWSRNGNLAYKGRGIQAGRVWTNCYHAYPAHAAFGGYKQS 510 GIGRETHKWMLEHYOOTKCLLVSYSDKPLGLF 512 GIGRETHKMMLEHYQOTKCLLVSYSDKPLGLF 542	Cispectes: Exercions coll Cispectes: Exercision 16-Feb 2001 #text_change 02-Nov-2001 Cidete: 16-Feb-2001 #sequence_revision 16-Feb 2001 #text_change 02-Nov-2001 CiAccession: 686033 CiAccession: 686033 Riperna, N. T. Plunkert III, c.; Rurland, V.; Man, N.; Glasnor, I. D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001 Affilted: Genome sequence of enterchangic Percharical Activity Activity Activity Activity (1015) 10157.H7.
RESULT 2 H91186 a104186 a104186 c) Specie C) Date: C, Date: C, Date: C, Acsayara DNA Res. A) TILLE: A) Refere A) Status A) Sta	e dehy es: Es 18-Ju sion. hi, N., 18, 11 components sions si	RESULT 2 ### RESULT 2 ### RESULT 2 ### RESULT 2 ### RESULT 2 ### RESULT 2 ### RESULT 2 ### RESULT 3 ### RESUL	A.Accession: G8603 A.Status: preliminary A.Molecule type: DNA A.Residues: 1-542 - CSTO A.Cross-references. GB:AE005174; NID.g12518326, PIDN:AAG58731.1; GSPDH:GN00145; UMGP: A.Cross-references. GB:AE005174; NID.g12518326, PIDN:AAG58731.1; GSPDH:GN00145; UMGP: A.Cross-references. GB:AE005174; NID.g12518326, PIDN:AAG58731.1; GSPDH:GN00145; UMGP: A.Cross-references. GB:AE005174; NID.g12518326, PIDN:AAG58731.1; GSPDH:GN00145; UMGP: C.Generics: A.Generics: A.Gener
Query Match Best Local Matches 500	Match Local		DD 91 KPDIDLALIDAAHKVKDKWAHTSVQDRAATLEKTADEMEQNISTLATAFANDAGKPTRETS 150  QY 121 AADVELATDHEKYFASCTRAQEAGTSEVDSETVAVHEHEDGAVVGQTTCWNEFDLMASWK 180  DA 353 AADVELATDHEKYFASCTRAQEAGTSEVDSETVAVHEHEDGAVVGQTTCWNEFDLMASWK 180  DA 353 AADVELATORE OF A STANDARD CONTRACTOR OF A STA
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R;Priefert, H.; Kruger, N.; Jendrossek, D.; Schmidt, B.; Steinbuchel, A. J. Bacteriol. 174, 899-907, 1992
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C.Species: Salmonella enterica subsp. enterica serovar Typhi
C.Species: Salmonella enterica subsp. enterica serovar Typhi
C.Species: Salmonella enterica subsp. enterica serovar Typhi
C.Species: O9-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C.Accession: AF0977
R.Parkhill. J.: Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
T.; Connerton, P.; Cronin, A.; Davis, P.; Provies, R.M.; Pickard, D.; Wain, J.; Churcher,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skeiton, J.; Stevens, K.;
A.Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A.Rocession: AF0977
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-512 *PAR
A.Residues: 1-512 *PAR
A.Residues: 1-512 *PAR
A.Residues: J. Stevenson Sequences: G. Superfamily: G.Superfamily: G
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aldehyde dehydrogenase B [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: B87693
B;Nierman, W C;Feldhynm, T V;Panlsen, I.T;Nelson, K F; Eisen, J;Heidelberg, B;Nierman, W C;Feldhynm, T V;Panlsen, I.T;Nelson, K F; Eisen, J;Heidelberg, B;Nierman, M C;Feldhynm, T V;Panlsen, F J; Purkin, A S; Gwinn, M L;Hatt, D H; Ko n, J; Ermolaeva, M;White, O;Salzberg, S.L;Shapiro, L;Venter, J.C.;Fraser, C Proc Nat]. Acad Sci n;SA, 98, 4136-4141, 2001
A;Tille: Complete Genome Sequence of Caulobacter crescentus.
A;Tille: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: AR7249; Millo:21174698; PMillo:11254647
A;Accession: B87693
A;Molecule type: DNA
A;Residues: 1-506 <SFO>
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C)Genetics:
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Best Local Similarity 71.7%; Pred. No. 5.5e-140;
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RESULT 5
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A:Status: preliminary
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A:Title. Identification and molecular characterization of the gene coding for acetaldehy
A;Reference number: A42597; MUID:92121129; PMID:1732222
A;Accession: A42597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aldehydrogenase aldA [imported] - Agrobacterium tumefaciens (strain C58, Dupont) (Species: Agrobacterium tumefaciens (Cipate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change U1-Feb-2002 (Cipate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change U1-Feb-2002 Revision AC2849 Rivod, D.W.: Setubal. J.C., Kaul, R., M.d.ks, D., Chen, L., Wood, G.E., Chen, Y., Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D., Kutyavin, T., Levy, R.; Li, M.; McCLeil science 294, 2317-2323, 2001
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Ster, E.W.
A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A.Reference number: AB2877; PMID:11743193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SILVLMEVIGDLLPPGVVNVINGFGLEAGKPLASSPRISKVAFTGETTTGRLIMQYASQN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 TRDGARAFRMGRGIQAGRVWTNCYHAYPAHAAFGGYKQSGIGRENHRMMLDHYQQTKNLL 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 SVQDRAAILFKIADRMEQNLELLATAFTWDNGKPIRETSAADVPLAIDHFRYFASCIRAQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGNCVVLKPARLTPL, 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVLLLMEIVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVGQQIMQYATQN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 IIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVCTCPSRALVQESIYE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFMERAIRRVESIRSCNPLDSVTQMGAQVSHGQLETILNYIDIGKKEGADVLTGGRRKLL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 EGELKDGYYLEPTILFGQNNMRVFQEEIFGPVLAVTTFKTMEEALELANDTQYGLGAGVW 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 DGDLAGGYYVKPTVFAGHNKMRIFQEEIFGPVVSVTTFKDEEEALAIANDTLYGLGAGVW 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442 SRNGNLAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKQSGIGRETHKMMLEHYQQTKCLL 501
                                                                                                                                                                                                                                                                    C.Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology C.Keywords. NAD, oxidoreductase (F.57-31/Commin: aldehyde dehydrogenase homology <ALED> F:57-31/Active site: 01u, Cys #status predicted
F:262.301/Active site: 01u, Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 KARYDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDAAHKVKDKWAHT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 KQQYENYIGGAWVPPAGGEYFESTTPITGKPFTRVPRSGQQDVDAALDAAHAAKAAWART 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                     A; Cross·references GR M74003; NID. 9141885; PIFN: AAA21943.1; PID: 9141886
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73; Indels
                                                                                                                                                                         A; Experimental source: strain TF93
A;Note: sequence extracted from NCBI backbone (NCBIP:77618)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                       71.5%; Score 1910; DB 1;
71.5%; Pred, No. 2.3e-139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 351; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                 A; Residues: 1-506 <PRI>
                                                                                   A; Status: preliminary
                                                                                                       A; Molecule type: DNA
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chloroacetaldehyde dehydroqenase (AF029733) [imported] - Aqrobacterium tumetariens (s
C;Species: Agrobacterium tumefaciens
C;Date: 30 Sep 2001 #sequence_revision 30 Sep-2001 #text_change 11 Jan 2002
C;Accession: E97626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ridoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJTILLE: Genome Sequence of the Plant Pathoden and Riotechnology Agent Agrobacterium A, Reference number: A97359; PMID:11743194
A.McJecule type: DNA
A.Residues: 1-505 «KRR»
A.Cross-reterences: GB:AE00868; PIDN:AALA*21*.1; PID:q17740695; GSPDH:GNO0186
A.Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  £0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 DAAHKWERMARISVQDRAATEELADRINEDLAATAETWDNGRPTRETSAADVITAT 128
| [1]| [1] :: [1 | 1]: : [1 | 1] :1 | 1: [1 | 1]: [1: [1 | 1] | 1]: [1: [1 | 1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 DAAHKAREKWGKTSITEKSNILLAHAQRIEDNLDLAARAFTWDNGKPLRETTNAD1PLTI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .29 DHFRYFASC1RAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAG 1H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 GADVLTGGRRKILLEGELKIKSYLEPTTILFGONNMRVFOEETFGPVLAVITFKIMELALEI, 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 GAKVLTGGDRKTLTGDLKDGYYLOPTVFEGNNKMRLFQEELFGPVVSVTTFKTVEEALEL 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.29 ANDTQYGLGAGVWSRNGNLAYKMGRGTQAGRVWTNCYHAYPAHAAFGGYKQSGTGRETHK 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Cross-references: GB: AEG07869: PIDN: AAKB7966.1: PID: q1515/3/4: GSPDH: GN00169
                                                                                                                                                                                                            A,Map position, circular chromosome
C;Superfamily; aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Map position: circular chromosome
C.Superfamily: aldehyde dehydrogemace (NAPP); aldehyde dehydrogenase homelowy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 QQKAGEAPFKLK----YGNY GGGWWFPKSGPYMON SPYGGHK CFVPPSDASDIEFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.9 EVGÖĞLMQYATONLI PVTLELKIĞKSPILI VEAFVMDEEDAFFIKALEGFALFAFINGGEVET
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 QIKPGEYGFPLKLKARYDNF1GGEWVAPAIKHEYYQNLTPVFGQLLCEVASSGKRD1DLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 NOVVEKPARLTPLSVELLIMETVGDELFPGVVNVNVNGAGGVIGEVIALSKRIAKVAFTGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 CPSKALVĢESIYEREMEKAIKKVESIKSGNPIDSVTOMGAQVSHGOLETIINYIDIGKKE
                                                                                                                                                                                                                                                                                                                      70,9%; Score 1895; DB 2; Length 505;
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                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.2e 138;
                                                                                                                                                                                                                                                                                                                                                                                    68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       489 MMLEHYQQTKCLLVSYSDKPLGLF 512
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                                                                                                                                                                                                                                                                                                                                                          69.08;
                                                                                                                                                                                                                                                                                                                                                                                       348; Conservative
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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A.Molecule type: DNA
A:Residues: 1:540 <KUR>
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                                                                                                                                                                                                                                                                                                                      Query Match
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Matches 34	hes 348, Conservative 68, Mismatches 84; Indels 4; Gaps 1;	qrı	125 FRYFAGAIRAQBGTLSQIDNDFVARHFHEFLGVVGQIIFWNFFILMAIWKLAFALAAGNC 184
Qy	9 QIKPGEYGFPLKLKAPYDNEIGSFWVAPARGEYYQNJTPVTGQLLZEVASSSKRDIDLAL BR 	.tઝ 1.b	191 VVI.KPAPLTPLSVLILMFIVGDLI PPSVVNVVNGAGGVIGEVLATSKPTAKVAFTGSTEV 250 1111   1   1   1   1   1   1   1   1
Qy Db	69 DAAHKVRDKWAHTSVQDPAATLEKTADPMEQNLELLATAETWDDGKPIRETSAADVPLAI 128 	O.y.	251 GGGLMGYAPGNIJPVILELGGKSPNIVPABVMDEEGAFBVALESFALFAFNQGEVCTCP 310 [1:1][1:1:1][1:1][1][1][1][1][1][1][1][1][1][1][1][1][1
Qy Db	129 DHFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIFWNFPLLMASWKMAPALAAG 188 	cy Dp	311 SFALVUESIYERFMEHAIPRUESIRSSMPLUSVTQMGALVSHBGLEFILNYTUTGKFEGA 370 
ΟΥ Db	189 NCVVLKPARLTPLSVLLLMEIVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGST 248 	Qy Db	371 DVLFGGRKKLLEGELKDGYYLEPTILFGQNNMKVFQEEIFGPVLAVTTFKTMEEALELAN 430 
Qy hu	249 EVGQOIMQYATQNIIPVTLELGGKSPNIVFADVMDEEDAFFUKALEGEALEAFALUGEVCT 308 	රි සි	4.31 ETGYGLGAGVWSRNGNLAYKMGRGLGAGRVTNCYHAYPAHAAPGGYKUSGLGRETHKMM. 4.90 
Oy Db	309 OPSPALVQESTYEPPREPALPRVESTESGNPLDSVTQMGAQVSHGQLETTLNYTHJGKKE 358 	5 ž	491_LEHYQQTKGJLVSYSDKPLGLF_512 
Qy Db	369 GADVITGGPRKILEGEIKDGYYLEPTILEGQNNMRVEQEEIFGPVLAVTTEKTMEEALEL 428 	RESULT 10 H75589	10
Qy Db	429 ANDTQYGLGAGVWSRNGNIAYKMGRGTQAGRVWTNGYHAYFAHAAFGGYKQSGIGRETHK 488 	aldehyd C;Speci C;Date: C;Acces	
Oy Db	489 MMLEHYQUIKCLLVSYSDKPLGLF 512 	R;White , M.; S S.; Smi Science	, O.; Eisen, J.A.; Heidelkerg, J.F.; Hickey, E.K.; Peterson, J.D.; Dudson, R.J. hen, M., Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; th, H.O.; Venter, J.C.; Fraser, C.M. 286, 1571-1577, 1999
RESULT A83735 aldehyd C;Speci C;Date: C;Acces R;Takam Nucleic A;Title	RESULT 9 A83735 aldehyde dehydrogenase aldA [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun.2001 C;Accession: A83735 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83560; MUTD, 29512582; MUTD, 11059132	A Title A Refer A Statu A Statu A Molec A Cross A Gene C Mone C	A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RI. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Recession: H7589 A;Status: preliminary A;Moteoule type: DNA A;Residues: preliminary A;Residues: 1-515 AWHD A;Residues: 1-515 AWHD A;Residues: GB:AE001863; GB:AE001825; NID:96460670, PIDN:AAF12436.1; PID:9646 A;Reperimental source: strain RI C;Genetics: A;Genetics: A;Gen
A; Accet A; Statt A; Molec A; Resid	ssion: A83735 cule type: DNA cule type: DNA cule type: ONA cule ty	Query M Best Lo Matches	69 2%; Scorp 1849 5; DR 2; Length 515; nilarity 69.1%; Pred. No. 1.1e-134; Conservative 59, Mismatches 95, indels 1,
A; Experior (C; Genet A; Genet C; Super C; Senet	Coloss tretrences: delarollor, in magninus; miliginizitin; pinn manusuul); GSPDB:GNUQ Genetics: Genetics: Stinerfamily: aldohide debudronomses (MADI): aldohida dohudronomses homolom		12 PGEVGEFELELKAPVINETGTEWVAFADESYYGNI TPVINGELFFVASSKKUIDLAIDAA 71 
Ouery Marches	Ouery Match 70.3%, Score 1878; DB 2; Length 506, Best Local Similarity 68.3%, Pre-3. N. 6.72.137, Indels 0; Gaps 0; Matches 346; Conservative 67; Mismatches 89; Indels 0; Gaps 0;	Åð d	72 HKVKDKWAHTSVQDRAATLEKTADRMEQNLELLATAETWINGKPTRETSAADVPLAIDHF 131 
ςς Op	11 KPGEYGFPLKLKARYDNPTGGEWVAPADGETYQNLTFVTGGLLGEVASSGKEDIT 	2y 2b	132 RYFASCIKAÇEĞƏISEVISETVAYHEHERLƏVVĞQIIPWNFPLLMASWKMAPALAAĞNCV 191 
Oy Dh	AHKVKDKWAHTSVQDRAAILFKIADRMEQNLELLATAETWUNGKEIKETSAADVELAIDH	Qy Dp	192 VLKPARLTPLSVLLLMEIVGDLLPPGVVNVVNCAGGVIGEYLATSKRIAKVAFTGSTEVG 251 
Οy		ΟΥ	252 QQIMQYAIQNIIPVTLELGGKSPNIVFADVMDEBDAFFDKALEGFALFAFNQGEVCTCPS 311 :

QY         427 ELANDTQYGLGAGVWSPNGNLAYKMGKOLQAGKWTNCYHAYFAHAAFGGYKQSGLGRET 44KL           ED         +111   11   111	PRSULT 12 F83142 probable aldehyde dehydrogenase PA4022 [imported] Pseudomonas aeruqinosa (strain c)species: Pseudomonas aeruqinosa (strain c)species: Pseudomonas aeruqinosa (c)species: Pseudomonas aeruqinosa (s)species: Pseud	Cens tess tens		192 VEKFARITELSVILJANSTVANHIHTTITTITTITTITTITTITTITTITTITTITTITTIT	252 VOLMOVATON I IVA LETIAGRANIA MARMINERAM PAKADARA MARMAGANIA MAGANA TANAGANIA MAGANA  97   972 VITGERKILEGELEGGYYLEPTILEGUNMENFOEETFOLVIAVTIETIMEALELAND 4 41   1   1   1   1   1   1   1   1	
Db   256   RLIMGYAADNI,IPVTLELGGKSPNIFFDDVMMEDDAFLDKAVEGMVMFALNGGEVCTCPS   315	09         432 TQYGLGAGYWSRNONLAYKMGRGTQAGRVWTNCYHAYPAHAAFGGYKQSGTGRETHKMML 491           1	RESULT 11 AB3470 aldehydrogenase (NAD) (EC 1.2.1.3) [imported] - Brucclla melitensis (strain 1 c; Species: Brucella melitensis C; Species: Brucella melitensis C; Date: 01'reb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002 C; Date: 01'reb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002 R; DelVerchio, V G : Kapatral. V : Pedkar. P I., Patra, G; Mujor, C; Los, T; Ivano, J; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lo, Proc. Natl. Acad. Soi. U.S.A. 99, 443-448, 2002 A,Title: The genome sequence of the facultative intraveliular pathogen brucella meii A; Reference number: Ana252; PMTD:11756688 A; Accession: AE3470 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-505 ckUk> A; Cross: references G; A ABDÜRNIZ: PHANAMICESER I. PH. 917484776, GSPÜRL: NUDGUN A; Experimental source: strain 16M C; Genetics:	Asgene: BME11747  Aswap position: I  C.Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology C.Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology C.Superfamily: aldehyde dehydrogenase homology C.Superfamily: aldehyde dehydrogenase homology C.Superfamily: aldehyde dehydrogenase homology C.Superfamily: aldehyde dehydrogenase homology C.Superfamily: aldehyde dehydrogenase homology C.Superfamily: aldehyde homology C.Superfamily: aldehyde dehydrogenase homology C.Superfamily: aldehyde dehydrogen	SAQIKPGEYGFELKIKARYDNFIGGEWVAPADGEYYQNUTPVIGQILGEVASSGKREFEL, 6    III	127 AIDHPRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALA 120 AVDHFRYFACVIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALA 120 AVDHFRYFACVIRAQEGGISEIDHDTVAYHFHEPLGVVGQIIPWNPPLLMATWKLAPALA 187 AGNCVVLKPARITPLSVLLLMFIVGDILDPCVVNVNGAGGVIGFYLATSKRIAKVAFTG 110 AND AND AND AND AND AND AND AND AND AND	DD 180 AGNCYVLKPARQIPASTIVI,MELTADITEPROVNIVNGFGLEAGKPLASSPRIAKTAFTG 239  OY 247 STEVGOLMOYATONI PYTLELGGKSPNIVFALVMUCHELAFERALEGFALFAFNUGEV 30b    1

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aldehyde dehydrogenase VC1819 [imported] - Vibrio cholerae (strain N16961 serogroup O C;Species: Vibrio cholerae
C;Species: Nibrio cholerae
C;Date: 18:Aug-2000 #sequence_revision 20:Aug-2000 #text_change 02:Feb-2001
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adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Fölger, K.R., Kas, A.; Larbiq, K.,
.; Lory, S.; Olson, M.V.
Nature 406, 959 964, 2000
                                                                                     A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic
A,Roterence number: A82950; Multi-20437 (47; PMJD-10984043
A,Accession: H83396
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A,Reference number: A82035, MUID-20406833, PMID-10952301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.32 TQYSLSASVWSFNSNLAYKMSFSLQAGPVWTNCYHAYPAHAAFGGYFQSGIGRETHKMML, 4.9.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 VEKPARLTPESVELLMEIVGDEEPGVVNVVNGAGGVIGEYLATSKPIAKVAFTGSTEVG
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A;Residues: 1-506 <HEI>
A,Cr.ss.reterendes GB.A
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R,Stover, C.K.; Pham. X Q.; Erwis, A L.; Michguchi, S.D.; Warrener, P., Hiekey, M.J.; Rd
                                                                                                                                     Cyccession: F708.7

Rychery S. T.; Prosch, P. Parkhill, T.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Conter, S. T.; Prosch, P. Parkhill, T.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Conter, M. A.; Mayers, J.; Futter, S.; Serjer, K.; Skelton, S.; Squares, S.; Hamlin, N.; Holroyd, S. Nature 393, 537-544, 1998

A; Rajandream, M. A.; Ruster, S.; Stutter, S.; Serjer, K.; Skelton, S.; Squares, S.; Sartier, S.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barreil, B.G.

A; Reference number: A70500; MUID:98295987; PMID:9634230

A; Reference number: A70807

A; Return Sprellminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA
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C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #seqwestrevision 15-Sep-2000 #text_change 31 Dec 2000
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Ajgross references (GR.A) 02:033, 08:AL120456 NH: garafere; FIFN:CAA17413.1, FID-garage.
Apperimental source: strain H37Rv
CyGenetics:
                                                  probable aldehyde dehydrogenase (NAD) (EC 1.2.1.3) RV0458 [similarity] - Mycobacterium C;Species: Mycobacterium tuberculosis
C;Species: 17-1u1-1998 #sequeuro_revision 17-1u1-1998 #text_change 03-Jun-2002
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C,Superfamily, aldehyde dehydrogenase (NAD+); aldehyde dehydrögenase homology
C;Keywords: oxidoreductase
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65, Mismatches 105;
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Matches 332, Conservative 6
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H83396
RESULT 13
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A; Experimental source: serogroup 01; strain N16961; biotype El Tor

A; Gene: VC1819

A:Map position: 1 C:Superfamily: aldehyde dehydrogenase (NAD:); aldehyde dehydrogenase homology

Gaps 0 Ouery Match 67 0%; Score 1791; PR 2; Length 506; Best Local Similarity 64 9%; Pred No. 3.4e-130; Matches 326; Conservative 74; Mismatches 102; Indels ( 11 KPGEYGFPLKLKARYDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDA 70

71 AHKVKDKWAHTSVQDRAAILFKIADRMEQNLELLATAETWDNGKPIRETSAADVPLAIDH 130

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191 VVLKPARLTPLSVLLLMEIVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEV 250

g

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251 GQQIMQYATQNIIPVTLELAGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVGTCP 310

371 DVLTGGRRKLLEGELKDGYYLEPTILFGQNNMRVFQEETFGPVLAVTTFKTMEEALELAN 430  $^{\circ}$ QQ

431 DTQYGLGAGVWSPNGNLAYKMGRGIQAGPVWTNCYHAYPAHAAFGGYKQSGIGRETHKMM 490 q

 $^{\circ}$ 

491 LEHYQQTKCLLVSYSDKPLGLF 512

LNHYONTKNLLISYDVNPLGFF 506

Search completed: June 24, 2003, 10:18:33 Job time : 21.5932 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
GenCore version 5 1 6
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OM protein - protein search, using sw model

June 24, 2003, 16:02:55; Search time 10.3122 Seconds (without alignments) 2059.300 Million cell updates/sec Run on:

US-09-830-751-8 Perfect score:

HYQQTKCLLVSYSDKPLGLF 512 1 MTNNPPSAQIKPGEYGFPLK Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

length: 2000000000 Minimum DB seq length: 0 Maximum DB seq

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 08

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

#### SUMMARIES

Result		% Query				
NO.	Score	Match	Match Length	DB	qi	Description
1	2668	8.66	512	1	AL.DB_ECOLI	585
CI		1	506	_	PHA2_ALCEU	i,
æ	1849 5	69.2	515	П	DHAL_DEIRA	
4	1810	7.	506	٦	DHAL_RHORU	09zall rhodospiril
เร		67.3	507	_	DHAL_MYCTU	
ء	17 H Y	٤	ر ا	-	THCA_PHOER	P46369 rhodococcus
7	1760	δ.	507	-	DHAL_STRCO	Q9rjz6 streptomyce
80	1682	-1	G.	-	PHAL_VIBCH	
6	981	9	519	7	DHAM_MOUSE	~
10	975	9	519	Н	DHAM_RAT	P11884 rattus norv
11	971	9	517	~	DHAM_HUMAN	P05091 homo sapien
12	968	٠.	005	<del>, -</del>	DHAM_MESAU	_
13	953	2	520	+	DHAM_BOVIN	P20000 bos taurus
14	952	N	500	-	DHAM_HORSE	
15	940.5		519		DHA4_YEAST	P46367 saccharomyc
	936	'n.	517	<del></del> 4	DHA5_HUMAN	
17	935 5	ıc	499	-	DHA2_HMAN	homo:
18	931.5	4	497	~	DHAL_EMENI	emeri
19	929.5	4	200	-	DHAL_AGABI	074187 agaricus bi
50	926.5	4	499	-+	DHA2_RAT	
2.1	C1	3.4 F	499		PHA2_MOUSE	Q62148 mus muscalu
Ci	955	4	6.1.	٠.	DHA5_YEAST	
53	921 5	٠,	190		- 1	-93344 gallus gall
2.4	010	<del></del>	490		DHAB_BACSII	
i.		٣.	512	r1	DHA6_HTMAN	ιζ
26	903.5	ω,	497	7	DHAL_ASPNG	
1.1	835		503	+ →	DHA1_CHICK	P27463 gallus gail
28	881	'n	497	~	- 1	
53	880.5	ص د: د:	664	-	DHA6_YEAST	P54115 saccharomyc
30	873 5		500	_	- 1	P00352 home sapien
3.1	870.5	32.6	500	-	DHA1_HORSE	snnbə
CI CN	870	3.2	49.	_	DHAL_ALTAL	2041 altern
33.3	868	32 5	ר (י	_	DHAB_CRYSA	024174 oryza sativ

601 rattus norv	P51977 ovis aries	644 bos taurus	417 leishmania	883 escherichia	549 mus musculu	895 amaranthus	647 rattus norv	237 beta vulgar	024 hordeum vul	490 macroscelid	
P13	151	P48	025	P23	P24	004	P51	F28	040	029	0 <b>7</b> 40
DHAC_RAT	DHA1_SHEEP	DHA1_BOVIN	DHAM_LEITA	DHAL_ECOLI	DHA1_MOUSE	DHAB_AMAHP	CHA1_RAT	DHAB_BETVU	DHAB_HORVU	DHAE_MACPR	DHAL_CLAHE
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200	500	500	498	495	200	501	500	500	505	501	496
32.4	32.2	32.1	31.9	31.9	31.8	31.7	31.6	31.6	31.6	31.4	31.3
		m	5	52	349	8.5	846	846	845	840	7.5
867	860	858	852	80	w	84					83

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                                                                                                                                                                                                                                                                                                                                    MFDINE-94316500; PubMed-8041620;
Sofia H.J. Burland V., Daniels D.E., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes.";
Nucloir Acids Pos. 22:2876-2886(1994).
                                                                                                                      01-0CT-1994 (Rel. 30, Created)
01 NNY-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase B (EC 1.2.1.22) (Lactaldehyde dehydrogenase).
ALDB OR B3588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu J., Johnson R.C.; "aldB, an RpoS dependent gene in Escherichia coli encoding an aldehyde dehydrogenase that is repressed by Fis and activated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 177:3166-3175(1995).
CATALYTIC ACTIVITY: (S) Lactaldehyde + NAD(+) + H(2)0 = (S)-lactate + NADH.
                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase, NAD, Complète proteome.
ACT_SITE 268 268 BY SIMILARITY.
ACT_SITE 307 BY SIMILARITY.
SECURNCE 512 AA: 56306 MW; E673034334004680D CRC64;
                                                                                        512 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFam: PF00171; aldedh: 1.
PROSITE: PS00070; ALLEHYDE_DEHYDE_CYS; I.
PROSITE: PS00687; ALDEHYDE_DEHYDE_GLU; I.
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, U00039, AAB18565.1; ALT_INIT.
EMB., AE030435, AA726512.1; ALT_INIT.
EMBL: L40742, AA726539.1; -.
HSSP: P40591; 1CW3.
                                                                                        PRT;
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SPOURNEE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE-95286498; PubMed=7768815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         512 AA; 56306 MW;
                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ecodone, Egi2292, aldB.
InterPro, IPP002086, Al
                                                                                                                                                                                                                                                                                       (1)
SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                    Escherichia coli.
                                                                                      ALDB_ECOLI 8
P37685; P78118;
                                                                                                                                                                                                                                                                    NCBI_TaxID=562;
                                                                                                                                                                                                                                                    Escherichia
                                                                 ALDB_ECOL1
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                                                                                                                                                                                61 KRDIDLALDAAHKVKDKWAHTSVQDPAATLFKTADPMFQNLFLLATAETWDNGKPIRETS 120
                                                                                                                                                                                                                                                              121 AADVPLAIDHFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWK 180
                                                                                                                                                                                                                                                                                                                                          MAPALAAGNCVVLKPARLTPLSVLLLMEIVGDLLPPGVVNVVNGAGGVIGEYLATSKRIA 240
                                                                                                                                                                                                                                                                                                                                                                                                                        KVAFTGSTEVGQQIMQYATQNIIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 FNQGEVCTCPSRALVQESTYBREMBRAIPRVESTRSGNPLDSVTGMGAQVSHGQLETILN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 YIDIGKKESADVLTGGRRKLLEGELKDGYYLEPTILFGUNNMRVFQEEIFGPVLAVTTFK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 YIDIGKKEGADVLTGGRRKLLEGELKDGYLEPTILFGQNNMRVFQEEIFGPVLAVTTFK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 TMEEALELANDTÖYGLGAGVWSKNGNLAYKMGKGIOAGKVWTNCYHAYPAHAAFGGYKOS 480
                                                                                                  1 MTNNPPSAQIKPGEYGFPLKLKARYINFIGGEWVAPARGEYYQNLTPVTGQLLGEVASSG 60
                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
MEDILIDS-121129; Pubmed 1732222;
Priefert H , Kruges, Jedfressek D., Schmidt B., Steinbuechel A.;
"Identification and molecular characterization of the gene coding for acctaldebyde dehydrogenase II (acob) of Alcaligenes eutrophus.";
J. Hacteriol 174.849-97(1992)
-i. FUNCTION: INVOLVED IN THE CATABOLISM OF ACETOIN AND FTHANOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 - an acid + NADH.
! PATHWAY. Ethonol utilization, second step.
-i- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                               Caps
                                                             ċ
                  99.8%, Score 2668, DB 1, Length 512; 99.8%, Pred No 1 2c 192; 1ve 0; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alcaligenes eutrophus (Ralstonia eutropha).
Bacteria, Proteobacteria, beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
U-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetaldehyde dehydrogenase II (EC 1.2.1.3) (ACDH-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 GIGRETHKMMLEHYQQTKCLLVSYSDKPLGLF 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 GIGRETHKMMLEHYQQTKCLLVSYSDKPLGLF 512
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Query Match
Hest Local Similarity 99 55
Thest Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 IIPVTLELGGKSPNIVFADVMDEEDAFDKALEGFALFAFAFOGEVOTOFSBALVQESIFF (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 LIPVTLELGGKSPNIFFEDVLAADDAFFDKALEGFAMFALNGGEVCTCPSRALIOESIYD 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 KARYDNFIGGEWVAPADGERYQNLTPVTGQLLCEVASSGKRDIDLALDAAHKVKDKWAHT HI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 KQOYENYIGGAWVPPAGGEYFESTTPITGKPFTRVPRSGQQDVDAALDAAHAAKAAWART 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 SVELLEMET VCDITTPPGVVNVVNGARGV I GEYLAT SKRT AKVAFTGST FVGQOT MQYAT ON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S76 DODLAGGYYVAPTVFACHNAMKTPOELFOPVSVTIFITIT | 111 :1111 | 11111 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ċ
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                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 71.5%; Score 1910; DB 1; Length 506; Hest Local Similarity 71.5%; Pred. No. 8.7e-146;
                                                                                                                                                                                                                                                     NAP (APP PART) (BY SIMILARITY).
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67; Mismatches 74;
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16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                               BY SIMILARITY BY SIMILARITY
                                                                                                                                  PROSITE, PS00070, ALDEHYDE DEHYDR_CYS;
PROSITE, PS00687; ALDEHYDE_DEHYDR_GLU;
                                                                  InterPro; IPR002086; Aldehyde_dehydr.
Pfam; PF00171; aldedh; 1.
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09RYG9: 042502;
16-orr-2001 (Rel. 40, created)
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PMRL; M74003; AAA21943.1;
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                                        JOM3.
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262
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                                                                                                                                                                                                                                                                                  Submitted (APK-1997) to the EMBL/35chEark/EGRJ databases
-!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
-!- SIMILARITY: RELONSS TO THE ALBEHYDE DEHYDROSENASES FAMILY
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Moffat K.S., Gin H., Jiang L., Famphile W., Crosby M., Shen M., Vandarbevan J.J., Lam P., McChonald L., Ifterback T., Zalewski C., Makarrova K.S., Aravind L., Daly M.J., Mintcon K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzkwig S., Smith H.G., Venter J.C.,
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                                                                                                                                                                                                                         Narumi I., Du 2., Alatas 2., Kitayama S., Watanabe H.; "Isolation and characterization of pprA, a novel beinococcus radiodurans gene involved in DNA repair ":
                                                                                                    Genome sequence of the radioresistant bacterium Deinococcus
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PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1
Oxidoreducteses; NaD; Complete proteome.
NP_BIND 228 234 NAD (APP PAR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                          Science 286:1571-1577(1999).
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                                                                                                                                                                                  SEQUENCE OF 1-258 FROM N.A.
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                                                                                Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 PYFASCTPAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGNCV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 PYFAACIPAQEGSLSQIDETTIAYHFNEPLGVVGQTIPWKFPTLMATWKLAPALAAGNCL 185
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                                                                                                                                                                                                                                                                                                          Phodospirillum rubrum.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY; An aldebyde + NAD(+) + H(2)O = an acid + NADH.
-:- SIMILAPITY - BELIONGS TO THE ALDEHYDE DEHYPPOGENASES FAMILY.
                                                                                                                                                                                                                                                                       \operatorname{Ok1he} N., Amada K , Morikawa M., Kanaya S ; "Cloning of aldehyde dehydrogenase gene from photosynthetic bacterium
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                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
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                                                                                               (Pel. 40, Last annotation update)
                                                                             Last sequence update)
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PROSITE; PS00687; ALDEHYDR_GLU; 1.
PPOSITE; PS00070; ALDEHYDR_DEHYDR_CYS; 1
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                      STANDARD
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NP_BIND 218 2
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                         372 VIÆGGRRKILLEGELKFGYYLEPTILFGQNNMKVFØEHTFGPVLAVTTFKTMEFALELAND 431
                                                                                                              432 TÖYGLGAGVWSKNGNLAYKMGKGIQAGRVWTNCYHAYPAHAAFGGYKQSGIGRETHKMML 491
                                                                                                                                                                                                   312 RALVQESIYEREMERAIRRVESIRSGNPLDSVTÖMGALVSHGÖLETILNYILLIGKKEGAD 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CDC 1551 / Oshkosh,
Fletschmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fletschmann R.D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Folomay J.F., Nelson W.C., Umayam L.A., Ermolæeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 * an acid + NADH.
-1- SIMILARITY: RELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cole S.T., Brosch K., Parkhill J., Garnier T., Churcher C., Harris D., Gurdon S.V., Eiglmeier N., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor P., Davies R., Deviln K., Firwell T., Gentles S., Hamlin N., Hoiroyd S., Hornsby T., Jaqels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne I., Quail M. A., Pajandream M. A., Rogars J., Sulston J.E., Taylor K., Whitehead S., Squares R., Seeger K., Skelton S., Squares S., Squares R., Taylor K., Whitehead S., Barrell B.G.; Taylor K., Whitehead S., Barrell B.G.; Mycobacterium tuberculosis from the Complete genome sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable aldehyde dehydrogenase (EC 1.2.1.3).
                                                                                                                                                                                                                                                             492 EHYQQTKCLLVSYSDKPLGLF 512
                                                                                                                                                                                                                                                                                                        486 DHYQQTKNLLVSYDPKAMGFF 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98295987; PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RV0458 OR MT0474 OR MTV038.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; ALO21933; CAA17413.1; -. EMBL; AE006950; AAK44698.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                              DHAL_MYCTU
053743;
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Tuberculist, Rv0458;

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71 AHKVKDKWAHTSVQDRAAILFKIADRMEGNI.ELLATAETWINGKPIRETSAADVPLAIDH 130
                                                                                                                                                                                                                                                                                                                                                                                     66 AHAAAPGWGKTAPAERAAIIJMIADRIDKNAAALAVAEVWDNGKPVREALAADIIIJAVDH 125
                                                                                                                                                                                                                                                                                                                                                                                                                          131 FRYFASCIRAGEGGISEVDSETVAYHFHEDLGVVGQTIPWNFPLLMASWKMAPALAAGNY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                191 VVLKPARLTPLSVLLLMETVGDLLPPGVVNVVNGAGGVTGFYLATSKRTAKVAFTGSTEV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 GQQTMQYATQNTTPVTLELGGKSPNTVPADVMDEEDAFFDKALEGFALFAFNGGEVCTCP (10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 GRLIMQYASHNLIPVTLELGGKSPNIFFADVLAAHDDFCDKALEGFIMFALNOGEVCTCP 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 DTOYGLGAGVWSRNGNLAYKWGROLQAGRVWTNCYHAYPAHAAFOOCYKOSGLGRETHKMM 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 KPGEYGFPLKLKARPINFIGGEWVAPADGPFYGNITPVTGQLLGFVASGRKDIDLALDA 70
                                                                                                                                                                                                                                                                                                            6 RPGSAGALMSYESRYQNFIGGQWVAPVHGRYFENPTPVTGQPFCEVPRSDAADIDKALDA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 SKALVQESTYERFMEKATIRKVESTKSGNPLDSVTQMGAQVSHGQLETILNYTDIGKKEGA
                                                                                                                                                                                                                                   0; Gaps
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Actinomycetales, Corynebacterineae; Nocardiaceae; Rhodococcus.
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NIBC/21 inclie an indusible eptochrome P 450 system and aldehydo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schoofs G., Compernolle F., Proost P., Vanderleyden J.,
                                                                                               NAD (ADP PART) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                              Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Degradation of the thiocarbamate herbicide EPPC (Sethyl
                                                                                                                                                                                                                                   Indels
                                                                                                                                                          4AB57CB742244451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Greated)
11-NOV-1995 (Rel. 32, Last sequence update)
11-OGT-2001 (Rel. 40, Last amnotation update)
EPTC-inducible aldebyde dehydrosenase (EC 1.2.1.5).
                                                                                                                                                                                                             5 Fred. Nc. 2.2e 127;
65; Mismatches 105;
                                                                                                                                                                                              67.3%; Score 1798; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 505 AA
                    Pfam: PF00171; aldedh: 1.
PROSITE: PS00687; ALDEHYDE_DEHYDE_CLU; 1.
PROSITE: PS00070; ALDEHYDE_DEHYDE_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                 Oxidoreductase; NAD; Complete profeome.
InterPro; IPR002086; Aldehyde_dehydr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                      507 AA; 54574 MW;
                                                                                                                                                                                                                 66.18;
                                                                                                                                                                                                               Best Local Similarity 66.19
Matches 332; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodococcus erythropolis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                 219
263
302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mot. R.;
                                                                                                                   ACT_SITE
ACT_SITE
                                                                                                                                                        SEQUENCE
                                                                                                                                                                                              Query Match
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                                                                                                   NP_BIND
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    REE SETTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 AHAAAPAWGKTSVAEFATTLNKIAFPMEENLESTALAESWINGKPTFETLNADIPLAIDH 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 FRYFASCIRAGEGGISEVDSEIVAYHFHEFLGVVGQIIPWNFFLLMASWKMAPALAAGNG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 VVLKPARLTPLSVLLLMEIVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQQIMQYATQNIIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVCTCP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRALVQESIYERFMERAIRRVESIRSGNPLDSVTQMGAQVSHGQLETII,NYIDIGKKEGA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 DVLTGGRRKIJEGELKDGYFLEPTILFGQNNMRVFQEEJFGPVLAVTTFKTMEEALELAN 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 KPGEYGFPLKLKARYDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDA 70
                                FUNCTION: DEGRADES ALL ALDEHYDES POTENTIALLY GENERATED BY N
BEALKYLATION OF THIOGARAMATES AND MAY ALES PARELICIPATE IN
ETHANOLAMINE METABOLLS MAND FURTHER SSIMILATION OF DESKADATION
PRODUCTS BY THIOCARRAMATE-INDUCED CYTOCHPOME P.4.6.0
CATALYTIC ACTIVITY: An aladbyde + NAD(+) + H(2)0 - an acid + NADH.
INDUCTION: BY EPPC (S-ETHYL DIPROPALICARE)
SIMILARITY: RELONAS TO THE ALOBHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 RPGTADAIMSFQSRYDNWIGNEWVAPVKGQYFENPIPVTGQNFGDVARSTAEDIELALDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 IVLKPAEQTPVSILHLIGIIGDLLPAGVLNIVNGFGVEAGKPLASSPRIKKIAFTGETTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1768.5; DR 1; Length 505;
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00171, aldedh, 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                      IPR002086; Aldehyde_dehydr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  505 AA; 54863 MW;
                                                                                                                                                                                                                                                                                                                                            EMBL; U17129; AAC77472.1; ·..
HSSP; P05091: 1CW3
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hes 331, Conservative
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dehydrogenase.";
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262
301
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ACT_SITE
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PPCT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation-the Burge-an Broin-remains Institute, there are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 VLKPAEQTPASIHYWLSLVADLLDPGVLNVVNGFGVFAGKPLASSPPVAKVAFTGETTTG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 HEAAPGWSPTSVTEBSDITLKIANPMPANLEP!AVAFSWFNGKPVRETLAADIPLATDHF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 QQIMQYATQNITEVTLELGGKSFNIVPADVMDPPDAFPDKALEGFALFAFNGGEVCTGPS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 HKVKDKWAHTSVQDKAAILFKIADKMKQNLELLATAETWONGKPIRETSAADVPLAIDHF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 PGEYGFPLKLKARYDNFIGGEWVAPANGEYYQNLTPVTGQLLGEVASSGKRDIDLALDAA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 PGTEGALVSYQSPYDHFIGGEYVPPARGQYFENPSPVNGDPFIEIAHGTADDVEPALDAA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 PYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFFLLMASWKMAFALAAGUCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 VERPARLIFISVLLLMEIVGDLLFFGVVNVVNGAGGVIGEYLATSKKIAKVAPTGSTEVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- CATALYTI' ACTIVITY. An aldehyde + NAD(+) + H(\lambda)0 = an acid + NADH -1- SIMILAPITY: RELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                             STRAIN-A3(2) / M145;

BELLINE-13-5-41;

Fentley S. D., Chater K., Cerdeno-Tarraga A.-M., Challis G. L.,

Thomson N.R., James K.D., Harris D. E., Quail M.A., Kieser H.,

Thomson N.R., Datemenn A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornshy T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Stabbinowlisch E., Kajandeam M.A., Rulherford K., Rutter S.,

Seeger K., Sannders D., Sharp S., Squares P., Squares S.,

Warren T., Wictzorrek A., Woodward J., Parrell B.G., Parkhill J.,
                                                                                                                                                   Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                 Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; NAD; Complete proteome.

NP_BIND 219 225 NAD (APP PAPT) (RY SIMILAPITY)

ACT_SITE 263 263 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.8%; Score 1760; DB 1;
65.9%; Pred. No. 1.6e-124;
7ative 64; Mismatches 107;
                                                           16-0CT-2001 (Pel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable aldehyde dehydrogenase (RC 1.2.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00171; aldedh; 1.
PROSITE: PS00087; ALDEHYDE_DEHYDR_GLU; 1.
PROSITE: PS00076; ALDEHYDE_DEHYDR_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002086; Aldchyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY
                                           16-00T-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; ALL13210; CAB61586.1; -. HSSP; P05091; 1CW3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      507 AA; 55673 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity 65.99
330; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coelicolor A3(2).",
Nature 417:141:147(2002).
  STANDARD;
                                                                                                                                 SCC1174 OR SCS11A.05
                                                                                                                                                                                                                                                                SEQUENCE FROM N A.
                                                                                                                                                                                                                    NCB1_Tax1D=1902;
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DHAL_STRCO
Q9RJZ6;
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                              312 RALVQESIYERFMERAIRRVESIRSGNPLDSVTÜMGAÜVSHÖLLETILNYIDIGKKEGAD 371
                                                             307 RALVORGVYAEFWEAAVARTELIKPGHPLDTDTMIGAQASNDQLEKILSYLDIGRGEGAK 366
                                                                                                              TQYGLGASVWSRNGNLAYKMGRGIQAGRVWTNCYHAYFAHAAFGGYKQSGIGRETHKMML 491
                                                                                                                                                                           247 RLIMQYASENIKPVTLELGGKSPNIFFEDVWARDDDFRDKALEGFTMFALNGGEVCTCPS 306
                                                                                               372 VLTGGRRKI.LEGELKDGYYLEPTI.LFGONNMRVFQEEIFGPVI.AVTTFKTMEEALELAND 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20406833, PubMed-10552301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D. B.
Ermoitaeva M.D., Vannathevan J., Hass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karaolis D.K.R., Johnson J.A., Bailey C.C., Boedeker E.C., Kaper J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A Vibrio cholerae pathogenicity island associated with epidemic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteobacteria, gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: MAY BE INVOLVED IN V.CHOLERAE VIRULENCE, AS ITS EXPRESSION IS UNDER THE CONTROL OF TOXE, A TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parsot C., Mekalanos J.J.; "Expression of the Vibrio cholerae gene encoding aldehyde dehydrogenase is under control of Toxk, the cholera toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Classical Ogawa 395 / ATCC 39541 / Serotype 01;
MEDLINE=21117025; PubMed-11179381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 95:3134-3139(1998).
                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1991 (Rel 20, fast sequence update)
15-JUN-2002 (Rel 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                          Aldehyde dehydrogenase (EC 1.2.1.3),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN*EL TOR N16961 / Serotype 01;
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=El Tor N16961 / Serotype 01;
                                                                                                                                                                                                                           492 EHYQQTKCLLVSYSDKPLGLF 512
                                                                                                                                                                                                                                            487 EHYQQTKNILCSYSPKKLGFF 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcríptional activator.";
J. Bacteriol, 173:2842-2851(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immun. 69:1947-1952(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91210174; PubMed-1902210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98169509; PubMed-9501228;
                                                                                                                                                                                                                                                                                                                                                       P23240; Q9KTS0;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seventh pandemic strains.
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                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pandemic strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ALDA OR VC0819.
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                                                                                                                                                                                                                                                                                                                                          DHAL_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cholerae.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation has European Bioinformatics institute. There are no restrictions on its use by non-profit this statement as lond a usage by and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ab/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 DRAAILFKIADRMEONLEILATAFTWDNGKPIRFTSAADVPLAIDHFRYFASCIRAQEGG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 ISEVDSETVAYHFHEPLGVVGOTTPWNFPLLMASWKMAPALAAGNCVVLKPARLTTLGSVL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 LLMETVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVGQQIMQYATQN111º 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 VTLELGOKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVCTCPSRALVQESTYERFM 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 FPATPPVESTPSGNPLDSVTGMGAQVSHGGLETTLNVTDTGKKFGADVLTGGPFKLLEGE 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 LKDGYYLEPTILFGONNMRVFQEEIFGPVLAVTTFKTMEEALELANDTQYGLGAGVWSRN 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 LSGGYYIKPTLFFGHNQMHIFQEEIFGPVIAITKFKDEIEALHLANDTVYGLGAGVWTKD 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 YDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDAAHKVKDKWAHTSVQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 YDNY IGGQWMKPHSGEYFSNTSPVNGLVFCRVARSSSQDVELALDAAHNALESWSTTSAV 78
                 CATALYTIC ACTIVITY: An aldehyde + NAb(+) + H(2)O - an acid + NAbH.
PATHWAY: Ethanol utilization; second step.
SIMILARITY: BELONGS TO THE ALLEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 FLMELIGDLIPAGVINVVNGFGSFAGNALATSQRIDKLAFTGSTFLIGNHILKCAADNLIP
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ACTIVATOR OF SEVERAL GENES ASSOCIATED WITH VIRULENME.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69E7F561D6CFED07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.9%; Score 1682; DB 1; 63.3%; Pred, No. 1.1e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                519 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_CLU; 1.
                                                                                                                                                                                                                                                                                                or send an email to licensedishesib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase, NAD; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                 EMBL; M60658; AAA03051.1; -.
EMBL; AT034434; AAC12273.1; -.
EMBL; AF125733; AAK20747.1; -.
EMBL; AG04167; AAK3982.1; ALT_INIT.
HSSP; P05091; ICW3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR002086; Aldehyde_dehydr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00171; aldedh;
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262
301
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42 EINNEWHDAVSEKIEFTVNPSTGEVICOVAEGNKEDVDKAVKAAPAAFOLGSPWPRMDAS 101

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FER-1996 (Pel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogensse, mitochendrial previous (ET 1.2 1.3) (ALUH class 2) (AHD-M1) (ALDH1) (ALDH-E2).
ALDH2 OE AHD1 OP AHF-1
                                                                                                      Eukaryota, Metazoa, Chordutu, Cianiutu, Vertebrutu, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase, NAD; Acetylation; Mitochondrion; Transit peptide.
TRANSIT 1 19 MITOCHONDELON (FY SIMILARITY).
CHAIN 20 519 ALDEHYDE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                               PATHWAY. Ethanol utilization, second step.
SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLUIAR LOCATION MITCORDONATION MITCORDONATION.
INDUCTION: By Tection's acid; 3-5 fold increase.
SIMILARITY: RELOWIS TO THE ALMEHYDE DEHYDROGENASES FAMILY.
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BY SIMILARITY.
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                                                                                                                                                                                                                  "Cloning and characterization of the gene encoding mouse mitochondrial aldehyde dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200806P63048F40A CRO54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACETYLATION (PROBABLE)
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AF -> C (IN PEF 2)

MISSING (IN REF. 2).
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S \rightarrow M \text{ (IN REF. 2)}.

D \rightarrow V \text{ (IN REF. 2)}.
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-> G (IN REF. 2).
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PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002086; Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                      MEDLINE=94335908; PubMed=8058062;
                                                                                                                                                                                       MEDLINE=95047445; PubMed=7958964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56537 MW;
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MGD; MGI:99600, ALHE
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181
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                                                                                                                                                                                                       Chang C., Yoshida A.;
                                                                                              (Mouse)
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                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                   NOBI_TaxID=10090;
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321 EPFMERAJPPVESIRSGNPLDSVTQMGAQVSHGQLETILNYIDJGKKEGAPVLTGGRRKL 380
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                                                                                                                                                                                                                                                                                                                                                                                             34] --GAAADPGYFLOPIV-FGDVKLØMIIAKEEIFGPVMOILKFKTIEEVVGFANDSKYGLA 447
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                    263 IPVILELGGKSPNIVFADVMDEEDAFFDKALE--GFALFAFNQGEVCTCPSRALVQESIY 320
                                                                                                                                                                                                                                                282 KRVTLELGGKSPNIIMS------DADMEWAVEDAHFALF-FNOGODOGAGSFIFVOENVY 334
95 DPAAILEKIADPMEQNLEILATAETWDNOKPIPETSAADVDIAIDHEBYFASCIPAGEOS 144
                                                                                                                                                                            222 YVANLIKEAGFPFGVVNIVFGFGFTAGAAIASHEGVEKVAFTGSFEVEHLIQVAAGSSNL
                                                                      145 ISEVDSETVAYHEHEFLGVVGQIILEWNFFLLMASWKMAPALAAGNCVVLKFAFLEFLSVL
                                                                                         205 LEMELVGDL-LPPGVVNVVNGAGGVTGBYLATSKRTARVAPTGSTBVGQQIMQYA-TQNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jeng J., Weiner H.;
"Purification and characterization of catalytically active precursor
of rat liver mitochondrial aldehyde dehydrogenase expressed in
Escherichia culi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotu, Metusuaj Chordata, Craciata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Podentia, Sciurognathi, Muridae, Murinae, Pattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parres J , Guan K -L , Weiner H.; "Sequence of the signal peptide for lat liver mitochondrial widehyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-00T-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase, mitochondrial precursor (RC 1 2 1.3) (ALDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-892[0855; PubMcd-2549003;
Parres J., Guan K.-L., Weiner H.;
"Primary structures of rat and bovine liver mitochondrial aldehyde
dehydrogenases deduced from cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys Pos Commun 150 1083-1087(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley; TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biochem. 180.67-74(1989).
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12, Last sequ
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SEQUENCE OF 1-29 FROM N.A.
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01-00T-1989
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10;

24; Gaps

86, Mismatches 171, Indels

209; Conservative

Matches

Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 DRGRLLYRLADLIERDRTYLAALETLDNGKPYVISYLVDLUMVLKCLRYYAGWADKYHGK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 ISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGNCVVLKPARLTPLSVL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 TIPIDGDFESYTKHEPVGVOGQIIPWNFPLLMQAWKLGPALATGNVVVMKVAEQTPLTAL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 YVANLIKEAGFFFGVVNIVFGFGFTAGAAIASHEDVDKVAFTGSTFVGHLIQVAAGSSNL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 IPVTLELGGKSPNIVFADVMDEEDAFFDKALE--GFALFAFNQGEVCTCPSRALVQESIY 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 LEGELKO-GYYLEPTILEG--QNNMRVFQEEIFGPVLAVTTFKTMEEALELANDTQYGLG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 --GAAADRGYFIQPTV-FGDVKDGMTIAKEEIFGPVMQILKFKTIEEVVGRANNSKYGIA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 AGVWSRNGNLAYKMGPGIQAGPVWTNCYHAYPAHAAFGGYKQSGIGRETHKMMLEHYQQT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 F1GGEWVAPADGEYYONLTPVTGQLLCEVASSGKRDIDLAL---DAAHKVKDKWAHTSVQ 84
Arch Riochem, Riophys. 289:214-222(1991).
-i- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; NAD; Acetylation; Mitochondrion; Transit peptide.
                                                                                                   -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 975; DB 1; Length 519;
; Pred. No. 1.2e-65;
86; Mismatches 172; Indels :
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BY SIMILARITY.

75C748202F1333E5 CRC64;
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                                                                                SHBCELLHLAR LOCATION: Mitochondrial matrix
                                        PATHWAY: Ethanol utilization; second step. SUBUNIT: HOMOTETRAMER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Pram: PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GIU; 1.
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MEDLINE:88256152; PubMed:2848413;
Hsu L.C., Bendel R.E., Yoshida A.;
"Genomic structure of the human mitochondrial aldehyde dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Braun T., Buber E., Singh S., Agarwal D.P., Goedde H.W.; "Isolation and sequence analysis of a full length cDNA clone coding for human mitochondrial aldehyde dehydrogenase.";
                      p05091; 003639;
13-ANG-1987 (Rel. 05, Created)
11-JAN-1990 (Rel. 13, Last sequence update)
15-JIN-2002 (Pel. 41 last annotation update)
Aldehyde dehydrogenae, mitochondrial precursor (EC 1.2.1.3) (ALDH
class 2) (ALDHI) (ALDH-E2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Braun T., Bober E., Singh S., Adarwal D.P., Goedde H.W.: "Evidence for a signal peptide at the amino terminal end of human mitochondrial aldehyde dehydrogenase.";
                                                                                                                                                                                                                                   Hómo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Enteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hempel J., Kaiser R., Joernvall H.;
"Mitochodrial aldebyde dehydrogenase from human liver. Primary
stracture, differences in relation to the cytosolic enzyme, and
functional correlations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hsu L.C., Tani K., Fullyoshi T., Kurachi K., Yoshida A.; "Cloning of cDNAs for human aldehyde dehydrouenases I and 2."; Proc. Natl. Acad. Sci. U.S.A. 82:8771-8775(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular abnormality and conn cloning of human aldehyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Braun T., Bober E., Singh S., Agarwal D.P., Goedde H.W.;
FERS Lett. 233:440-440(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-2001) to the EMBL/GerBank/DDBJ databases.
517 AA
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Yoshida A., Ikawa M., Hsu L.C., Tani K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 15:3179-3179(1987)
PRT;
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MEDLINE=87219091; PubMed=3582651;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE 87174836, PubMed=3562250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eur. J. Biochem. 153:13-28(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 215:233-236(1987).
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Senomics 2:57-65(1988).
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                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver;
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DHAM_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tene.
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                                  NA KARANA KARANA KANDANINA ```

SEQUENCE OF 214-500 FROM N.A.

EMBL, YOR199, CA468290 1; -.
EMBL, BCGC2957, AAH679671; -.
EMBL, KOROOT, AAR59500 1; -.
EMBL, MA-7500, AAA516941, -.
EMBL, MA-9501, AAA516941, -.

Genew; HGNC:404; ALDH2. MIM; 100650; -.

PDB; 1CW3; 10-JAN-00. EMBL, ME4931, AAACLET PIR, SOORO4; DRHUE2.

A29975; A29975

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   SINGLE ARID WALD EACHANGS.

SINGLE AND WALD THE ALDEHYDE DEHYDROGENASES FAMILY.

CAUTION: THE CONFLICTS BETWEEN THE SEQUENCE DETERMINED IN FEF.1

CAUTION: THE CONFLICTS BETWEEN THE SEQUENCE DETERMINED IN FEF.1

FRAMESHIET OF SEQUENCING REPORTS AS DESCRIBED IN FEF.5

THE SEQUENCE DESCRIBED IN REF.9 LIFFERS FROM THAT SHOWN DIE TO TWO
   Hempel J., Hoeoeg J.-O., Joernvall H., "Mitochondrial aldehyde dehydrogenase. Homology of putative targeting sequence to that of carbamyl phosphate synthetase I revealed by Correlation of CDNA and protein data."; FEBS Lett 222:95-08(1987)
  CATALYTIC ACTIVITY: A aldehyde + NAb(+) + H(Z)O = an acid + NAbH. PATHWAY: Ethanol utilization; second step.
SUBUNIT: HOMOTETPAMER
  Yoshida A., Huang I.-Y., Ikawa M.; "Molecular abnormality of an inactive aldehyde dehydrogenase variant commonly found in Orientals ";
   Vi L , Zhon T , Hurley T D , Weiner H ;
Human liver mitochondrial aldehyde dehydrogenase  three-dimensional
   structure and the restoration of solubility and activity of chimerio
   ORTENTALS AND SOUTH AMERICAN INDIANS, AS COMPAPED TO CAUCASIANS, CAN BE DIPECTLY ATTRIBUTED TO AN ENZYMATICALLY IMPAIRED ALDH ISOZYME. THE INACTIVE VARIANT (ALLELE 2 OR ALDH2*2) IS DUE TO
  SHRCELLUJAR LOCATION: Mitochondrial matrix.
DISEASE: A VERY HIGH INCIDENCE OF ACUFE ALCOHOL INFOXICATION IN
  DESCRIPTION OF ORIGIN OF CONFLICTS BETWEEN REF.Z AND INA SEQUENCES
   Agarwal D P , Goedde H.W ;
"Human aldehyde debydrogenase is aymos and ulcohol scusitivity.",
Isorymos Curr Top Biol. Mod Ros Proledk(1987)
  "Mitochondrial aidehyde dehydrouenase polymerphism in Asian and American Indian populations: detection of new ALDH2 alleles."; Alcohol. Clin. Exp. Res. 19-1105-1110(1995)
  Novoradovsky A., Tsai S.J., Goldfarb I., Peterson P., Long J.C.
   Natl. Acad Sci. H.S.A. 81:258-261(1984)
  X-RAY CRYSTALLOGRAFHY (2.58 ANGSTROMS)
   MEDLINE=20095857; PubMed=10641996;
   MEDLINE=84119449; PubMed=6582480;
MEDLINE=87279033, PubMed-3610592,
  MEDLINE-88005159; PubMed=3653404;
  MEDLINE=96119362; PubMed=8561277;
   SINGLE AMINO ACID EXCHANGE.
   Protein Sci. 8:2784-2790(1999).
   FRAMESHIFTS.
  VARIANT LYS-504
  VARIANT LYS-496
   Goldman D.;
   forms ";
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10:
   263 - IEVTLELDTKSPNIVFALVMIGERAFFIFAI E - 1971 FAFNZTEVTI TESPALVQESTY - 300
   0 H ×
   333 DEFVERSVARAKSRVVGNPFDSKI EDGPLVDETDFRKI LIGY INTGROEGAKLLDGG---- 388
  381 LEGELKD-GYYLFPTILFG--ONNMHVPQEFIFGPVLAVTTFRTMEEALELANDTQYGLG 437
   89 --GIAADRGYFIQPTV-FGDVQDGMTIAKERIFGDVMQILKFKTIEEVVGRANNSTYGLA 445
   438 AGVWSRNGNLAYKMGPGIQAGPVWTNCYHAYPAHAAFGGYKQSGIGPETHKMMLEHYQQT 497
   85 EPAATLEKTADEMEDNIELLATAETWINGKPIPETSAADVPLAIDHEPYFASCIPAQEGG 144
   145 ISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGNCVVLKPARI.TPLSVL 204
  28 FIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDAAH----KVKDKWAHTSVQ 84
  40 FINNEWHDAVSPKTFPTVNPSFGEVICQVAFGDKEDVDKAVKAAPAAFQLGSPWPRMDAS 99
  · AWPAWAPPLVSRFHFGR
   205 LLMEIVSEL-LEFSVVNVNBASSVISEYLAISKETAKVAFIGSIEVSSJMEYA-TERI
   3.21. EREMEPATREVESTRSSNPLICSVTGMGAGVSHGGLETTLINYTFFGRKEGALVLFGGEPRE
   84; Mismatches 173; Indels 24; Gaps
  E\to K (IN ALSH2*2; DRASTIC REDUCTION OF BNZYME ACTIVITY).
  Oxidoreductase; NAD; Mitochondrion; Transit peptide; Polymorphism;
   S -> A (IN RÉF. 2).
VKAAPA -> PPCPPG (IN PEP. 3 AND 4).
   ALDEHYDE DEHYDROGENASE.
NAD (ADP PART) (BY SIMILARITY).
   Score 971; DB 1; Length 517; Prod No 2 4e-65;
  /FTId-VAR_002248.
PFGPPL -> ARAPP (IN REF. 5)
  -> V (IN DBSNP:1062136).
   E8F74D44D285A00E CRC64;
  KESTERLOFF LUSAAATOAVE
  E -> K (IN ALDH2*3).
/FTId=VAR_011302.
   A -> P (IN REF. 9).
E -> Q (IN REF. 1).
AL -> SP (IN REF. 9)
   -> S (1N REF. 9).
   /FTId=VAR_011869.
   MITOCHONDPION
  A (IN REF. 3)
S -> A (IN RE
  Pfam: PF00171; aldedh: 1.
FF0SIIE: FS00670; ALDEHYDE_DEHYDP_CYS: 1.
PROSIIE: PS00687; ALDEHYDE_DEHYDR_GLU: 1.
  InterPro; IPR002086; Aldehyde_dehydr.
  م
د -
   56381 MW;
   36.38;
   Matches 209; Conservative
  18
85
216
218
247
  285
   496
  £ 0.4
   216
218
247
380
462
4
   Similarity
   18
262
285
   319
   496
  504
   3D-structure.
  NF_BIND
ACT_SITE
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AAA51693.1; JOTNED. AAA51693.1; JOTNED. AAA51693.1; JOTNED. AAA51693.1; JOTNED. CAA28990.1.

M20453;

M20454; X05409

AAA51693.1; JOINED.

M20450;

AAA51693 1;

AAA51693.1; JOINED AAA51693.1; JOINED

AAA51693 1; JOINED. AAA51693 1; JOINED AAA51693.1; JOINED.

M20445; M20446; M20447: M20448; M20449;

EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL;

EMBL, M20456; AAA51633 1.

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   24; Caps 10;
85 DRAAILFKIADRMEQNLELLATAETWDNGKPIRETSAADVPLAIDHFRYFASCIRAQEGG 144
   205 LIAMETVGDL-LPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEVGQQIMQYA-TQNT 262
   203 YVANI.IKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVAFTGSTEVGHLIQVAAGSSNI, 262
  263 IPVTLELGGKSPNIVFADVMDEEDAFFDKALE--GFALFAFNQGEVGTGPSRALVQESIY 320
  145 ISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGNCVVIKPARITPLSVL 204
   23 FINNEWHDAVSKKTFPTVNPSTGEVICQVAEGSKEDVDKAVKAARAAFQLGSPWRRMDAS 82
   28 FIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDAAH---KVKDKWAHTSVQ
  15-JUL-1998 (Ref. 36, Last sequence update)
15-JUN-2002 (Ref. 41, Last annotation update)
Aldehyde dehydrogenase, mitochondrial (EC 1.2.1.3) (ALDH class 2)
  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Rodentia, Sciuroguathi; Muridar; Crietinar;
Mesocricetus.
   Hjelmqvist L., Lundgren R., Norin A., Joernvall H., Vallee B., Klyosov A., Keung W.M.; "Class 2 aldehyde dehydrogenase. Characterization of the hamster enzyme, sensitive to daidzin and conserved within the family of multiple forms.";
  -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
  NAD (ADP PART) (BY SIMILARITY).
   36.2%; Score 968; DB 1; Length 500; Best Local Similarity 42.2%; Pred. No. 3. 96-65; Matches 207; Conservative ac......
  8B81886AB04F493F CRC64;
  500 AA.
   BY SIMILARITY.
BY SIMILARITY.
  PROSITE; PS00687, ALUMHYDE_DEHYDR_GLU; 1.
PROSITE; PS00070, ALUMHYDE_DEHYDR_CYS; 1.
OXidooreductase; NAD; Mitochondrion.
NP_BIND 245 250
NP_BIND (ADP PAR
   Mesocricetus auratus (Golden hamster).
  IPR002086; Aldehyde_dehydr.
  PPT;
  MEDLINE=98034175; Pubmed=9369242;
  15-JUL-1998 (Rel. 36, Created)
   500 AA; 54334 MW;
  STANDARD;
  Pfam; PF00171; aldedh; 1
   498 KCLLVSYSDK 507
   506 KTVTVKVPQK 515
  268
   HSSP; P05091; 1CW3
   (ALDH1) (ALDH-E2).
   NCB1_TaxID=10036;
   268
302
  TISSUE=Liver;
   DHAM_MESAU
   interPro;
  SECUENCE
  ACT_SITE
  ACT_SITE
  SEQUENCE
   DHAM MESAU
   ALDH2
   RESULT 12
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   q
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   Q
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421 ERFMERATRRVESTRSGNPTDSVTgMGAgVSHGGLETTINYTFFFGKREGAFVLFGGREKT, 480
  881 LEGBELKD-GYYLEPTILFG--QNNMRVFQEBIFGPVLAVTTFKTMBEALELANDTQYGLK3-4-(7)
   438 AGVWSRNGNLAYKMGRGTQAGRVWTNCYHAYPAHAAFGGGRGGGGGGRETHKMMLEHYOOT 497
   an acid + NADH
   01-FEB-1991 (Rel. 17, Created)
17-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldebyde debydrogenase, mitochondrial precursor (EC 1.2.1.3) (ALDH
class 2) (ALDHI) (ALDH-E2).
   "Primary structures of rat and bovine liver mitochondrial aldehyde dehydrogenases deduced from cDNA sequences.";
                             316 DEFVERSVARAKSRVVCNPFDSRTFQGPQVDFTQFKKILAYIKSAQQFCAKLLAGG
  Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Hovoldea;
  "Sequence of the precursor of bovine liver mitochandrial aldehyde dehydroqenase as determined from its cDNA, its quie, and its
  Oxidoreductase; NAD; Mitochondrion; Transit peptide; 0 structure. TEANSIT 1 21 MITOCHONDRION.
  MEGLINE 97341232; PubMed-9195888;
Steinmetz C.G., Xie P., Weiner H., Hurley 1.D.;
"Structure of mitochondrial aldebyde debydrogenase: the genetic
   SUBCELLULAR LOCATION: Mitochondrial matrix.
SUBCARTION: Mitochondrial matrix.
SUBLARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
SUBSES. SUBSES.
SUBSES. SUBSES.
   ALDEHYDE DEHYDROGENASE, NAD (ADP PART) (BY SIMILARITY).
   CATALITIC ACTIVITY: An aldebyde + NAD(+) + H(2)0
  PATHWAY: Ethanol utilization; second step. SUBUNIT: HOMOTETRAMER.
  520 AA.
  BY SIMILARITY.
  Arch. Biochem. Biophys. 277:351-360(1990).
  PROSTTE: PSGU070; ALDEHYDE_DEHYDE_CYS; 1.
PROSTTE; PSGU687; ALDEHYDE_DEHYDE_GLU; 1.
  X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS).
   FDB, 1A42; 08-APR-98.
InterPro; IPR002086; Aldehyde_dehydr.
  PRT;
  MEDLINE-89210865; PubMed-2540003;
Farres J., Guan K.L., Weiner H.;
  MEDLINE: 90179198; PubMed=1689984;
  Eur. J. Hiochem. 180:67-74(1989).
  component of ethanol aversion.";
Structure 5:701-711(1997).
   SEQUENCE OF 92-520 FROM N.A.
  STANDARD;
   498 KCLLVSYSDK 507
   489 KTVTIKVPOK 498
  Pfam; PF00171; aldedh;
   520
270
288
   Bovidae; Bovinae; Bos.
  PDB; 1AG8; 08-OCT-97.
   Bos taurus (Bovine).
   Suan K., Weiner H.;
   SEQUENCE FROM N.A.
  NCBI_TaxID-9913;
   25
265
288
   functionality.
  TISSUE=Liver;
  DHAM_BOVIN
  NP_BIND
ACT_SITE
   DHAM_BOVIN
  ALDH2
   CHAIN
  RESULT 13
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43 FINNEWHDAVSKKTFPTVNPSTGDVICHVAEGDKADVDRAVKAARAAFQLGSPWRRMDAS 102
  145 ISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGNCVVLKPARLTPL,SVL 204
  163 TIPIDGOYESYTPHEPVGVGGGIIPWNFPLLMQAWKLGPALATGNVVVMKVAEQTPLTAL 222
  205 LLMEIVGDL-EPPGVVNVVNBAGGVIGEYLATSKRIAKVAFTGSTEVGQQIMQYA-TQNI 26.2
  263 IFVILELGGKSPNIVFADVMDREFAFFFKALE--GFALFAFNQGEVATAPSPALVQESIY 320
   3.2. ERFMERAIRPVESIPSGNPLDSVTQMGAQVSHGQLETILNYIFTGKKFGADVLLGGPFKL, 380
  336 AEFVERSVARAKSPVVGNPFDSRTEMGPQVI BITGFKKVLISY IKSGKEBILKLLIGGT---- 391
   381 LEGELKD-GYYLEPTILFG--QNNMRVFQEEIFGPVLAVTTFKTMEEALELANDTQYGLG 437
   438 AGVWSRNGNI.AYKMGRGIQAGRVWTNCYHAYPAHAAFRGYKQSGIGPETHKMMLEHYQQT 497
  85 DRAAILFKIADRMEQNLELLATAETWDNGKPIRETSAADVPLAIDHFPYFASCIFAQESG 144
  28 FIGGEWVAPADGEYYQNLTPVTGQLL"EVASSGKPOLOLALDAAH----KVKDKWAHTSVQ 84
   223 YVANLIKEAGFPPGVVNVIPGFGPTAGAAÍASHEDVEKVAFTGSTFVGHLIQVAAGKSNI.
   an acid + NADH
  24; Galys
   "Mitochondrial aldehyde dehydrogenase from horse liver Correlations of the same species variants for both the cytosolic and the mitochondrial forms of an ontyme ";
   Equus caballus (Horse).
Eukaryota, Metazoa, Chordata, Cianiata, Veitebrata; Euteleostomi;
Mammalia, Eutheria; Perissodactyka; Equidae, Equus.
NCBL_TaxiD=9796,
   01-0c1-1989 (Rel. 12, Created)
01-0c1-1989 (Rel. 12, Last sequence update)
15-JW1-2002 (Rel. 41, Last unnotation update)
Aidehyde dehydrogenase, mitochondrial (EC 1.2.1.3) (ALDH class (ALDHI) (ALDH-E2).
   -!- SUBCELLUIAR LOCATION: Mitochondrial matrix.
  Johansson J., von Bahr-Lindstrom H., Jeck P., Weenekhaus P.,
Joernvall H.;
   Length 520;
  81, Mismatches 178, indels
   Eur T Ricchem, 172-527-533(1988).
-!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0
                56708 MW; P920BCPC05B5AB5B CRC64;
   Score 953, DB 1,
Pred. No. 5.4e-64;
  PATHWAY: Ethanol utilization; second step. SUKUNIT: HOMOIETRAMER.
  500 AA
BY SIMILARITY
   ΡkT;
   MEDLINE=88166730; PubMed=3350012;
   35.78,
42.28,
  Best Local Similarity 42.29
Matches 207; Conservative
  STANDARD;
  498 KCLLVSYSDK 507
   509 KTVTVRVPQK 518
  PIR; S00364; S00364.
                520 AA
  mitochondrial
  DHAM_HORSE
                SEQUENCE
   Query Match
   SEQUENCE
  RESULT 14
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   3.20
   85 DRAALCPKIADPMEGNIELLATAFTWDNGKPIPETSAANVPIA (THEPYPAS?TPAQESG 144
  34 DECELLINELARILIERRETYLAALETLINGKEVVISYLVILIMULYLLEYYA:WALKYBCK 142
  145 ISEVDSETVAYHFHEPLGVVGQ11PWNFPLLMASWKMAPALAAGNCVVLKPAKLTPLSVL 204
  263 KKVTLELGGKSPNIIVS-----DADMDWAVEQAHFALF-FNQGQCCGAGSRTFVQEDVY 315
  3.21 EREMEPATPPVESTPSGNPLDSVTQM3AQVSH3QLETILNYTHIGKKEGADVLF3GPPKL 380
   116 AEFVERSVARAKSRVVGNPFDSQTFDSPQFDVDFTQFNKVJ.GYTKSGKFFSAKLLCGG---- 371
   381 LEGELKD-GYYLEPTILFG--QNNMRVFQEEIFGPVLAVTTFKTMEEALELANDTQYGLG 437
   438 AGVWSRNGNIAYKMCRGIQAGRVWINCYHAYPAHAAPGGYKQSGIGREIHKMMIEHYQQI 497
  23 FINNEWHDAVSKRTEFTVNESTGEVICQVAACDREDVDFAVRAAFAAFGLGSFWFEMDAS 82
   28 FIGGEWVAFADGEYYQNLIEVIGQLLCEVASSGKRDIDLALDAAH ····KVKDKWAHTSVQ 84
  P46357, U08898;
(1-NV-1995 (Pel. 32, Created)
16-OCT-2001 (Pel. 40, Last annotation update)
Potassium-activated aldohyde dehydrogenase, mitochondrial procursor
(Br 1 2 1 3) (K(+)-activated acetalehyde dehyde dehydrogenase) (K(+)-ACDH).
Aluk ur ALD? ur ALUH our YUKA74W up 06730.
   205 LLMFTVGDL-LPP3VVNVVN3AGGVTGEYLATSKRIAKVAFTGSTEV0QQ1MQXA-TQNI
   203 YVANLTKEAGFPFGVVNVVPGFGPTAGAAIASHEDVDKVAFTGSTEVGHLIQVAAGRSNL
   263 IPVTEBEGGKSPNIVFADVMDBEDAFFDKALE--GFALFAFNUGEVCTOPSRALVQBSIY
  24; Gaps
   Eukarjota, Fungi, Ascongcola, Saccharomýcotina, Saccharomycetes;
Saccharomycetales; Saccharomycetuceae, Saccharomyces.
   NAD (ADP PART) (BY SIMILARITY).
  Length 500;
  ; Score 952; DB 1; Length 50; Pred. No. 6.1e-64; 81; Mismatches 177; Indels
  SEQUENCE FROM N.A. Delius H., Hofmann B.; Submitted (JUL-1995) to the EMBL/SenBank/DUBJ databases.
  7895364A73383B24 CRC64;
   519 AA
   BY SIMILARITY
BY SIMILARITY
                            Pfam, PF00171; aldedh; 1.
PROSLIE; PSOOO70; ALDEHYDE_DEHYDE_CYS; 1.
PROSLIE; PSOO687; ALDEHYDE_DEHYDE_CLU; 1.
          interproj IPPRO2086; Aldebyde_dobydr.
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   A -> L.
   OXIGOTE-dust dset, NAP, Mitochondrion NP_BIND 245 250 NAD (A ACT_SITE 268 268 BY SIM
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   54166 MW;
  35.68;
  42.48;
  208; Conservative
   STANDARD
  498 KCLLVSYSDK 507
  489 KTVTIKVPQK 498
   305
  500 AA;
HSSF, P05091, 1CW3.
  Similarity
   302
   NCBI_TaxID=4932;
   LHA4_YEAST
   NP_BIND
ACT_SITE
ACT_SITE
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  Query Match
   VARIANT
   VARIANT
   DHA4_YEAST
  Matches
   RESULT 15
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib ch/announce) or send an email to license@isb-sib.ch).
  211 TVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVGEAITHHPRIKKVAFTGST 270
   72 HKV--KDKWAHTSVQDRAAILFKIADRMEQNLELLATAETWDNGKPIRETSAADVPLAID 129
   92 DRAFSNGSWNGIDPIDRGKALYRLAELIEQDKDVIASIETLDNGKAI-SSSRGDVDLVIN 150
  190 CVVLKPARLTPLSVIJIMETVGDI-IPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGST 248
   30 HFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGN 189
  18 PLKLK--ARYDN----FIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDAA 71
  Tessier W D , Meaden P G , Dickinson F.M , Midgley M.; "Identification and distuption of the gene encoding the K(+)-activated aretaldehyde dehydrogenase of Saccharomyces cerevisiae.";
                                  Chalmers R.M., Keen J.N., Fewson C.A.;
"Comparison of benzyl alcohol dehydrogenases and benzaidehyde
dehydrogenases from the benzyl alcohol and mandelate pathways in
Acinetobacter calcoaceticus and from the TOL-plasmid-encoded toluene
pathway in Pseudomonas putida. N-terminal amino acid sequences, amino
acid compositions and immunological cross-reactions.";
   + NAD(+) + H(2)O = an acid + NADH.
  Identification of two dimensional gel electrophoresis resolved yeast
  32 PIKLPNGLEYEQPTGLFINNKFVPSKONKTFEVINPSTEEEICHIYEGREDDVFFAVQAA
   Gaps
  Larsson T., Norbeck J., Karlsson H., Karlsson K.-A., Blomberg A.;
   -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
  proteins by matrix-assisted laser desorption ionization mass
   35.2%; Score 940.5; DB 1, Length 519, 41.4%; Pred. No. 4.7e-63;
   NAD (ADP PART) (BY SIMILARITY).
   POTASSIUM-ACTIVATED ALDEHYDE
   Indels
  E7D9944EA25F948E CRC64;
   Oxidoreductase; NAD; Mitochondrion; Transit peptide.
TRANSIT 1 24 MITOCHONDRION.
  N -> NN (IN REF. 2).
E -> V (IN REF. 2).
   177;
   88; Mismatches
   DEHYDROGENASE
  PROSITE; PSOU070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PSOU0687; ALDEHYDE_DEHYDR_GLU; 1.
   PARTIAL SEQUENCE, AND CHARACTERIZATION.
  POTENTIAL.
  POTENTIAL
  Lett. 164:29-34(1998).
  IPPÓ02086; Aldehyde_dehydr.
   CATALYTIC ACTIVITY: An aldehyde
                  MEDILINE=91113163; PubMed=1989592;
  PubMed 9150920,
   Electrophoresis 18:418-423(1997)
  PubMed = 9675847
  SEQUENCE OF 25-34 AND 378-386.
  56723 MW;
   EMBL; 275282; CAA99705.1; -.
   41.48;
   Conservative
  Pfam; PF00171; aldedh; 1
   519
   SGD; S0005901; ALD4.
  519 AA;
   1CW3
   Local Similarity
es 205; Conserv
  MEDLINE=97295278;
  MEDLINE=98340498,
  FEMS Microbiol.
   P05091:
  ACT_SITE
ACT_SITE
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   Query Match
  CONFLICT
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FIAELKKAVONI ITSTYYNSGEVC 3.24
  308 TOPSRALVOESTYERFMERATHRVESTRSGNPLDSVTOMGAGVSHGOLFTILNYTFFGRK 367
  325 CAGSEVYVEESTYDKFTLEFKAASESTKVGDPFDESTFGGAGTSGMGTNKTTRYVDTGKN 384
   368 EGADVLTGGRRKLLEGELKDGYYLEPTTLPG QNNMRVFQEFTFGPVLAVTTFKTMEEA 425
   GSERTYFIARIV FRANKLIMETVERFIRMFVVIVIAREKSADEV 438
  4.26 LELANDFOYGLAJAGVWSKNGNLAYKMGKGTQAGKVWTNCYHAYPAHAAFGGYKQSGTGRE 445
  249 EVGQQIMQYATQNIIPVILELGGKSPNIVFADVMDEEDAFFDKALEGFAL FAFNQGEVC
  Search completed: June 24, 2003, 10:14:31
   486 THKMMLEHYOOTKCL 500
   499 MSVDALQNYLQVKAV 513
   385 BEATLITGGEFT.
  Job time : 12.3122 secs
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GenCore version 5.1 \kappa Copyright (c) 1993 - 2003 - compagen and
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OM profein - protein search, using sw model

June 24, 2003, 10:08-15; Search time 39 1863 Seconds (without alignments) 2692.168 Million cell updates/sec Run on:

115-09-830-751-8 Title.

HYQQTROLLUSYSDKPIDILE 512 1 MTNNPPSAQIKPGEYGFPLK... Perfect soore Sednence.

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

671580 seqs, 205047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length. 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100% Listing first 45 summaries

SPTREMBL\_21:\* Database :

sp\_unclassified.\* sp\_human:\*
sp\_invertebrate:\* sp\_vertebrate:\* sp\_rvilus:\*
sp\_bacteriap:\* sp\_organelle:\* sp\_phage:\* sp\_archea:\*
sp\_bacteria:\* sp\_plant:\* sp\_rodent:\* sp\_mammal:\* sp\_virus:\* sp\_fungi:\* sp\_mhc:\* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

#### SUMMARIES

|   | Dogariation              | norodinsea | 1 C8xd)1 escherichia |         | 365280 | 592n70   |        | 98860  | 08uda3 | 0      |        |        | Q9fds1 |        |        | 5 pseudomonas |        | 4 PSCHOMONAS |
|---|--------------------------|------------|----------------------|---------|--------|----------|--------|--------|--------|--------|--------|--------|--------|--------|--------|---------------|--------|--------------|
|   | E                        |            | CRXDJ                | QRZ1.72 | O87.25 | CASAS    | Q9A2T1 | 908800 | ORUDA  | 050203 | Q9KF16 | 816260 | Q9FDS1 | 902050 | ORYEYO | Q9HX05        | Q9KR28 | 041204       |
|   | a                        | :          | 3                    | 16      | 16     | <u>.</u> | 16     | 16     | 1      | C1     | 16     | C1     | 71     | C-4    | 16     | 16            | 16     | <u></u>      |
|   | Query<br>Match Length DR | 110 6110   | 543                  | 512     | F12    | 205      | 505    | 505    | 540    | 505    | 206    | 206    | 503    | ėÚ's   | 7.05   | 905           | 506    | 506          |
| æ | Query                    |            | 99.2                 | 47 3    | ৬ ৬৮   | 6 CL     | 71.8   | 71.3   | 70.4   | 70 3   | 70.3   | 70.0   | 69.5   | 69     | 69.2   | 67.4          | 0.79   | 67 û         |
|   | S. O.S.                  |            | 2651                 | 1097    | 2589   | 1948     | 1918   | 1905   | 1895   | 1879   | 1878   | 1870   | 1850.5 | 1850.5 | 1848 5 | 1802          | 1791   | 1791         |
|   | Result                   |            | 1                    | CI      | 3      | 4        | S      | 9      | 7      | 8      | 6      | 10     | 11     | 12     | 13     | 14            | 15     | 16           |

| Ogzaal pseudomonas<br>1948:02 arotobacter<br>1959:09 alteromonas<br>1939:42 halomonas<br>1980:08 ralstonia s | กูจงสุดริ yersinia ps<br>มูจจลสุด yersinia ps<br>มูจงสุด yersinia ps<br>บดิเชต์ริ fusobacteri | ogyvaką staphylogoc<br>Cyxyge sphingomona<br>Qarks bacillus st<br>UPKCC hacillus ha<br>OytxmO caenorhabdi | 085973 sphingomona<br>Q9wxh6 aloaligenes<br>C34666 bacillus su<br>Q9398 sphingomona<br>O14293 schingomona | 094je6 oryza sativ<br>Q20780 caenorhabdi<br>Q8x014 neurospora<br>G81gq2 brachydanio<br>Q90y03 brachydanio | Q8525 25a mays (m<br>Q869q1 brachydanio<br>Q40xsB brachydanio<br>Q9cxsl mus musculu<br>Q9v1c5 drosophila       |
|--------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------|
| 2 092AA1<br>2 094KH07<br>7 650A04<br>2 093042<br>16 08XU08                                                   | 2 093AP3<br>2 09AG19<br>2 093AC1<br>16 08RG63                                                 | 18 094X54<br>2 09X908<br>2 09KFUS<br>16 09KFUS<br>5 09TXM0                                                |                                                                                                           | 20                                                                                                        | 10 088529<br>13 080601<br>13 090888<br>11 090881<br>5 09VLC5                                                   |
| 506<br>5115<br>506<br>506                                                                                    | 505<br>506<br>491                                                                             | 4 4 4 4 4 9 4 9 4 9 4 9 4 9 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5                                         | 501<br>511<br>495<br>501<br>503                                                                           | 507<br>510<br>494<br>515<br>518                                                                           | 511<br>518<br>519<br>520                                                                                       |
| 66<br>66<br>66<br>66<br>66<br>66<br>66<br>86                                                                 | 65.7<br>65.7<br>67.6<br>67.6                                                                  | കയയും<br>ഒയയും<br>ഉയയും<br>ഉയയും<br>ഉയ                                                                    | 37.8<br>37.7<br>36.9<br>36.4                                                                              | 36.3<br>25.0<br>35.7<br>7.5                                                                               | 35.7<br>35.6<br>35.6                                                                                           |
| 1789<br>1781<br>1780, 5<br>1774<br>1772                                                                      | 1756<br>1755<br>1754<br>1257.5                                                                | 1085.5<br>1052<br>1038<br>1032<br>1032                                                                    | 1010<br>1008.5<br>986<br>972                                                                              | 969.5<br>453.5<br>954.5<br>954.5                                                                          | 25<br>25<br>25<br>25<br>25<br>25<br>26<br>26<br>26<br>26<br>26<br>26<br>26<br>26<br>26<br>26<br>26<br>26<br>26 |
| 17<br>18<br>14<br>20<br>21                                                                                   | 2.44<br>2.44<br>2.44                                                                          | 4 17 8 17 3<br>4 17 8 17 3                                                                                | вопек<br>Помеже                                                                                           | 88 8 8 9 0 1 4 4 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9                                                        | 1 4 4 4 4<br>1 4 6 4 4 5                                                                                       |

#### ALIGNMENTS

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SERVINGOLS FROM N.A.
STRAIN COLSTITY / FIND 0509952;
MEDLINE-21156231; PubMed=11258736;
Hayashi T., Makiso K., Chhishi W., Minita T., Tanaka M., Tehe T.,
Han C. G., Chishe E., Nakayama K., Minita T., Tanaka M., Tehe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kibara S., Shiha T., Hatteri M., Shinagawa H.,
Complete genome sequence of enterchemorrhagic Escherichia coli
O157.H7 and genome comparison with a laboratory strain K-12.";
DNA PAS B:11-22(2001).
ENBL, ARO05585, ABS37887.1;
InterPro; IPPUGLOSS ABS37887.1;
InterPro; IPPUGLOSS ABS37887.1;
  STRAIN-0157-H7 / EDL933 / ATCC 700927;
BEDLINE-21074935; PUDMEd-11206551;
Perna NT., Plunkett G. III, Burland V., Mau B., Glasner J.D., Pose D J, Mayhew G F, Evans P.S., Gregor J., Kirkpatrick H.A., Pose D J, Mayhew G F, Evans P.S., Gregor J., Kirkpatrick H.A., Grospeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., "Genome sequence of enterphase of sequence sequence of sequence sequence of sequence of sequence of sequence sequence of sequence of sequence sequence of sequence of sequence sequence of sequence sequence of sequence sequence of sequence sequence of sequence se
  Bacteria; Frotecbacteria, gamma subdivision, Enterobacteriaceae,
Escherichia.
  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Aldehyde dehydrogenase B (lactaldehyde dehydrogenase).
ALDE OR FRING OF FIZA454.
Escherichia coli 0157:H7.
   542 AA.
   PRT;
   PRELIMINARY;
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  NCB1_TaxID=83334;
   Q8XDJ1
RESULT 1
  08xDJ1
  COCCONNER REPARENTANT SEED DAGE OF COCCONNER REPARENT SEED OF COCCONNER REP
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121 AADVPLAIDHFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWK 180
   361 YIDIGKKEGADVLTGGRRKLLEGELKFGYYLEPTILEGGNNMRVFQHETFGPVLAVTTFK 420
  391 YIDIGKKEGADVLTGGRRKLLEGELKDGYYLEPTILFGONNMRVFQEEIFGPVLAVTTFK 450
  421 TMEEALELANDTOYGLGAGVWSRNGNLAYKMGRGIQAGKVWINCYHAYPAHAAFGGYKŲS 480
   KRDIDLALDAAHKVKDKWAHTSVQDRAAILFKIADRMEGNLELLATAETWDNGKPIPETS 120
  MAPALAAGNCVVLKPARLTPLSVLLJJMEIVGDLJPPGVVNVVNGAGGVIGEYIJATSKRIA 240
  KVAFTGSTEVGQQIMQYATQNIIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFA 300
   1 MTNNPPSAQ1KPGEYGFPLKLKARYDNFIGGEWVAPADGEYYQNLTPVTGQ1LCEVASSG 60
  31 MINNPPSAQIKPGEYGFPLKLKNRYDNFIGGEWVAPALGEYYQNLIPVIGULLCEVASSG 90
  STRAIN=LT2 / SGSC1412 / ATCC 700720, MEDLINE=21534948: PubMed=11677609; MCDLINE=21534948: PubMed=11677609; MCCLelland M., Sandedrson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
   Gaps
   "Complete genome sequence of Salmonella enterica serovar Typhimurium
  Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
   0
  99.2%; Score 2651; DB 16; Length 542; 99.2%; Pred. No. 1.4e-198; Live 0; Mismatches 4; Indels 0
   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M Waterston R., Wilson R.K.;
  01-MAP-2802 (TrEMBLIcel. 20, Greated)
01-MAP-2802 (TrEMBLIcel. 20, Last sequence update)
01-MAP-2802 (TrEMBLIcel. 20, Last annotation update)
01-MAP-2802 (TREMBLICE) 21, Last annotation update)
Aldehyde dehydrogenase R (lacraldehyde dehydrogenase) (EC
   542 AA; 59768 MW; FAU87A4BEE902A70 CRC64;
PIAM; PF00171; aldedh; 1.
PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
  481 GIGPETHKMMLEHYQQTKCLLVSYSDKPLGLF 512
  511 GIGRETHKMMLEHYQQTKCLLVSYSDKPLGLF 542
  PRT;
  508; Conservative
   Nature 413:852 856(2001).
   PRELIMINARY;
  Query Match
Best Local Similarity
  Complete proteome.
SEQUENCE 542 AA;
   SEQUENCE FROM N.A
   ALDB OR STM3680.
   NCBI_TaxID=602;
  Salmonella.
  181
  Q8ZL72
  Matches
   RESULT 2
   Q8ZL72
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   121 AADVPLAIDHFRYFASC1RAQEGGISEVDSETVAYHFHEPLGVVGQ11FWNFPLLMASWK 1R0
  181 MAPALAAGUÇVVLKPAPLITPI SVLJLIMFI LGDIJ PPRIVVNGAGGFLGPYLATSKRTA 240
  301 FNGGEVCTCPSPALVQESTYEFFMERATRRVESTRSGNPLDSVTQMGAQVSHQLFTTLN 460
  361 YIDIGKKECADVLTGGRRKLIJEGELKDGYYLEPTILFGQNNMRVFQEETFGPVLAVTTFK 420
   421 TMEEALELANDTGYGLGAGVWSENGNLAYKMGRGLGAGRVWTNCYHAYPAHAAFOGYKOS 480
  61 KPDIDLALDAAHKVKDKWAHTSVQDRAATLFKTADPMFQNIFTLATAFTWDNGKPTRETS 120
  35.1. YIDIGKKEGADILIGGKRKELDGELKEGYYLEFT ILEGKNNMKVEQEELEGFULAVITEK 4.20
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  3
  MEDLINE-2154947; PubMed-11677608; Merchill J., Pongat G., James K.D., Thomson N.P., Fickard D., Main J., Charcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Schaihia M., Raker S., Rasham D., Brooks K., Chillingworth T., Connection P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrat J., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrat J., Krogh A., Hien T., Load Her S., Moule S., O'Gaora P., Jaqels K., Graffi M., Futherford K., Simmonds M., Skelton I., Stooms F.,
   241 KVAFTGSTEVGQOIMOYATQN11PVTLELGGKSPN1VFADVMDEEDAFFDKALEGFALFA
   1 MINNPPSAQIKPGEYGEPLKLKARYDNETGGEWVAPAKKEYYQNLTPVTGQLLCEVASSG
   MAPALAAGNCVVLKPARLTPLSVLLLMETVGDLLPPGVVNVVNGAGGVTGEYLATSKRTA
  Bacteria, Proteobacteria, gamma subdivis.on, Enterobacteriaceae,
  ;;
;;
   Length 512;
  7; Indels
   770D89E35EC587DA CRC64;
   01-MAR 2302 (TrEMBLiel. 20, Created)
01-MAR-2302 (TrEMBLiel. 20, Last sequence update)
01-30N-2002 (TrEMBLiel. 21, Last annotation update)
   PROSITE; PSO0070; ALDEHYDE_DEHYDK_CYS; UNKNOWN_I.
PROSITE; PSO0687; ALDEHYDE_DEHYDK_GIU; I.
OXIGOTEGIASE; COMPLETE PFOLEOME: T.
SEQUENCE 512 AA; 56326 MW; 770089E35E75R7DA C
   Score 2601, DB 16;
Pred, No. 1.1e 194;
   481 GIGRETHKMMLEHYQQTKCLLVSYSDKPLGLF 512
  11; Mismatches
  Aldehyde dehydrogenase B (EC 1.2.1.22).
EMBL; AE008870; AAL22539.1; ·.
InterPro; IPR002086; Aldehyde_dehydr.
Pfam; PF00171; aldedh; 1.
  97.4%;
  96.5%;
  Matches 494; Conservative
   PRELIMINARY;
   Query Match
Best Local Similarity
  SEQUENCE FROM N.A.
   Salmonella typhi.
  NCBI_TaxID=601;
   STRAIN-CT18;
   Salmonella.
   181
   STY4116
   RESULT 3
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   421 TMEEALELANDIQYGLGAGVWSRNGNLAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKQS 480
   61 KRDIDLALDAAHKVKDKWAHTSVQDRAAILFKIADRMEQNLELLATAETWDNGKPIRETS 120
  121 AADVELAIDHERYFASCIRAQEGGISEVUSETVAYHFHEPLGVVGOIIPWNFPLLMASWK 180
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  361 YIDIGKKEGADVLIGGPPKLLFGELKPGYLEPITLFGONNMRVFQEELFGDVLAVITFK 420
  1 MINNPPSAQIKPGEYGFPLKLKARYDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSG 60
  1 MINNPPSTRIQPSEYGYPLKLKARYDNFIGGDWVAPADGEYYQNLTPVTGQPLCEVASSG 60
   Gaps
  Capela D., Rarloy Hubler F., Gonzy T., Rothe G., Ampe F., Batut J.,
Bolstard D., Recker A., Routry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
                             "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.", Nature 413:848-852(2001).
   Bacteria; Proteobacteria; alpha subdivision; Khizobiaceae group;
Rhicobiaceae, Sinothicobium.
   .;
  96.9%; Score 2589; DB 16; Length 512;
   Indels
  56355 MW; A64CD3COFA7E394D CRC64;
   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel 19, Last sequence update)
01-JUN-2002 (TrEMBLrel 21, Last admination, pdate)
01-JUN-2002 (TrEMBLrel 21, Last admination, parabale aldehyde dehydrogenase protein (ET 1-2 1).)
  Pfam: PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU, 1.
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   9.2e-194;
   # GIGRETHKMMLEHYQQTKCLLVSYSDKPLGLF 512
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Matches 490; Conservative 14; Mismatches
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   STRAIN=1021:
  361
  SEQUENCE
   Query Match
   Q92N70
   RESULT 4
  Q92N70
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82 SVQDRAATLFKIAD#MEGNLFLLATAETWINGKPIRETSAADVPLAIDHFKYFASCIRAG 141
   72 STTERSNILMKTAARMEDNLELLAPARTWPWGKPTPFTMARD1P1ATDHFFYFAAC1FAQ 131
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  202 SVLLLMEIVGDLLPPGVVNVVNGAGGVIGRYLATSKRIAKVAFTGSTEVGQQIMQYATON 261
  252 LIPVTLELGGKSPNIFFADVASEDDDFFDKALEGFAMFALNQGEVCTCPSRALVQESIYD 311
  322 REMERAIRPVESIPSGNPLDSVTQMGAQVSHGQLETI1.NYIDIGKKEGADVLTGGRPKLL 381
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   442 SKNONLAYKMSRSIQAGRVWINCYBAYPAHAARGGYKQSSIGRFIHKMMJFHYQQIKGIL 501
  192 SILVWAELIGDLLPPGVLNIVNGFĞLEAGKPLATSPRIAKIAFTGETTTGRLIMQYASON 251
   262 IIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVCTCPSRALVQESIYE 321
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  22 KARYDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLALDAAHKVKDKWAHT
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  , Nelson K E
  STRAIN-ATCC 19089 / CB15; MEDLLNE-21173698; PubMcd-11259647; Nelson K Nierman W O'. Belddyum T V Laub M T , Paulsen I.T , Nelson K Eisen J., Heidelberg I.F., Alley M.P.K., Ohta N., Maddock J.R.,
  0,
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group,
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  17, Tast sequence update)
20, Last annotation update)
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PMOSI1E; PS00070; ALDEHYDE_GEHYDE_CYS; UNKNOMN_1.
PMOSITE; PS00687; ALDEHYDE_FFHYDE_GIU; UNKNOMN_1.
  79,
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51, Mismatches
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Matches 361, Conservative 5
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   502 VSYSDKPLGLF 512
   492 VSYSPKALGFF 502
  PRELIMINARY,
   (TrEMELrel
  01-MMN-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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  Q9A211
Q9A211;
  RESULT 5
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   82 SVQDRAAILFKIADRMEQNLELLATAETWDNGKPIRETSAADVPLAIDHFRYFASCIRAQ 141
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   376 PGQLADGYYVEPTVFEGHNKMRIFQEEIFGPVLAVTTFKTEEEALEIANDTAFGLGAGVW 435
   22 KARYDNFIGGEWVAPADGEYYQNLIPVTGQLLCEVASSGKRDIDLALDAAHKVKDKWAHT 81
  16 KARYDNFIGGGWVAPADGRYFDNSSPIHGKKICEIARSQAIDIERALDAAHAAKAGWART 75
  SRNGNLAYKMGRG1QAGRVWTNCYHAYPAHAAFGGYKQSGIGRETHKMMLEHYQQTKCLL.
Potocka I., Nelson W.C., Newton A., Stephens C., Phadko N.D., Riy R., DeBONY R., Pordson P. I., Purkin A.S., Gwinn M.L., Haft D.H., Kolongy R., Smit J., Craven M. B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Well A., Vamathevan T., Frmolaeva M., White O., Salzberg S., Venter J. Shapiro L., Fraser C.M.:
"Complete genome sequence of Caulobacter researchs.";
Proc. Natl., Acad. Sci. U.S.A. 98:4136-4141(2001).
  Gaps
   Bacteria, Frote-obacteria, alpha subdivision; khizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID-381;
  ò
  Length 506;
  Indels
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   01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel 21, Last annotation update)
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71.7%; Pred. No. 2.4e-141;
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Rhizobium loti (Mescrhizobium loti).
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01-OCT-2001 (TrEMBLrel. 18,
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Best Local Similarity 71.74
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   502 VSYSDKPLGLF 512
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  proteome
   SEQUENCE FROM N.A.
   CC3580;
   SEQUENCE
   Complete
  908860
  HSSP;
  TIGR;
   RESULT 6
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132 RYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAFALAAGNCV 191
  ÷0.4
   464
  4.5]
  72 HKVKDKWAHTSVQDRAAII,FKIADKMEONIELI,ATAETWDNGKPIRETSAADVPIAIDHF 141
  125 PYPASAVEGGESLSQ110PTVAYHEHEPLGVVGQ11PWNFPLLMACWKLAPALAAGNCV 1B4
   252 QCIMQYATQNIIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALEAFNQGEVCTOPS (11
   312 PALVQESIYERFMEPATRPVFSTPSGNPLDSVTGMCAGVSHGGLFTTLNYTD1GKKFGAD 371
   7.
   7.
   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Suqimoto M.,
Takouchi C., Yamada M., Tabata S.;
"Gomplete genome thrusture of the ultregen fixing symbiotic bacterium
Mesochizobium Lot.";
  14 EYGEPEK - - EKARYDNF I GGEWVAPADGEYYONLTPVTGOLLCEVASSGKRD I DLALDAA
   5 EFSRPVKAPFDKRYGNFIGGKWTEPRSGRYFENHSPVNGQLLCEVARSDADDIEAALDAA
  192 VERPARLIPLSVILLMETVEHERVOURPANOVNER STEVENERE ATSEKTAR VAN DESTEVO
   432 TQYGLGAGVWSRNGNLAYKMGRG1QAGRVWTN/YHAYPAHAAFGGYKGSG1GRETHKMML
  305 PALTHESTYDPEMERALK PVEATVOODPLDPATMICAGASSEGLEKTLSYTDICKQEGAF
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   Agrobacterium tumefaciens (strain (58 / ATCC 1970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae qroup;
Rhizobiaceae; Rhizobium.
STRAIN-MAFFTO1099;
MEDLINE-2108290; PubMed 11214968;
RAIN-2108290; PubMed 11214968;
RAIN-2108290; PubMed 11214968;
RAIN-2108290; PubMed 112, Sato I., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kiwashima K., Kimura T., Watanabe A., Kiyokawa C., Koluda M., Matsumoto M., Matsumo A., Kishida Y., Kiyokawa C., Koluda M., Matsumoto M., Matsumoto M., Matsumoto M., Makayama S., Nakazaki N., Shimpo S., Sudimoto M.
  7
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  01-JUN-2002 (TrEMBLrel, 21, Last sequence update)
01-JUN-2002 (TrEMBLrel, 21, Last annotation update)
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  Pfam; FF00171; aldedh; 1. PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
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   54C AA
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   01-JUN-2002 (TrEMBLrel: 21, Created)
   PRT;
  492 EHYQQTKCLLVSYSDKPLGLF 512
   485 DHYQQTKNMLVSYSPKKLGPF 505
  ALDA ÓR ATUZZZ4 ÓR AGR_C_4041.
  DNA Res. 7:331-338(2000).
EMBL; AP003009; BAB52891.1;
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   NCBI_TaxID:176299;
   152;
  SEQUENCE
  Query Match
  Complete
   Q8UDA3;
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  Matches
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   217 NOVVERPARQIPASILIVMELIRDILIPROVENEVAGGGRAGERIAQSNRIAKIARIQST 276
  309 CPSRALVQESIYERFMERATRRVESTRSGNPLDSVTOMGAQVSHGQLETILNYIDIGKKE 368
  997 GAKVLTGGDPKTLTGDLKDGYYLQPTVPEGNNKMPLFQEELFGPVVSVTTFKTVEEALEL 456
   429 ANDIQYGLGAGVWSKNGNLAYKMGKGIQAGKVWTNQYHAYPAHAAFGGYKQSGIGRETHK 488
   69 DAAHKVKDKWAHTSVQDPAAILFKIADRMEQNLELLATAETWDNGKPIPETSAADVPLAI 128
  97 DAAHKAREKWGKTSTTERSNILLRIAQRIEDNI,DIJARAETWDNGKPI,RETTNADIPLTI 156
   129 DHFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAG 188
  189 NOVVERPARLIPLSVLLLMETVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGST 248
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   337 CPSRALVHESIYDRFMEKAIKRVQAISQDDPLNPSTMLGAQASQEQFDKIMSYLEIGKKE 396
   369 GATVILIGGFRKLLBGELKIKTYYLEFFILFGDNNMPVFQERIFGPVLAVTTFKTMEEALEL 428
   9 QIKPGEYGEPLKLKARYDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDLAL 68
   41 QQKAGEAPFKLK----YGNYIGGKWVEPKSGPYMNNISPVTCHKITFVPPSDASDIEFAI, 96
  "The genome of the natural genetic engineer Agrobacterium tumefaciens {\sf C58."}:
   SEQUENCE FROM N.A.
MEDLINE-2160854; PubMcd-11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B. C. Faro Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Tartchouk D., Epp A., Liu F.,
Wollam C., Alingel M., Doughty D., Scott C., Lappas C., Markelz B.,
Elanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
   Gaps
            MEDLINF-2169856, pubMed=11743193;
Mood D.W., Serutal T.C., Kaul P., Monks D.E., Kitajima T.P.,
Gutra V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Kahmeida N.F., Jr., Woo L.,
Chapman P., Clendenning J., Leatherage G., Gillet W., Grant C.,
Rutyavin T., Lovy P., Li M.-J., McClelland E., Falmnori A.,
Raymond C., Konse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.
Zhang S., Yoo H., Fild M.-J., Jung M., Krespan W., Perry M.,
Cordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.
   4
   "Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens CSB.";
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  84,
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   517 MMLDHYQQTKNLLVSYSPNKVGFF 540
   Science 244.2424.2328(2001)
EMBL: AE009172: AAL43213.1; ALT_INIT.
EMBL: AE008138; AAK87966 1;
  489 MMLEHYQQTKCLLVSYSDKPLGLF 512
   Science 294:2317-2323(2001).
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SEQUENCE FROM N.A.
   Complete proteome.
  Nester E.W.,
  SEQUENCE
   Query Match
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56 DIEKALDAAHAAKDAWGKTSAAVKALILINKJADRMEENLDILALAEAETWDNGKPIRETTAA 115
   235
  303
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  236 AFTGETTTGRLIMQYASQNLIPVTLELGGKSPNIFFADVVAEDDDFFDKAVFGFVMFALN 295
   296 OGEVCTOPSPALIOESIYDPFMEKALKPVAAIVOGSPLDPATMIGAQASSEQLEKILSYI 355
  363 HIRKERADULDSGERKLLEGELKEGYIEPTILFGGNNMRVFQEEIFGFVLAVITFKIM 422
  356 DIGKQEGAEVLIGGEPNIFGGDLAGGYYVKPTVFKGHNKMRIFQEFIFGPVVSVTTFTDD 415
   423 FEALELANDTOYGLGAGVWSRNGNLAYKMGRGTQAGRVWTNCYHAYPAHAAFGGYKQSGT 482
   3 NNPPSAGIIKPGEYGFPLKLKARYDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKF 62
   2 NKPETATTKQSPF-----KAPYGNFIGGKFVEPVGGPYFDNTSPVTGGKIGETARSDAD 55
  STRAIN=GJ10;
MEDLINE-98172729; PubMed-9511738;
Pergeron H., Labbe P., Turmel C., Lau P.C.;
Pergeron H., Labbe D., Turmel C., Lau P.C.;
"Cloning, sequence and extrussion of a linear plasmid based and a chromosomal homolog of chloroacetaldehyde dehydrogenase-encoding genes
  176 PALAAGNCVVLKPAEQTPASILVLAELIADLLPPGVLNIVNGFGLEAGKPLASSSRIAKI
   303 GSEVCTOPSRALVQESIYERFMERATRRVESTRSGNPLDSVTQMGAQVSHGQLETILNYI
   6; Gaps
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Hyphomicrobium group; Manthobacter.
  -i- SIMILAKITY: BELLANGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
FMHL, AFD29733, AAC13641.1; -.
HSSP, POS091; LCW3.
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  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
  Pfam; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
  Best Local Similarity 69.2%; Fred. No. 2.7e
Matches 353; Conservative 58; Mismatches
   483 GPETHKMMLEHYQQTKCLLVSYSDKPLGLF 512
   476 GRENHKMMLDHYQQTKNMLVSYSPKKLGFF 505
  in Xanthobacter autotrophicus GJ10.";
Gene 207:9-18(1998).
   TPP002086; Aldehyde_dehydr
   PPT:
   ol-MAR-2002 (TrEMBLrel, 20, Last
Chloroacetaldehyde dehydrogenase
  Plasmid linear plasmid pXAU1.
  Xanthobarter autotrophirus
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  251 GQQIMQYATQNIIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVCTCP
   Gaps
  "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Pes 28-4317-433(2000).
   STRAIN-C-125 / JCM 9153;
MEDLINE-2051.28E1; PubMed 11058132,
Takami H., Nakasone K., Takaki Y., Macno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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   Bacillus halodurans.
Bacteria; Firmicutes, Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
   70.3%; Score 1878; DB 16; Length 506; 68.9%; Pred. No. 3.3e-138;
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19, Last annotation update)
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PROSITE: PS00070; ALDEHYDE_DEHYDE_CYS; UNKNOWN_1.
PROSITE: PS00687; ALDEHYDE_DEHYDE_GLU: 1.
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                                 PRT;
   491 LEHYQQTKCLLVSYSDKPLGLF 512
   485 LSHYOQTKNLLVSYSEDALGFF 506
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  346; Conservative
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   Best Local Similarity
   P05091; ICW3
   SEQUENCE FROM N.A.
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  NCBI_TaxID*86665;
  ALDA OR BH0681
  01 - OCT - 2000
  01-DEC-2001
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  Query Match
  Q9KF16;
                               Q9KF16
   HSSP:
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                  09KF16
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  73 GPTSVAERARLINKTADPMEEKLDLLAMVETTINGKPTRETKAADLPLATOHFPFFASCV 132
  <u>~</u>
  253 SENLIPPTLELGGKSPNIPHEDVAAEDDDPFDKAIEGEVLFALNQGEVCTCPSRAITHEK 412
  79 AHISVQDRAAILEKIADKMEQNEELLATAETWDNGKPIRETSAADVELAIDHERFEASCI 138
  139 RAQEGGISEVDSETVAYHFHEPLGVVGGIIPWNFPLLMASWKMAPALAAGN/VVLKFARL 198
  319 TYEKFMEKATRKVESTRSGNPTDSVTÇMGAÇVSHÖÇLETTÜNYTDTÖKKFGADVLTGORR (78
  379 KILEGELKDGYYLEPTILEGGNNMEVFQEETFEFPLAVTTEKTMEEALELANDLOYGLAA 438
  439 GVWSPNGNI,AYYKMGPGTQAGPVWTNCYHAYPAGAAFGSGYRGPFTHYMMI FHYGGTK 459
  7 8
  13 IAFRSRYDNFIGGKWVAPVRGQYFDNITPITGMPVAQIARSTAEDIELALDAAHAAKDAW 72
  259 FONT IPVIEEGGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNOGSEV TOPSKALVOES
  19 LIKEKARYDNF1GGEWVAPADGERYQNLTPVTGQLLCEVASSGKRU1DLALDAAHKVKDKW
  313 IYDKEMERALARVAAIKQGSPIJEAATMIGAQASNIQIJEKILISYIDIGKABGAELLIGGER
  Okibe N. Amada K. Haruki M. Imanaka T. Morikawa M. Kanaya S.; "Gene cloning and characterization of aldehyde dehydrogenase from a petroleum degrading bacterium strain HD-1."; Submitted (PEB-1999) to the EMBL/Genkank/DBMJ databases. -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY. BENBL; AND2.840; BAA75508.1; ·. HSSP; P05091; ICW3.
   Sdpp
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  Length 506;
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   596 AA; 55582 MW; 13FC7781D0F1C6B9 CRC64;
   01-MAY-1999 (TrEMBLiel, 10, Created)
01-MAY-1999 (TrEMBLiel, 10, Last sequence update)
01-MAR-2002 (TrEMBLiel, 20, Last annotation update)
  PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOMN_1.
PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
   # Match 70.0%; Score 1870; DH 2; Local Similarity 69.0%; Pred. No. 1.40 187;
  œ
                        506 AA
  Bacteria, Proteobacteria, alpha subdivision
  68; Mismatches
  InterPro; 1PR002086; Aldehyde, dehydr.
  petroleum-degrading bacterium HD-1.
   499 CLLVSYSDKPLGLF 512
  Conservative
                        PRELIMINARY;
   Aldehyde dehydrogenase.
  Pfam; PF00171; aldedh;
  SEQUENCE FROM N.A.
  NCBI_TaxID=89018;
   Oxidoreductase.
  341;
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   HD-ALD.
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  64 AAHKAKKEWNKSSPTTRSNLLLKIADRMEANLEMLAVAETWDNGKPVRETLAADIPLAID 123
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   70 AAHKVKDKWAHTSVQDRAAILFKIADRMEQNLELLATAETWDNGKPTRETSAADVPLAID 129
  130 HFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALAAGN 189
   190 CVVLKFAFLTPLSVLLEMEIVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTE 249
  250 VGQQIMQYATQNITEVTLELAGKSENIVFADVMDEEDAFFDKALEGFALFAFNQGEVÇTÇ AU9
  370 ADVLTGGRRKLLEGELKDGYYLEPTILFGQNNMRVFQEEIFGPVLAVTTFKTMEEALELA 429
  364 AEVLLGGHGR---QEVGNGYYIEPTIFKGHNNMQVFQEEIFGPVLSVTTFKDFDFAIQIA 420
  430 NDTQYGLGAGVWSRNGNLAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKQSGIGRETHKM 489
  10 IKPGEYGFPLKLKARYDNFIGGEWVAPADGEYYÖNL1FVTGQLLCEVASSGKKUIDLALD 69
   4 VDPNQSGSKIHFKDQYENFIGGQWVAPVKGVYFDNISPVDGKSFTRIPRSSARDIELALD 63
  utilization and wax ester synthesis in Acinetobacter sp. strain M-1.";
Appl Environ Microbiol. 66.3481-3486(2000)
-!- SIMILMARITY: BELCNGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
EMBL, AB042203: BAB11888.1;
-.
HSSP; P05091; 1CW3.
  310 PSRALVQESIYERFMERATRRVESIRSGNPLESVTÖMGAÐVSHGÓLETTLNYTEFGKKEG
   ishige T., Tani A., Sakai Y., Kato N.;
"Long-chain aldehyde dehydrogenase that participates in n-alkane
  DB 2, Length 503,
   Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
   503 AA; 55499 MW; 3254DBACCC65F246 CRC64;
                     01-WAR-2001 (TrEMBLrel, 16, Created)
01-WAR-2001 (TrEMBLrel, 16, inst sequence update)
01-JUN-2002 (TrEMBLrel, 21, Last annotation update)
   Pfam; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_5LU; 1.
  .06
   69.2%; Score 1850.5, PB 2, 67.6%; Pred. No. 4.5e-136; Live 70; Mismatches 90;
 503 AA
  InterPro; IPP002086: Aldehyde_dehydr.
   490 MIRHYQQTKÇLIVSYSDKPLGLF 512
   MLDHYQQTKNLLVSYSTKAMGFF 503
  PRT;
   MEDLINE=20378657; PubMed=10919810;
  340; Conservative
   Aldehyde dehydrogenase 1.
 PRELIMINARY;
  Local Similarity
  NCBI_TaxID=123502;
  SEQUENCE FROM N.A.
   Acinetobacter sp
   Oxidoreductase.
SEQUENCE 503
  Acinetobacter
  STRAIN=M-1
   481
   Query Match
Q9FDS1
  Matches
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  354 SYIDIGRAEGAQVLAGGERNVLTGELADGFYVKPTVFLGKNNMRIFQEEIFGPVVSVTTF 413
   6.0 GKEDTITLALDAAHKVKDKWAHTSVQDFAATLFKTADMEGNIELLATAETWONGKPTPFT 119
  180 KMAPALAAGNIVVIJKHARIJHH,SVELEMETVGOJJHPGVVNVVNGAGGVIGEYEATSKRI 239
  300 APNQGEVCTOPSPALVQESTYEFPMEPATPPVESTPSONPLOSVTQMGAQVSHGQLETIL 359
   294 ALNQGEVCTCPSKALVQESIFDKFMEKALAKVAAIKQGSPLDPSIMIGAQASSEQMHKIL 353
   NYIDIGKKEGADVLTGGRRKLLEGELKDGYYLEPTILFGQNNMRVFQEEIFGPVLAVTTF 419
  4.20 KTMEEALELANFILIYGLGARIVWSPNINLAYKMIRITQAGRVWTNIYHAYBAHAAFIG 479
   120 SAADVPLA1DHERYFASC1KAQEGGISEVDSETVAYHEHEPLGVVGQ11PWNFPLLMASW 179
  3 NNP---PSAQIKPGEYGFPLKLKARYDNFIGGEWVAPADGEYYQNLTPVIGQLLCEVASS 59
   2 NSPAFIJSSAHTSP-----FKPPYGNFIGGTFVEPVSGPYFENTSPITGKVIGEVPPS 53
  Bergeron H., Labbe D., Turmel C., Lau P.C.; "Cloning, sequence and expression of a linear plasmid-based and a chromosomal homolog of chloroacetaldehyde dehydrogenase-encoding genes
   174 KLAPALGAGNCVVLKPAFOTPASILVLAELIAMLDPPGVLNIVNGFGLFAGKPLASSPRI
  240 AKVAPTGSTEVGQQIMQYATQNIIPVILELGGKSPNIVFADVMDEEDAFFDKALEGFALF
   Bacteria, Proteobacteria, alpha subdivision, Phicobiaceae group,
  DR 2, Longth 506;
   Indels
  506 AA; 54885 MW; C92B41F49C38AAB7 CRC64;
01-JUN-1998 (TrEMBLrel. 05, Created)
01-JUN-1998 (TrEMBLrel. 05, Last Sequence update)
01-MAR-1998 (TrEMBLrel., 0, Last annotation update)
NAD-dependent chloroacetaldehyde dehydrogenase
   Pfam; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
PROSITE; PS00687; ALDEHYDE_DFHYDP_GLU; 1
  ; Pred. No. 4.6e-136; 71, Mismatches 90,
   480 SGIGRETHKMMLEHYQQTK711.VSYSDKFLGLF 512
   69.78, Sporter 1850 F,
65.5%; Pred. No. 4.56
   TPF007086, Aldebyde_debydr.
   Hyphomicrobium group; Xanthobacter.
  MEDLINE=98172729; PubMed=9511738;
   Xanthobacter autotrophicus.
   Matches 341, Conservative
   Hest Local Similarity
   SEQUENCE FROM N.A.
   NCBI_Tax1D=280;
  Oxidoreductase.
   InterPro,
  SEQUENCE
   Suery Match
   RESULT 13
  Q8YEY0
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505 AA.

PRT;

PRELIMINARY:

OBYEYO

506 AA.

PRT;

PRELIMINARY;

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60 ALDAAHAARELWGRTSVAERALILNRIADRIEENLPALAAAAETWDNGKPIRETTNADLPL 119
   67 ALDAAHKVKDKWAHTSVQDRAAILFKIADRMEQNLELLATAETWDNGKPIRETSAADVPL 126
  127 AIDHFRYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQIIPWNFPLLMASWKMAPALA 186
   247 STEVGQQIMQYATQNIIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEV 306
  307 CTCPSRALVQESIYERFMERAIRRVESIRSGNPLDSVTQMGAQVSHGQLETILNYIDIGK 366
   300 CICPSRALIQESIYDRFMEKALKRVEAIVQGDPLDPATMIGAQASSEQLEKILSYLDIGR 359
  367 KEGADVIJTGGRRKLLEGELKEGYYLEPTILFGQNNMKVFQEEIFGPVLAVTJPKIMEEAL 426
   427 ELANDTQYGLGAGVWSRNGNLAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKQSGIGRET 486
  7 SAQIKPGEYGFPLKLKARYDNFIGGEWVAPADGEYYQNLTPVTGQLLCEVASSGKRDIDL 66
  DelVecchio V.G., Kapatral V., Pedkar R.T., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn K., Kyrphides N., Overbeek R.; "The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
   187 AGNCVVLKPARLTPLSVLLLMEIVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTG
   240 ETTTGRLIMQYASQNLIPVTLELGGRSPNIFFKDVAAEDDDFLDKAIEGFVMFALNQGEV
  Gaps
   Bacteria; Proteubacteria, alpha subdivision; Khizubiaceae group;
  7,
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  93, Indels
  2E57ACC86ED187BD CRC64;
                            01-MAR-2002 (TrEMBLrel, 20, Created)
01-MAR-2002 (TrEMBLrel, 20, Last sequence update)
01-JUN-2002 (TrEMBLrel, 21, Last annotation update)
   Query Match
Best Local Similarity 67 4%; Pred. No. 6 5e-136;
  PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
  Proc. Natl. Acad Sci U.S.A. 99:443-448(2002).
EMBL: AE009608; AAL52928.1;
  65; Mismatches
  487 HKMMLEHYQQTKCLLVSYSDKPLGLF 512
   InterPro, IPR002086; Aldehyde_dehydi.
   SEQUENCE FROM N.A.
STRAIN=16M / ATCC 23456 / BIOTYPE 1;
MEDLINE=20020109; Pubmed-11756688;
  Aldehyde dehydrogenase (EC 1.2.1.3).
   Oxidoreductase; Complete proteome
SEQUENCE 505 AA; 55313 MW; 2E
   Matches 341; Conservative
  Brucellaceae; Brucella.
   Pfam; PF00171; aldedh;
   Brucella melitensis
  NCBI_TaxID=29459;
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   72 HKVKDKWAHTSVQDRAAILFKIADRMEQNLELLATAEFWDNGKPIRETSAADVPLAIDHF 131
  132 RYFASCIRAQEGGISEVDSETVAYHFHEPLGVVGQI1PWNFPLLMASWKMAPALAAGN/V 191
   3.1.2. PALVĢESTYEPFMEPATPRVESTRSONICLISVIÇMOAQVŞHOQLICTILINYTD GAKKBOAD (3.1.)
  372 VLTGGREKLLEGELKIKGYYLEPTILFGQNNMRVFQEELFGPVLAVTTFKTMEFALELAND 431
   12 PGEYGFPLKLKARYDNF1GGEWVAPADGEYYQNIJTPVTGQIJICEVASSGKRDIDI,ALDAA 71
   6 PGSEGAIVSFKARYGNYIGGEFVPPVKGQYFTNTSPVNGQPIAEFPKSTAEDIDKALDAA 65
  192 VEKPAPLTPLSVELLIMETVGDELPPGVVNVVNGAGGVEGEVLATSKELAKVAFTGSTEVG
  186 VLKPAEQTPLGICVLLELIGDLLPPGVLNVVQGFGREAGFALATSKRIAKIAFTGSTPVG
  SIRAIN=AICC 15592 / PAO1;
MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoquchi S.D., Warrener P.,
Stover C.K., Pham X.-C.T., Erwin A.L., Mizoquchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hundaqle W.O., Kowelik D.J., Lagrou M.,
Garber R.L., Golftry L., Tolentino F., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Forger K.R., Kas A., Larbiq K., Lim K.M.,
Smith K.A., Spencer D.H., Wond G.K.-S., Wu Z., Paulsen LT.,
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
  252_QQIMQYATQNI IPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVCTCPS
   0; Gaps
   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadareae;
   67.4%; Score 1802; DB 16; Length 506; 67.1%; Pred. No. 2.8e 142;
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  506 AA; 54979 MW; 48E2E3295086E3004 CR064;
  16, Last sequence update)
19, Last annotation update)
   PROSITE; PSOU070; ALDEHYDE_DEHYDE_CYS; UNKNOMN_I. PROSITE; PSOU687; ALDEHYDE_DEHYDE_GLU; UNKNOMN_I.
   59; Mismatches 106;
  506 AA.
   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
   InterPro; IPE002086; Aldehyde_debydr.
  492 EHYQQTKCLLVSYSDKPLGLF 512
  486 DHYQQTKNLLVSYDINPLGFF 506
  Probable aldehyde dehydrogenase.
  EMBL; AE004819; AAG07409.1; -. HSSP; P05091; 1CW3.
   opportunistic pathogen.";
   336; Conservative
   PRELIMINARY;
  Nature 4118-454-464(2000)
   Pfam; PF00171; aldedh; 1
   Pseudomonas aeruginosa.
  Best Local Similarity
  SEQUENCE FROM N.A.
  Complete proteome.
  NCBI_TaxID=287;
   Pseudomonas
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   Query Match
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   Matches
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  71 AHKVKDKWAHTSVQDRAAILFKIADRMEQNLELLATAETWDNGKPIRETSAADVPLAIDH 130
  131 FRYFASCIRAGEGGISEVDSETVAYHFHEFLGVVGQIIPWNFPLLMASWKMAPALAAGNC 190
  191 VVLKPARLTPLSVLLLMETVGDLLPPGVVNVVNGAGGVIGEYLATSKRIAKVAFTGSTEV 250
  Z51 GQQIMQYATQNIIPVTLELGGKSPNIVFADVMDEEDAFFDKALEGFALFAFNQGEVCTCP 310
  311 SRALVQESIYERFMERAIRRVESIRSGNPLDSVTQMGAQVSHGQLETILNYIDIGKKEGA 370
   305 SRVLVHESIYDRFVAKVAERAKGIKOGNPLDTATQVGAQASQEQFUKILSYLDIGKQEGA 364
  371 DVIJIGGRRKIJEGELKESYYLEPTILFGUNNMKVFUEEIFGPVLAVTTFKTMEEALELAN 430
  431 DTQYGLGAGVWSRNGNLAYKMGRGIQAGRVWTNCYHAYPAHAAFGGYKQSGIGRETHKMM 490
  11 KPGEYGFPLKLKARYDNF1GGEWVAPADGEYYQNLTFVTGQLLCEVASSGKKDIDLALDA 70
  SEQUENCE FROM N.A.
STRAIN-EL TOR NI566 / SEKUTYPE UI;
MEDLINE-20406833; Pubmed-10952301;
MEDLINE-20406833; Pubmed-10952301;
Dodson R.J., Haft D.H., Hickoy E.K., Peterson J.D., Umayam I.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H. Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDondad L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell P.R., Mekalanos J.J., Venter J.C.,
  0; Gaps
   Bacteria, Protecbactelia, gamma subdivision, Viblionaceae, Vibrio.
  "DNA sequence of both chromosomes of the cholera pathogen Vibrio
  67 0%; Score 1791; PB 16: Length 506; 64.9%; Pied. No. 2e-131; ative 74, Mismatches 102, Indels 0.
  506 AA; 55308 MW; 21ECC981411C8663 CRC64;
  01-OCT-2000 (TrEMHLFel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
  PROSITE: PS00070; ALDEHYDE_DEHYDE_CYS; UNKNOWN_1.
PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
                                   506 AA
  InterPro; IPRAA2A86; Aldehyde_dehydr
  15, Created)
                                     PRT;
  EMBL; AE004258; AAF94967.1; -.
HSSP; P05091; 1CW3.
  326; Conservative
  Nature 406:477-483(2000).
                                 PRELIMINARY;
   01-OCT-2000 (TrEMRLrel
   Aldehyde dehydrogenase.
  Pfam; PF00171; aldedh;
  Local Similarity
  Complete proteome.
   Vibrio cholerae.
  NCBI_TaxID=666;
  VC1819;
  Fraser C.M.;
  SEQUENCE
  Query Match
   cholerae
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